
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:05:40 1999: MasPar time 4.00 Seconds

Tabular output not generated. 63.853 Million cell updates/sec

Title: >US-09-150-947-1

Description: (1-12) from US09150947.pap

Sequence: 1 TNKKKVTAGELD 12

Scoring table: PAM 150

Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 16.236; Variance 48.115; scale 0.337

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description | Pred. No. |
|------------|-------|--------------------|--------|-------------|---------------------------------|
| 1 | 74 | 100.0 | 12 34 | W64636 | Synthetic SEB peptide 1.06e-01 |
| 2 | 74 | 100.0 | 13 34 | W64640 | Synthetic SEB peptide 1.06e-01 |
| 3 | 74 | 100.0 | 239 3 | R13206 | Staphylococcal entero 1.06e-01 |
| 4 | 74 | 100.0 | 239 34 | W64647 | Synthetic SEB protein 1.06e-01 |
| 5 | 74 | 100.0 | 239 8 | R45014 | Staphylococcal entero 1.06e-01 |
| 6 | 74 | 100.0 | 255 20 | W06737 | Staphylococcal entero 1.06e-01 |
| 7 | 68 | 91.9 | 221 3 | R13209 | Staphylococcal entero 5.57e-01 |
| 8 | 68 | 91.9 | 221 8 | R45017 | Staphylococcal entero 5.57e-01 |
| 9 | 68 | 91.9 | 251 24 | W12145 | Streptococcus pyogenes 5.57e-01 |
| 10 | 68 | 91.9 | 251 24 | W12146 | Streptococcus pyogenes 5.57e-01 |
| 11 | 68 | 91.9 | 251 24 | W12153 | Streptococcus pyogenes 5.57e-01 |
| 12 | 68 | 91.9 | 251 24 | W12152 | Streptococcus pyogenes 5.57e-01 |
| 13 | 68 | 91.9 | 251 24 | W12152 | Streptococcus pyogenes 5.57e-01 |
| 14 | 68 | 91.9 | 251 24 | W12097 | Streptococcus pyogenes 5.57e-01 |
| 15 | 68 | 91.9 | 251 24 | W12147 | Streptococcus pyogenes 5.57e-01 |
| 16 | 68 | 91.9 | 251 24 | W12151 | Streptococcus pyogenes 5.57e-01 |

| Result ID | Score | Query Match Length | ID | Description | Pred. No. |
|-----------|-------|--------------------|--------|-------------|---------------------------------|
| 17 | 68 | 91.9 | 251 33 | W59781 | Amino acid sequence o 5.57e-01 |
| 18 | 68 | 91.9 | 251 33 | W59780 | Amino acid sequence o 5.57e-01 |
| 19 | 68 | 91.9 | 251 24 | W12150 | Streptococcus pyogenes 5.57e-01 |
| 20 | 68 | 91.9 | 251 24 | W12149 | Streptococcus pyogenes 5.57e-01 |
| 21 | 68 | 91.9 | 251 33 | W59798 | Amino acid sequence o 5.57e-01 |
| 22 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 23 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 24 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 25 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 26 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 27 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 28 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 29 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 30 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 31 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 32 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 33 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 34 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 35 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 36 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 37 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 38 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 39 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 40 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 41 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 42 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 43 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 44 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |
| 45 | 68 | 91.9 | 251 24 | W12148 | Streptococcus pyogenes 5.57e-01 |

ALIGNMENTS

RESULT 1
 ID W64636: standard; peptide; 12 AA.
 AC W64636:
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide PSEB(150-161).
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KW therapeutic; vaccine; food poisoning.
 OS Synthetic.
 OS Staphylococcus aureus.
 PM W09629444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G. Kampferer.
 DR WPI: 96-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
 PT antagonising toxin-mediated activation of T cells and prevention of
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 6: Page 41: 68pp: English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced
 CC by PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 12 AA.

Query Match 100.0%; Score 74; DB 34; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.06e-01;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 tnkkvtageld 12

QY 1 TNRKRVTAQELD 12

RESULT 2
ID W64640 standard; peptide; 13 AA.

AC W64640;
DE 23-OCT-1998 (first entry)
DE Synthetic SEB peptide pSEBLC(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; T-cell; antagonist; inhibitor;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
OS Synthetic; vaccine; food poisoning.

OS Staphylococcus aureus.
FH key Location/Qualifiers
FT Modified_site 1 /note="N-terminal Thr modified by presence of
N-lauryl-cysteyl"

MO9829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 15; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced activation of T-cells, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 tnrkvtatageld 13
QY 1 TNRKRVTAQELD 12

RESULT 3
ID R13206 standard; protein; 239 AA.
AC R13206;
DE 15-OCT-1991 (first entry)
DE Staphylococcal enterotoxin B.
KW SEB; cancer treatment; pyrogen; tumouricide.
OS Staphylococcus aureus.
PN MO9110680-A.
PD 25-JUL-1991.
PF 17-JAN-1991; U00342.
PR 17-JAN-1990; US-466577.
PA (TERM) TERMAN D S.
PI Terman DS;
DR WPI: 91-237984/32.
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
PS Disclosure; Fig 1; 74pp; English.
CC SEB was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and prococagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The

CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEB. Synthetic
CC polypeptides having structural homology to Staphylococcal
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydrophathy profiles.
CC See R13203-R13211.
SQ Sequence 239 AA;

Query Match 100.0%; Score 74; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 150 tnrkvtatageld 161
QY 1 TNRKRVTAQELD 12

RESULT 4
ID W64647 standard; peptide; 239 AA.
AC W64647;
DE 23-OCT-1998 (first entry)
DE Synthetic SEB protein fragment.
KW Enterotoxin B; SEB; pyrogenic exotoxin; T-cell; antagonist; inhibitor;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
OS Synthetic; vaccine; food poisoning.
OS Staphylococcus aureus.
PN MO9829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Example 8; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced activation of T-cells, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 239 AA;

Query Match 100.0%; Score 74; DB 34; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 150 tnrkvtatageld 161
QY 1 TNRKRVTAQELD 12

RESULT 5
ID R45014 standard; protein; 239 AA.
AC R45014;
DE 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SEB.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; pertussis system.
OS Staphylococcus aureus.
PN MO9324136-A.
PD 09-DEC-1993.
PF 01-JUN-1993; U05213.

PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS Disclosure: Fig 1: 90pp; English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 SQ Sequence 239 AA;

Query Match 100.0%; Score 74; DB 8; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.06e-01;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 150 tkkktvtageld 161
 |||||
 QY 1 TNKKKVTAGELD 12

RESULT 6
 ID W06737 standard; Protein: 255 AA.
 AC W06737;
 DT 08-MAR-1997 (first entry)
 DE Staphylococcus enterotoxin B.
 KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
 KW vaccine; adjuvant.
 OS Staphylococcus sp.
 FH Key Location/Qualifiers
 FT peptide 1..15
 FT /label= Sig.peptide
 PN W09636366-A1.
 PD 21-NOV-1996.
 PR 20-MAY-1996; U07432.
 PR 18-MAY-1995; US-446918.
 PR 29-DEC-1995; US-580806.
 PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
 PI Dow SM, Elmstie RE, Potter TA;
 DR WPI: 97-011857/01.
 DR N-PSDB: T45698.
 PT Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer
 PS Example 1: Page 96-97; 131pp; English.
 CC A cDNA clone (T45698) codes for staphylococcal enterotoxin B
 CC (W06737) superantigen. Nucleic acids encoding superantigens (see
 CC also W06738-39), esp. truncated forms of the superantigen lacking
 CC the leader peptide, can be utilised in the gene therapy of cancer,
 CC infectious diseases and immunological disorders. The nucleic acid,
 CC optionally in combination with cytokine or chemokine nucleic acids,
 CC is delivered to an animal using e.g. liposomes. It acts by
 CC controlling the activity of effector cells, such as T-cells,
 CC macrophages, monocytes and/or natural killer cells. Localised
 CC prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal.
 SQ Sequence 255 AA;

Query Match 100.0%; Score 74; DB 20; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.06e-01;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 166 tkkktvtageld 177
 |||||
 QY 1 TNKKKVTAGELD 12

RESULT 7
 ID R13209 standard; Protein: 221 AA.
 AC R13209;
 DT 15-OCT-1991 (first entry)
 DE Streptococcal pyrogenic enterotoxin A.
 KW SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 OS Streptococcus Nr-5 strain.
 PN W09110680-A.
 PD 25-JUL-1991.
 PR 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumouricidal activity
 PT as staphylococcal protein A without potential toxic reactions
 PS Disclosure: Fig 1: 74pp; English.
 CC SPE A can be used for tumouricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to streptococcal
 CC pyrogenic exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of cysteine
 CC residues and similar hydrophathy profiles.
 CC See R13203-R13211.
 SQ Sequence 221 AA;

Query Match 91.9%; Score 68; DB 3; Length 221;
 Best Local Similarity 91.7%; Pred. No. 5.57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 135 tkkmtvtageld 146
 |||||
 QY 1 TNKKKVTAGELD 12

RESULT 8
 ID R45017 standard; protein: 221 AA.
 AC R45017;
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SPE A.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 OS Staphylococcus aureus.
 PN W09324136-A.
 PD 09-DEC-1993.
 PR 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS Disclosure: Fig 1: 90pp; English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 SQ Sequence 221 AA;

Query Match 91.9%; Score 68; DB 8; Length 221;
 Best Local Similarity 91.7%; Pred. No. 5.57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 135 tkkmtvtageld 146
 |||||
 QY 1 TNKKKVTAGELD 12

CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 CC Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
 Best Local Similarity 91.7%; Pred. No. 5,57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnkkmvtage1d 176
 |||||:|||||
 QY 1 TNKKVTAQELD 12

RESULT 12
 ID W12153 standard; Protein; 251 AA.
 AC W12153;
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 1..30
 FT /label= sig_peptide
 FT 31..251
 FT /label= mat_peptide
 FT Misc-difference 120
 FT /note= "wild type Cys replaced by Ser"
 FT W09640930-A1.
 PN 19-DEC-1996.
 PR 07-JUN-1996; U10252.
 PR 07-JUN-1995; US-480261.
 PA (MIND) UNIV MINNESOTA.
 PI Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;
 DR WPI: 97-099936/09.
 PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Example 4; Page -: 102pp; English.
 CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 CC Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
 Best Local Similarity 91.7%; Pred. No. 5,57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 165 tnkkmvtage1d 176
 |||||:|||||
 QY 1 TNKKVTAQELD 12

RESULT 13
 ID W12152 standard; Protein; 251 AA.

AC W12152;
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Cys98Ser.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 OS Synthetic.

FH Key Location/Qualifiers
 FT peptide 1..30
 FT /label= sig_peptide
 FT 31..251
 FT /label= mat_peptide
 FT Misc-difference 128
 FT /note= "wild type Cys replaced by Ser"

FT W09640930-A1.
 PN 19-DEC-1996.
 PR 07-JUN-1996; U10252.
 PR 07-JUN-1995; US-480261.
 PA (MIND) UNIV MINNESOTA.
 PI Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;
 DR WPI: 97-099936/09.
 PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Example 4; Page -: 102pp; English.
 CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 CC Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
 Best Local Similarity 91.7%; Pred. No. 5,57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnkkmvtage1d 176
 |||||:|||||
 QY 1 TNKKVTAQELD 12

RESULT 14
 ID W12097 standard; Protein; 251 AA.
 AC W12097;
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 1..30
 FT /label= sig_peptide
 FT 31..251
 FT /label= mat_peptide
 FT W09640930-A1.
 PN 19-DEC-1996.

(TM)

Distribution rights by Oxford Molecular Ltd

1 TNKKVTAQELD 12

PAM 150

122810 seqs, 40068593 residues

Listing first 45 summaries

1:plr1 2:plr2 3:plr3 4:plr4

Mean 23.119; Variance 28.486; scale 0.812

and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------|-----------------------|-----------|
| 1 | 74 | 100.0 | 266 | 1 | ENSAB6 | enterotoxin B precurs | 1.74e-04 |
| 2 | 68 | 91.9 | 236 | 6 | S18783 | exotoxin type A precu | 5.23e-04 |
| 3 | 68 | 91.9 | 236 | 2 | S18786 | exotoxin type A precu | 5.23e-04 |
| 4 | 68 | 91.9 | 251 | 2 | S28659 | exotoxin type A precu | 5.23e-04 |
| 5 | 64 | 86.5 | 233 | 2 | A29566 | enterotoxin A - Staph | 4.71e-03 |
| 6 | 64 | 86.5 | 236 | 2 | S18789 | exotoxin A precursor | 4.71e-03 |
| 7 | 64 | 86.5 | 257 | 2 | A28664 | enterotoxin A precurs | 4.71e-03 |
| 8 | 64 | 86.5 | 266 | 1 | ENSAC1 | enterotoxin C-1 precu | 4.71e-03 |
| 9 | 64 | 86.5 | 266 | 2 | A60114 | enterotoxin C-2 precu | 4.71e-03 |
| 10 | 64 | 86.5 | 266 | 2 | S18185 | enterotoxin C3 - Stap | 4.71e-03 |
| 11 | 62 | 83.8 | 258 | 2 | A33953 | enterotoxin D precurs | 1.38e-02 |
| 12 | 58 | 78.4 | 257 | 2 | A28179 | enterotoxin E precurs | 1.12e-01 |
| 13 | 52 | 70.3 | 807 | 2 | A64575 | Vib4 homolog - Helic | 2.24e-01 |
| 14 | 51 | 68.9 | 803 | 2 | A41793 | dipeptidyl aminopepti | 3.62e+00 |
| 15 | 51 | 68.9 | 803 | 2 | I68600 | dipeptidyl aminopepti | 3.62e+00 |
| 16 | 51 | 68.9 | 865 | 2 | I54331 | dipeptidyl aminopepti | 3.62e+00 |
| 17 | 50 | 67.6 | 1252 | 2 | T00263 | hypothetical protein | 5.82e+00 |
| 18 | 49 | 66.2 | 153 | 2 | S50431 | hypothetical protein | 9.28e+00 |
| 19 | 48 | 64.9 | 637 | 2 | E69627 | cell-division protein | 1.47e+01 |
| 20 | 48 | 64.9 | 1055 | 1 | A37205 | leukotoxin A - Actino | 1.47e+01 |
| 21 | 48 | 64.9 | 1782 | 2 | S45280 | vitellogenin precurs | 1.47e+01 |
| 22 | 48 | 64.9 | 4644 | 1 | A38905 | dysen heavy chain, C | 1.47e+01 |
| 23 | 47 | 63.5 | 148 | 2 | H69116 | conserved hypotetica | 2.31e+01 |

| | | | | | | | |
|----|----|------|------|---|--------|-----------------------|----------|
| 24 | 47 | 63.5 | 538 | 2 | S12570 | homeotic protein bico | 2.3ie+01 |
| 25 | 47 | 63.5 | 649 | 2 | S58097 | probable phosphoester | 2.3ie+01 |
| 26 | 46 | 62.2 | 200 | 2 | S23524 | GTP-binding protein N | 3.5ie+01 |
| 27 | 46 | 62.2 | 200 | 2 | S49225 | guanine nucleotide re | 3.5ie+01 |
| 28 | 46 | 62.2 | 257 | 2 | G64216 | ribosomal protein L3 | 3.5ie+01 |
| 29 | 46 | 62.2 | 264 | 2 | A47737 | osteonectin precursor | 3.5ie+01 |
| 30 | 46 | 62.2 | 417 | 2 | C32185 | Frz CD protein - Myxo | 3.5ie+01 |
| 31 | 46 | 62.2 | 489 | 2 | SA0731 | ATP-dependent RNA hel | 3.5ie+01 |
| 32 | 46 | 62.2 | 489 | 2 | T01959 | hypothetical protein | 3.5ie+01 |
| 33 | 46 | 62.2 | 589 | 2 | T01163 | hypothetical protein | 3.5ie+01 |
| 34 | 46 | 62.2 | 727 | 2 | S57056 | neurotransmitter Cran | 3.5ie+01 |
| 35 | 46 | 62.2 | 727 | 2 | I65704 | Na+/Cl(-)-dependent t | 3.5ie+01 |
| 36 | 46 | 62.2 | 818 | 2 | S57070 | probable protein kina | 3.5ie+01 |
| 37 | 46 | 62.2 | 1084 | 2 | A28555 | middle wall protein P | 3.5ie+01 |
| 38 | 46 | 62.2 | 1179 | 2 | C36792 | hypothetical protein | 3.5ie+01 |
| 39 | 45 | 60.8 | 212 | 2 | C71633 | hypothetical protein | 5.60e+01 |
| 40 | 45 | 60.8 | 230 | 2 | S09648 | nucleoprotein NS1 - 1 | 5.60e+01 |
| 41 | 45 | 60.8 | 230 | 1 | NM1V1 | nonstructural protein | 5.60e+01 |
| 42 | 45 | 60.8 | 351 | 1 | S49887 | hypothetical protein | 5.60e+01 |
| 43 | 45 | 60.8 | 466 | 2 | J65325 | processing peptidase | 5.60e+01 |
| 44 | 45 | 60.8 | 572 | 2 | S73730 | MG307 homolog H08.orf | 5.60e+01 |
| 45 | 45 | 60.8 | 793 | 1 | UC6161 | kinesin-associated pr | 5.60e+01 |

ALIGNMENTS

```

RESULT      1
ENTRY
TITLE       ENSAB6      #type complete
ORGANISM    enterotoxin B precursor - Staphylococcus aureus
DATE        #formal_name Staphylococcus aureus
            24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change
            11-Sep-1998
ACCESSIONS  S27360; A92065; S27240; A01815
REFERENCE   S27360
#authors    Jones, C.L.; Khan, S.A.
#journal     J. Bacteriol. (1986) 166:29-33
#title       Nucleotide sequence of the enterotoxin B gene from
            Staphylococcus aureus.
#cross-references MUID:86168029
#accession   S27360
#molecule-type DNA
#residues    1-266 ##label JON
#cross-references EMBL:M1118; NID:g152999; PID:g153000
#experimental_source strain S6
REFERENCE   A92065
#authors     Huang, I.Y.; Bergdoll, M.S.
#journal     J. Biol. Chem. (1970) 245:3518-3525
#title       The primary structure of staphylococcal enterotoxin B. III.
            The cyanogen bromide peptides of reduced and aminoethylated
            enterotoxin B. and the complete amino acid sequence.
#cross-references MUID:71007902
#accession   A92065
#molecule-type protein
#residues    28-55, 'NND', 59-68, 'NE', 71, 'FDLIV', 78-117, 119-127, 'N',
            129, 'D', 131-132, 'EMT', 136-148, 'GN', 151-156, 'Y',
            157-184, 'EQ', 187-232, 'N', 234-245, 'ND', 248-266 ##label
            HDA
#experimental_source strain S-6
REFERENCE   A92064
#authors     Huang, I.Y.; Bergdoll, M.S.
#journal     J. Biol. Chem. (1970) 245:3511-3517
#title       The primary structure of staphylococcal enterotoxin B. II.
            Isolation, composition, and sequence of chymotryptic
            peptides.
#cross-references MUID:71007901
#contents    annotation: chymotryptic peptides
REFERENCE   A92063
#authors     Huang, I.Y.; Bergdoll, M.S.
#journal     J. Biol. Chem. (1970) 245:3493-3510
#title       The primary structure of staphylococcal enterotoxin B. I.
            Isolation, composition, and sequence of tryptic peptides
            from oxidized entero-toxin B.
#cross-references MUID:71007900

```

REFERENCE #contents annotation: tryptic peptides
A90548
#authors Schatz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
Dunne, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin B.
#cross-references EMBL:66035792
#contents annotation: biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Kinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.;
Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of
staphylococcal enterotoxin B.
#accession S27240
#molecule-type protein
#residues 28-42;128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin; extracellular protein; toxin
FEATURE 1-27
#domain signal sequence #status predicted #label SIG
28-266 #product enterotoxin B #status experimental #label MAT
120-140 #disulfide bonds #status experimental
SUMMARY #length 266 #molecular-weight 31436 #checksum 4249
Query Match 100.0%; Score 74; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 177 TNKKVTAQELD 188
QY 1 TNKKVTAQELD 12
RESULT 2
ENTRY 518783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes
(fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS158 isolate Nebraska; strain MGAS485 isolate
Yugoslavia; strain MGAS491 isolate United Kingdom; strain
MGAS624 isolate Germany; strain MGAS495 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
ACCESSIONS 518783; 518793; 518801; 518798
REFERENCE 518782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUIID:92044323
#accession 518783
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61568; NID:947289; PID:947290
#experimental_source strain MGAS158 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518793
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEA
#cross-references EMBL:X61569; NID:947313; PID:947314
#experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518794
#status nucleic acid sequence not shown; translation not shown

REFERENCE #molecule-type DNA
#residues 1-236 #label NEZ
#cross-references EMBL:X61570; NID:947315; PID:947316
#experimental_source strain MGAS491 isolate United Kingdom unassigned
phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518801
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEY
#cross-references EMBL:X61572; NID:947333; PID:947334
#experimental_source strain MGAS624 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518798
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEO
#cross-references EMBL:X61571; NID:947323; PID:947324
#experimental_source strain MGAS495 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS #gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
#domain signal sequence (fragment) #status predicted
#label SIG
23-236 #product exotoxin type A (fragment) #status predicted
#label MAT
SUMMARY #length 236 #checksum 612
Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 5.23e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 157 TNKKVTAQELD 168
QY 1 TNKKVTAQELD 12
RESULT 3
ENTRY 518786 #type fragment
TITLE exotoxin type A precursor (allele 2) - Streptococcus pyogenes
(fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS250 isolate California; strain MGAS251 isolate
California; strain MGAS256 isolate California; strain
MGAS285 isolate Colorado; strain MGAS480 isolate
Yugoslavia; strain MGAS492 isolate United Kingdom; strain
MGAS496 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
ACCESSIONS 518786; 518787; 518788; 518790; 518792; 518795; 518799
REFERENCE 518782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUIID:92044323
#accession 518786
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61561; NID:947297; PID:947298
#experimental_source strain MGAS250 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

```
#accession S18787
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 ##label NEA
#cross-references EMBL:X61562; NID:947299; PID:947300
#experimental_source strain MGAS251 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18788
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 ##label NEZ
#cross-references EMBL:X61563; NID:947301; PID:947302
#experimental_source strain MGAS256 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18790
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 ##label NEY
#cross-references EMBL:X61564; NID:947305; PID:947306
#experimental_source strain MGAS285 isolate Colorado unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18792
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 ##label NEO
#cross-references EMBL:X61565; NID:947311; PID:947312
#experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18795
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 ##label NEH
#cross-references EMBL:X61566; NID:947317; PID:947318
#experimental_source strain MGAS492 isolate United Kingdom unassigned
phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18799
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 ##label NES
#cross-references EMBL:X61567; NID:947325; PID:947326
#experimental_source strain MGAS496 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

GENETICS
#gene SPEA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
1-22
23-235
#domain signal sequence (fragment) #status predicted
#product exotoxin type A (fragment) #status predicted
#label MAT
#label MAT
SUMMARY #length 236 #checksum 1685

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. NO. 5.23e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKKVTAQELD 168
|||||
1 TNKKVTAQELD 12

RESULT 4
ENTRY S29659 #type complete
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes
phage T12
```

```
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change
25-Mar-1998
ACCESSIONS S29659; S18782; S18784; S18785; S18791; S18796; S18797;
S18800
REFERENCE
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin
(erythrogenic toxin) gene from Streptococcus pyogenes
bacteriophage T12.
#cross-references MUID:86166804
#accession S29659
#molecule-type DNA
#residues 1-251 ##label WEE
#cross-references GB:040453; EMBL:M19350; NID:91877426; PID:91877430
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18782
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 ##label NEL
#cross-references EMBL:X61560; NID:947287; PID:947288
#experimental_source Streptococcus pyogenes strain MGAS156 isolate
Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18784
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 ##label NEA
#cross-references EMBL:X61556; NID:947291; PID:947292
#experimental_source Streptococcus pyogenes strain MGAS165 isolate
Minnesota unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18785
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 ##label NEZ
#cross-references EMBL:X61559; NID:947293; PID:947294
#experimental_source Streptococcus pyogenes strain MGAS167 isolate
Texas unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18791
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 ##label NEY
#cross-references EMBL:X61555; NID:947309; PID:947310
#experimental_source Streptococcus pyogenes strain MGAS327 isolate
Arizona unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18796
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 ##label NEO
#cross-references EMBL:X61557; NID:947319; PID:947320
#experimental_source Streptococcus pyogenes strain MGAS493 isolate
France unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18797
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 ##label NEH
```

```

##cross-references EMBL:X61558;NID:947321; PID:947322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18800
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-228 ##label NES
##cross-references EMBL:X61554; NID:947327; PID:947328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
Zealand unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

GENETICS
#gene speA; speAL
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
1-30 #domain signal sequence #status predicted #label SIG
31-251 #product exotoxin type A #status predicted #label MAT
SUMMARY #length 251 #molecular-weight 29246 #checksum 1475

Query Match 91.9%; Score 68; DB 2; Length 251;
Best Local Similarity 91.7%; Pred. No. 5,23e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 TNKKNVTAQELD 176
QY 1 TNKKNVTAQELD 12
||||:|||||

RESULT 5
ENTRY A29566 #type complete
TITLE enterotoxin A - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change
18-Jun-1993

ACCESSIONS A29566
REFERENCE A29566
#authors Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
#journal J. Biol. Chem. (1987) 262:7006-7013
#title Complete amino acid sequence of staphylococcal enterotoxin A
#cross-references MUID:87222293
#accession A29566
#molecule_type protein
#residues 1-233 #label HUA

GENETICS
#gene entA
SUMMARY #map_position 6 #length 233 #molecular-weight 27079 #checksum 9580

Query Match 86.5%; Score 64; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 4,71e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 145 TNKKNVTAQELD 156
QY 1 TNKKNVTAQELD 12
||||:|||||

RESULT 6
ENTRY S18789 #type fragment
TITLE exoC10 A precursor (allele 4) - Streptococcus pyogenes
(strain MGAS265 isolate California) (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes
strain MGAS265 isolate California
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
25-Mar-1998
S18789
S18782
REFERENCE Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#authors

```

```

#journal      J. Exp. Med. (1991) 174:1271-1274
#title        Characterization and clonal distribution of four alleles of
              the speA gene encoding pyrogenic exotoxin A (scarlet fever
              toxin) in Streptococcus pyogenes.
#cross-references NID:92044323
#accession    S18789
#status       nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEL
##cross-references EMBL:X61573; NID:g47303; PID:g47304
##note        The nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

GENETICS
#gene         speA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS       exotoxin
FEATURE        1-22
              23-236
SUMMARY        #length 236 #checksum 3493
              MW
Query Match    86.5%; Score 64; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 4,71e-03;
Matches        10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db            157 TSKKNTVQELD 168
              1::1::11111111
QY            1 TNKKVTQELD 12

RESULT 7
ENTRY      A28664 #type complete
TITLE      enterotoxin A precursor - Staphylococcus aureus (strain
            FRI337)
ORGANISM   #formal_name Staphylococcus aureus
            #cross-references GB:M18970; NID:g153120; PID:g153121
            ##experimental_source strain FRI337
            #journal #length 257 #molecular_weight 29669 #checksum 2543
            #title    Nucleotide sequence of the type A staphylococcal enterotoxin
            gene.
            #cross-references NID:88086892
            #accession A28664
            ##molecule_type DNA
            ##residues 1-257 ##label BET
            ##cross-references GB:M18970; NID:g153120; PID:g153121
            ##experimental_source strain FRI337
            #journal #length 257 #molecular_weight 29669 #checksum 2543
            #title    Nucleotide sequence of the type A staphylococcal enterotoxin
            gene.

SUMMARY
Query Match    86.5%; Score 64; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 4,71e-03;
Matches        10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db            169 TNKKNTVQELD 180
              111111111111
QY            1 TNKKVTQELD 12

RESULT 8
ENTRY      ENSAC1 #type complete
TITLE      enterotoxin C-1 precursor - Staphylococcus aureus
ORGANISM   #formal_name Staphylococcus aureus
            #cross-references GB:M18970; NID:g153120; PID:g153121
            ##experimental_source strain FRI337
            #journal #length 257 #molecular_weight 29669 #checksum 2543
            #title    Nucleotide sequence of the staphylococcal enterotoxin C1 gene.
            #cross-references NID:88086892
            #accession A28664
            ##molecule_type DNA
            ##residues 1-257 ##label BET
            ##cross-references GB:M18970; NID:g153120; PID:g153121
            ##experimental_source strain FRI337
            #journal #length 257 #molecular_weight 29669 #checksum 2543
            #title    Nucleotide sequence of the staphylococcal enterotoxin C1 gene.

ACCESSIONS
REFERENCE     S06356; A01816
#authors      Bohach, G.A.; Schlievert, P.M.
#journals     Mol. Gen. Genet. (1987) 209:15-20
#title        Nucleotide sequence of the staphylococcal enterotoxin C1 gene.

```

| | |
|---|---|
| 28-266 | #product enterotoxin C-2 #stratus predicted #label MAT |
| SUMMARY | #length 266 #molecule-weight 30604 #checksum 5494 |
| Query Match | 86.5%; Score 64; DB 2; Length 266; |
| Best Local Similarity | 83.3%; Pred. No. 4,71e-03; |
| Matches | 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; |
| Db | 176 TDKKSVTAQELD 187 |
| OY | 1 TNRKKVTAQELD 12 |
| RESULT | 10 |
| ENTRY | S11885 #type complete |
| TITLE | enterotoxin C3 - Staphylococcus aureus |
| ORGANISM | #formal_name Staphylococcus aureus |
| DATE | 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Mar-1998 |
| ACCESSIONS | S11885 |
| REFERENCE | S11885 |
| AUTHORS | Howde, C.J.; Hackett, S.P.; Bohach, G.A. |
| JOURNAL | Mol. Gen. Genet. (1990) 220:329-333 |
| TITLE | Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three Type C staphylococcal enterotoxins. |
| #cross-references MUID:90220508 | |
| #accession | S11885 |
| #status | Preliminary |
| #molecule_type | DNA |
| #residues | 1-266 #label HOV |
| #cross-references GB:X51661; NID:g46570; PID:g46571 | |
| CLASSIFICATION | #superfamily enterotoxin B |
| SUMMARY | #length 266 #molecular-weight 30671 #checksum 6135 |
| Query Match | 86.5%; Score 64; DB 2; Length 266; |
| Best Local Similarity | 83.3%; Pred. No. 4,71e-03; |
| Matches | 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; |
| Db | 176 TDKKSVTAQELD 187 |
| OY | 1 TNRKKVTAQELD 12 |
| RESULT | 11 |
| ENTRY | A33953 #type complete |
| TITLE | enterotoxin D precursor - Staphylococcus aureus |
| ORGANISM | #formal_name Staphylococcus aureus |
| DATE | 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Sep-1997 |
| ACCESSIONS | A33953 |
| REFERENCE | A33953 |
| AUTHORS | Bayles, K.W.; Iandolo, J.J. |
| JOURNAL | J. Bacteriol. (1989) 171:4799-4806 |
| TITLE | Genetic and molecular analyses of the gene encoding Staphylococcal enterotoxin D. |
| #cross-references MUID:89359112 | |
| #accession | A33953 |
| #status | Preliminary |
| #molecule_type | DNA |
| #residues | 1-258 #label BAY |
| #cross-references GB:M8521; NID:g1492109; PID:g758691 | |
| SUMMARY | #length 258 #molecular-weight 29746 #checksum 39 |
| Query Match | 83.8%; Score 62; DB 2; Length 258; |
| Best Local Similarity | 75.0%; Pred. No. 1,38e-02; |
| Matches | 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; |
| Db | 170 TDKKVTQVQELD 181 |
| OY | 1 TNRKKVTAQELD 12 |
| RESULT | 12 |

ENTRY A28179 #type complete
TITLE enterotoxin E precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Sep-1997

ACCESSIONS A28179
REFERENCE A28179
#authors Couch, J.L.; Solitis, M.T.; Betley, M.J.
#journal J. Bacteriol. (1988) 170:2954-2960
#title Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
#cross-references MUID:88257005
#accession A28179
##molecule_type DNA
##residues 1-257 #label COU
##cross-references GB:M1319; NID:g153001; PID:g153002
SUMMARY #length 257 #molecular-weight 29358 #checksum 2562

Query Match 78.4%; Score 58; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 1.12e+01;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 169 TSKEVYVQELD 180
QY 1 TNKKVTAQELD 12

RESULT 13
ENTRY A64575 #type complete
TITLE VirB4 homolog - Helicobacter pylori (strain 26695)
ORGANISM #formal_name Helicobacter pylori
DATE 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 10-Oct-1997

ACCESSIONS A64575
REFERENCE A64520
#authors Sutton, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Tomb, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpx, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.
#journal Nature (1997) 388:539-547
#title The complete genome sequence of the gastric pathogen Helicobacter pylori.
#cross-references MUID:97394467
#accession A64575
#status preliminary; nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-807 #label TOM
##cross-references GB:AE00559; GB:AE00511; NID:g2313536; PID:g2313543;
SUMMARY #length 807 #molecular-weight 93383 #checksum 7147

Query Match 70.3%; Score 52; DB 2; Length 807;
Best Local Similarity 60.0%; Pred. No. 2.24e+00;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 143 KKRITNELE 152
QY 3 KKRKTAQELD 12

RESULT 14
ENTRY A41793 #type complete
TITLE dipeptidyl aminopeptidase-like protein (EC 3.4.14.-) short form, DPPX-S - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle

DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999

ACCESSIONS A41793
REFERENCE A41793
#authors Wada, K.; Yokotani, N.; Hunter, C.; Doi, K.; Wenthold, R.J.; Shimasaki, S.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:197-201
#title Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family.
#cross-references MUID:92108018
#accession A41793
#status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-803 #label WAD
##cross-references GB:M76429; NID:g408719; PID:g408720
#note sequence extracted from NCBI backbone (NCBIP:75138)
KEYWORDS dipeptidylpeptide hydrolase; glycoprotein
FEATURE 257,342
#binding_site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 803 #molecular-weight 90459 #checksum 9315

Query Match 68.9%; Score 51; DB 2; Length 803;
Best Local Similarity 54.5%; Pred. No. 3.62e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 64 SQRKVTVEDE 74
QY 1 TNKKVTAQEL 11

RESULT 15
ENTRY 168600 #type complete
TITLE dipeptidyl aminopeptidase like protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 06-Sep-1996

ACCESSIONS 168600
REFERENCE 154331
#authors Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K.
#journal Hum. Mol. Genet. (1993) 2:1037-1039
#title Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-related protein encoded by a gene on human chromosome 7.
#cross-references MUID:93372805
#accession 168600
#status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-803 #label RES
##cross-references GB:M96860; NID:g306707; PID:g306708
SUMMARY #length 803 #molecular-weight 91355 #checksum 814

Query Match 68.9%; Score 51; DB 2; Length 803;
Best Local Similarity 54.5%; Pred. No. 3.62e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 64 SQRKVTVEDE 74
QY 1 TNKKVTAQEL 11

Search completed: Tue Aug 31 19:05:19 1999
Job time : 20 secs.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (C) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:03:16 1999; MasPar time 2.77 Seconds
Tabular output not generated. 122.380 Million cell updates/sec

Title: >US-09-150-947-1
Description: (1-12) from US09150947.pep
Perfect Score: 74
Sequence: 1 TNKKKVTAEELD 12

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 23.804; Variance 25.094; scale 0.949

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 74 | 100.0 | 266 | 1 | ETXB_STAAU ENTEROTOXIN TYPE B PRE | 8.34e-07 |
| 2 | 68 | 91.9 | 251 | 1 | SPEA_STRPY EXOTOXIN TYPE A PRECUR | 4.14e-05 |
| 3 | 64 | 86.5 | 257 | 1 | ETXA_STAAU ENTEROTOXIN TYPE A PRE | 5.12e-04 |
| 4 | 64 | 86.5 | 266 | 1 | ETC1_STAAU ENTEROTOXIN TYPE C-1 P | 5.12e-04 |
| 5 | 64 | 86.5 | 266 | 1 | ETC2_STAAU ENTEROTOXIN TYPE C-2 P | 5.12e-04 |
| 6 | 64 | 86.5 | 266 | 1 | ETXD_STAAU ENTEROTOXIN TYPE D PRE | 1.75e-03 |
| 7 | 62 | 83.8 | 258 | 1 | ETXE_STAAU ENTEROTOXIN TYPE E PRE | 1.92e-02 |
| 8 | 58 | 78.4 | 257 | 1 | DIPEPTIDYL PEPTIDASE I | 9.93e-01 |
| 9 | 51 | 68.9 | 863 | 1 | DIPEPTIDYL PEPTIDASE I | 9.93e-01 |
| 10 | 51 | 68.9 | 863 | 1 | DIPEPTIDYL PEPTIDASE I | 9.93e-01 |
| 11 | 51 | 68.9 | 863 | 1 | DIPEPTIDYL PEPTIDASE I | 9.93e-01 |
| 12 | 49 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 13 | 49 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 14 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 15 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 16 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 17 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 18 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 19 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 20 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 21 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 22 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |
| 23 | 48 | 66.2 | 153 | 1 | YEC8_YEAST HYPOTHETICAL 17.4 KD P | 2.88e+00 |

| | | | | | | |
|----|----|------|------|---|-----------------------------------|----------|
| 24 | 46 | 62.2 | 417 | 1 | FRZC_MYXXA FRZD PROTEIN (FRIZZY | 1.33e+01 |
| 25 | 46 | 62.2 | 489 | 1 | VN21_CAEEL PURATIVE ATP-DEPENDENT | 1.33e+01 |
| 26 | 46 | 62.2 | 572 | 1 | MOES_LYIVA MOESIN. | 1.33e+01 |
| 27 | 46 | 62.2 | 727 | 1 | NRT4_RAT SODIUM- AND CHLORIDE-D | 1.33e+01 |
| 28 | 46 | 62.2 | 818 | 1 | PRK2_YEAST SERINE/THREONINE-PROTE | 1.33e+01 |
| 29 | 46 | 62.2 | 1053 | 1 | SLPM_BACR MIDDLE CELL WALL PROTE | 1.33e+01 |
| 30 | 46 | 62.2 | 1179 | 1 | VG56_HSV1 HYPOTHETICAL GENE 56 P | 1.33e+01 |
| 31 | 45 | 60.8 | 90 | 1 | VNS1_IACNO NONSTRUCTURAL PROTEIN | 2.18e+01 |
| 32 | 45 | 60.8 | 127 | 1 | CU04_BLACK CUTICLE PROTEIN 4 (BC- | 2.18e+01 |
| 33 | 45 | 60.8 | 130 | 1 | TAT_HV2B TAT PROTEIN (TRANSACTI | 2.18e+01 |
| 34 | 45 | 60.8 | 202 | 1 | VNS1_IACOM NONSTRUCTURAL PROTEIN | 2.18e+01 |
| 35 | 45 | 60.8 | 207 | 1 | LEUD_BUCAP 3-ISOPROPYLMALATE DEHY | 2.18e+01 |
| 36 | 45 | 60.8 | 230 | 1 | VNS1_IACEN NONSTRUCTURAL PROTEIN | 2.18e+01 |
| 37 | 45 | 60.8 | 230 | 1 | VNS1_IACPE NONSTRUCTURAL PROTEIN | 2.18e+01 |
| 38 | 45 | 60.8 | 239 | 1 | YQAS_BACSU HYPOTHETICAL 27.7 KD P | 2.18e+01 |
| 39 | 45 | 60.8 | 269 | 1 | YD54_SCHPO HYPOTHETICAL 31.2 KD P | 2.18e+01 |
| 40 | 45 | 60.8 | 330 | 1 | YD54_SCHPO HYPOTHETICAL 31.2 KD P | 2.18e+01 |
| 41 | 45 | 60.8 | 351 | 1 | YIM2_YEAST HYPOTHETICAL 39.5 KD P | 2.18e+01 |
| 42 | 45 | 60.8 | 450 | 1 | INVO_LEMCA INVOLUCRIN | 2.18e+01 |
| 43 | 45 | 60.8 | 4639 | 1 | DYHC_DROME DYNEIN HEAVY CHAIN, CY | 2.18e+01 |
| 44 | 45 | 59.5 | 130 | 1 | VG67_BPH2 EARLY PROTEIN GP16.7. | 3.54e+01 |
| 45 | 44 | 59.5 | 1738 | 1 | YCF1_EPIVI HYPOTHETICAL 208 KD PR | 3.54e+01 |

ALIGNMENTS

| RESULT | ID | ETXB_STAAU | STANDARD: | PRT: | 266 | AA. |
|--------|---|------------|-----------|------|-----|-----|
| AC | P01552; | | | | | |
| DT | 21-JUL-1986 (REL. 01, CREATED) | | | | | |
| DT | 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE) | | | | | |
| DT | 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) | | | | | |
| DE | ENTEROTOXIN TYPE B PRECURSOR (SEB). | | | | | |
| GN | ENTB. | | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | | |
| OC | STAPHYLOCOCCUS. | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RA | JONES C.L., KHAN S.A.; | | | | | |
| RT | "Nucleotide sequence of the enterotoxin B gene from Staphylococcus | | | | | |
| RT | aureus."; | | | | | |
| RL | J. BACTERIOL. 166:29-33(1986). | | | | | |
| RN | [2] | | | | | |
| RP | SEQUENCE OF 40-91 FROM N.A. | | | | | |
| RA | RAMELLI D.M., JONES C.L., JOHNS M.B., MUSSERY G.J., KHAN S.A.; | | | | | |
| RT | "Molecular cloning of staphylococcal enterotoxin B gene in | | | | | |
| RT | Escherichia coli and Staphylococcus aureus."; | | | | | |
| RL | PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985). | | | | | |
| RN | [3] | | | | | |
| RP | SEQUENCE OF 28-266 (S-6). | | | | | |
| RA | HUANG I.-Y., BERGDOLL M.S.; | | | | | |
| RT | "The primary structure of staphylococcal enterotoxin B. 3. The | | | | | |
| RT | cyanogen bromide peptides of reduced and aminoethylated enterotoxin | | | | | |
| RT | B, and the complete amino acid sequence."; | | | | | |
| RL | J. BIOL. CHEM. 245:3518-3525(1970). | | | | | |
| RN | [4] | | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS). | | | | | |
| RA | MEDLINE: 93063291. | | | | | |
| RT | "Crystal structure of staphylococcal enterotoxin B, a superantigen."; | | | | | |
| RL | NATURE 359:801-806(1992). | | | | | |
| RN | [5] | | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II. | | | | | |
| RA | JADETZKY T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G., | | | | | |
| RT | CHI Y.I., STAUFACHER C., STROMINGER J.L., WILEY D.C.; | | | | | |
| RT | "Three-dimensional structure of a human class II histocompatibility | | | | | |
| RT | molecule complexed with superantigen."; | | | | | |
| RL | NATURE 368:711-718(1994). | | | | | |

[6]
 X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 MEDLINE: 98181012.
 RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.:
 RT "Crystal structure of microbial superantigen staphylococcal
 RT enterotoxin B at 1.5-A resolution: implications for superantigen
 RT recognition by MHC class II molecules and T-cell receptors.";
 RL J. MOL. BIOL. 277:61-79(1998).
 CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -!- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M1118; G153000; -
 CC PIR: A01815; ENSAB6.
 CC PIR: S27360; S27360.
 CC PDB: 1SEB; 20-JUN-96.
 CC PDB: 2SEB; 28-JAN-98.
 CC PDB: 3SEB; 27-MAY-98.
 CC PDB: 1SE3; 16-JUN-97.
 CC PDB: 1SE4; 15-OCT-97.
 CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 CC PFAM: PF01123; Staph_strep_toxin; 1.
 CC ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 266
 FT DISULFID 120 140
 FT CONFLICT 56 58
 FT CONFLICT 69 77
 FT CONFLICT 118 118
 FT CONFLICT 128 130
 FT CONFLICT 133 135
 FT CONFLICT 149 150
 FT CONFLICT 156 156
 FT CONFLICT 185 186
 FT CONFLICT 233 233
 FT CONFLICT 246 247
 FT SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
 SQ
 Query Match 100.0%; Score 74; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 8.34e-07;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 177 TNKKVTAQELD 188
 QY 1 TNKKVTAQELD 12
 RESULT 2
 ID SPEA_STRPY STANDARD; PRT; 251 AA.
 AC P08095;
 DT 01-AUG-1988 (REL. 08, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
 DE (SPE A).
 GN SPEA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 CC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 8616804.
 RA WEEKS C.R., FERRETTI J.J.;

"Nucleotide sequence of the type A streptococcal exotoxin
 (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 T12.";
 RT INFECT. IMMUN. 52:144-150(1986).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 86284313.
 RA JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.:
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 RT related to staphylococcus aureus enterotoxin B.";
 RL MOL. GEN. GENET. 203:354-356(1986).
 CC -!- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -!- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -!- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U0453; G1877430; -
 CC EMBL: X03929; G47442; -
 CC PIR: A26152; A26152.
 CC PIR: S29659; S29659.
 CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 CC PFAM: PF01123; Staph_strep_toxin; 1.
 CC HSP; P01552; 1SEB.
 DR TOXIN; SIGNAL.
 FT SIGNAL 1 30
 FT CHAIN 31 251
 FT CONFLICT 6 6
 FT CONFLICT 17 18
 FT CONFLICT 25 35
 FT CONFLICT 40 40
 FT CONFLICT 43 43
 FT CONFLICT 47 59
 FT CONFLICT 129 129
 FT CONFLICT 165 178
 FT SEQUENCE 251 AA; 29246 MW; 53FE465 CRC32;
 SQ
 Query Match 91.9%; Score 68; DB 1; Length 251;
 Best Local Similarity 91.7%; Pred. No. 4.14e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 165 TNKKVTAQELD 176
 QY 1 TNKKVTAQELD 12
 RESULT 3
 ID ETXA_STAUV STANDARD; PRT; 257 AA.
 AC P13163;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE A PRECURSOR (SEA).
 GN ENTA.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-FR1337;
 RX MEDLINE: 8808682.
 RA BETLEY M.J., MEKALANOS J.J.;
 PM "Nucleotide sequence of the type A staphylococcal enterotoxin gene";
 RL J. BACTERIOL. 170:34-41(1988).
 RN (2)
 RP SEQUENCE OF 25-257.
 RX MEDLINE: 87222293.
 RA HUANG I.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J.;
 RL "Complete amino acid sequence of staphylococcal enterotoxin A";
 RN J. BIOL. CHEM. 262:7006-7013(1987).
 RP [3]
 RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE: 95354648.
 RA SCHLIEVERT P.M., OHLENDORF D.H., SVENSSON L.A.;
 RL Crystal structure of the superantigen staphylococcal enterotoxin
 type A.";
 RN EMBO J. 14:3292-3301(1995).
 RP [4]
 RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RA SUNDBERG M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEN M.,
 RA ABRAHMSSEN L.;
 RL "The Co-crystal structure of staphylococcal enterotoxin type A with
 Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding";
 RN J. BIOL. CHEM. 271:32212-32216(1996).
 RP [5]
 RX 3D-STRUCTURE MODELLING.
 RA MEDLINE: 96022987.
 RA SWAMINATHAN S., FUREY M.F., JR., PLETCHER J., SAX M.;
 RL "Residues defining V beta specificity in staphylococcal
 enterotoxins";
 RN NAT. STRUCT. BIOL. 2:680-686(1995).
 RP [6]
 RX COMPARISON OF STRUCTURE OF SEA AND SECC.
 RA MEDLINE: 97334373.
 RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
 RL "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity";
 RN J. MOL. BIOL. 269:270-280(1997).
 RP [7]
 RX SUBUNIT: MONOMER.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M18970; G153121; -
 DR PIR: A28664; A28664.
 DR PIR: A29566; A29566.
 DR PDB: 1SEF; 1JUL-96.
 DR PDB: 1SEA; 15-OCT-95.
 DR PDB: 1SXT; 19-NOV-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
 KW SIGNAL
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN A.
 FT DISULFID 120 130
 FT METAL 25 25 ZINC.
 FT METAL 211 211 ZINC.

FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 2).
 SQ SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;
 Query Match 86.5%; Score 64; DB 1; Length 257;
 Best local Similarity 83.3%; Pred. No. 5,12e-04;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 169 TNKKVTQELD 180
 1111111111
 QY 1 TNKKVTQELD 12
 RESULT 4
 ID ETC1-STAU STANDARD; PRT; 266 AA.
 AC P01553;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).
 GN ETC1.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88038352.
 RA BOHACH G.A., SCHLIEVERT P.M.;
 RL "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
 relatedness to other pyrogenic toxins";
 RL MOL. GEN. GENET. 209:15-20(1987).
 RN (2)
 RP SEQUENCE OF 28-266.
 RX MEDLINE: 83213327.
 RA SCHMIDT J.J., SPERO L.;
 RL "The complete amino acid sequence of staphylococcal enterotoxin C1";
 RL J. BIOL. CHEM. 258:6300-6306(1983).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X05815; G46567; -
 DR PIR: A01816; ENSAC1.
 DR PIR: S06356; S06356.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 DR HSSP: P34071; 1SE2.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN C-1.
 FT DISULFID 120 137
 FT CONFLICT 177 177 D -> N (IN REF. 2).
 SQ SEQUENCE 266 AA; 30546 MW; FE00255A CRC32;
 Query Match 86.5%; Score 64; DB 1; Length 266;
 Best local Similarity 83.3%; Pred. No. 5,12e-04;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 176 TDKKVTQELD 187
 1111111111
 QY 1 TDKKVTQELD 12

RESULT 5
ID ETC3 STAU STANDARD: PRT: 266 AA.
AC P33313;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ENT3.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
LN STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90220508.
RA HOVDE C.J., HACKETT S.P., BOHACH G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene;
RT sequence comparison of all three type C staphylococcal
RT enterotoxins.";
RL MOL. GEN. GENET. 220:329-333(1990).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECP.
RA FIELDS B.A., MALCHIODI E.L., LI H., YSEBN X., STAUFFACHER C.V.,
RA SCHLIEVERT P.M., KARJALAINEN K., MARIUTZA R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen.";
RL NATURE 384:188-192(1996).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYOGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X51661; G46571; .
DR PIR: S11885; S11885.
DR PDB: 1JCK; 12-NOV-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph_Strep_Toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-3.
FT DISULFID 120 137 BY SIMILARITY
SQ SEQUENCE 266 AA; 30671 MW; 27B4DD0A CRC32;
Query Match 86.5%; Score 64; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 5.12e-04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 176 TDKSVTAQELD 187
OY 1 TNKKRYTAQELD 12

RESULT 6
ID ETC2 STAU STANDARD: PRT: 266 AA.
AC P34071;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ENT2.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
LN STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-66.
RX MEDLINE: 89277549.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxin C1 and C2.";
RL INFECT. IMMUN. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE: 96027099.
RA PAPAGEORGIOU A.C., ACHARYA K.R., SHAPIRO R., PASSALACQUA E.F.,
RA BREHM R.D., TRANTER H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT staphylococcus aureus reveals a zinc-binding site.";
RL STRUCTURE 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE: 96022987.
RA SWAMINATHAN S., FUREY W.F., JR., PLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL NAT. STRUCT. BIOL. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE: 97334373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity.";
RL J. MOL. BIOL. 269:270-280(1997).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYOGENIC EXOTOXINS ARE ALL RELATED.
CC -----
DR PIR: A60114; A60114.
DR PDB: 1STE; 23-DEC-96.
DR PDB: 1SE2; 08-MAR-96.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph_Strep_Toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; A115FD37 CRC32;
Query Match 86.5%; Score 64; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 5.12e-04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 176 TDKSVTAQELD 187
OY 1 TNKKRYTAQELD 12

RESULT 7
ID ETC2 STAU STANDARD: PRT: 258 AA.
AC P20723;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE D PRECURSOR (SED).
GN ENT2.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
LN STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89359112.

RA BAYLES K.W., IANDOLO J.J.:
 RT "Genetic and molecular analyses of the gene encoding staphylococcal
 RT enterotoxin D.";
 RL J. BACTERIOLOG. 171:4799-4806(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN-ATCC 23235;
 RX MEDLINE: 97157473.
 RA DOHSTEN M., ABRAMSEN L., ANTONSSON P., MEHNATE K., MOURAD W.,
 RT "The crystal structure of staphylococcal enterotoxin type D reveals
 RT Zn2+-mediated homodimerization.";
 RL EMBO J. 15:6832-6840(1996).
 CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M28521; G758691; -.
 DR PIR: A33953; A33953.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph-strep-toxin; 1.
 DR HSSP: P13163; 1SXT.
 DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
 FT SIGNAL 1 25
 FT CHAIN 26 258
 FT METAL 212 212
 FT METAL 250 250
 FT METAL 252 252
 FT VARIANT 114 114
 FT SEQUENCE 258 AA; 29746 MW; 2D1AA120 CRC32;
 SQ
 Query Match 83.8%; Score 62; DB 1; Length 258;
 Best Local Similarity 75.0%; Pred. No. 1.75e-03;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RA SWAMINATHAN S., FUREY W.F., JR., PLETCHER J., SAX M.:
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL NAT. STRUCT. BIOL. 2:680-686(1995).
 RN [2]
 RP -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M21319; G153002; -.
 DR PIR: A28179; A28179.
 DR PDB: 1SFE; 15-OCT-95.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph-strep-toxin; 1.
 DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 257
 FT SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;
 SQ
 Query Match 78.4%; Score 58; DB 1; Length 257;
 Best Local Similarity 75.0%; Pred. No. 1.92e-02;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/termsandconditions)
CC or send an email to license@ebi.ac.uk.
CC -----
DR EMBL; M76428; G408718; -.
DR EMBL; M76429; G408720; -.
DR PFAM; PF00326; Prol_1.Oligopep; 1.
DR PFAM; PF00930; DDPX_N.term; 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
FT DOMAIN 1 93 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT CARBOHD 171 171 POTENTIAL.
FT CARBOHD 402 402 POTENTIAL.
FT CARBOHD 469 469 POTENTIAL.
FT CARBOHD 533 533 POTENTIAL.
FT CARBOHD 564 564 POTENTIAL.
FT CARBOHD 811 811 POTENTIAL.
FT VARSPLIC 1 79 POTENTIAL.
SQ SEQUENCE 863 AA; 96556 MW; 8DA40472 CRC32;
MSTAQAPAAAPRERGGGAGGRPRFYQARSDDED ->
MTAKEPNASGSVYOQEQ (IN DPPX-S).
SO FT
FT FT
FT FT
Query Match 68.9%; Score 51.; DB 1; Length 863;
Best Local Similarity 54.5%; Pred. No. 9,93e-01;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
DB 124 SOKKRVEDL 134
OY : ||||| ::|
1 TNRKKVTNQL 11
RESULT 11
ID ID DP66 HUMAN STANDARD; PRT; 865 AA.
AC PA2658;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
GN DPP6.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HIPPOCAMPUS;
RA MEDLINE; 93372805.
RX YOKOTANI N., DOI K., WENTHOLD R.J., WADA K.;
RT "Non-conservation of a catalytic residue in a dipeptidyl
RT aminopeptidase IV-related protein encoded by a gene on human
RT chromosome 7.";
RL HUM. MOL. GENET. 2:1037-1039(1993).
CC -I- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
CC FUNCTION. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -I- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
CC -I- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM
CC (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE
CC SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
CC -----
CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.EBI.AC.UK/TERMSANDCONDITIONS)
CC OR SEND AN EMAIL TO LICENSE@EBI.AC.UK.
```



```

RT subtlis chromosome containing the replication origin."
RL DNA RES. 1:1-14(1994).
CC -1- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
CC (BY SIMILARITY).
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
CC METALLOPROTEASE).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D26185; G467458; -
CC DR EMBL: 299104; E1182002; -
CC DR SUBTLIST: BG10132; FTSH.
CC DR PROSITE: PS00674; AAA; 1.
CC PRAM: PF00004; AAA; 1.
CC KW CELL DIVISION; ATP-BINDING; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE;
CC ZINC.
CC FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 8 28 POTENTIAL.
CC FT DOMAIN 29 109 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 110 130 POTENTIAL.
CC FT DOMAIN 131 637 CYTOPLASMIC (POTENTIAL).
CC FT NE_BIND 139 146 ATP (POTENTIAL).
CC FT METAL 423 423 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT ACT SITE 424 424 BY SIMILARITY.
CC FT METAL 427 427 ZINC (CATALYTIC) (BY SIMILARITY).
CC SQ SEQUENCE 637 AA; 70937 MW; 08C92C38 CRC32;

Query Match 64.9%: Score 48; DB 1; Length 637;
Best Local Similarity 54.5%: Pred. No. 4.84e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 385 NKKKIDARDID 395
OY 2 NKKKVTAEELD 12

RESULT 15
ID VIT_BOMMO STANDARD; PRT; 1782 AA.
AC 027309;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE VITELLOGENIN PRECURSOR [CONTAINS: VITELLIN LIGHT CHAIN (VL); VITELLIN
DE HEAVY CHAIN (VH)].
GN VG.
OS BOMBYX MORI (SILK MOTH).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; LEPIDOPTERA; BOMBYCOIDEA; BOMBYCIDAE; BOMBYX.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-25 AND 367-380.
RC STRAIN-KINSHU X SHOMA; TISSUE=FAT BODY;
RX MEDLINE: 94250682.
RA YANO K.-I., SAKURAI M.T., MATSUE S., IZUMI S., TOMINO S.;
RT "Structure and expression of mRNA for vitellogenin in Bombyx mori.";
RL BIOCHIM. BIOPHYS. ACTA 1218:1-10(1994).
CC -1- FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF
CC NUTRIENTS DURING EMBRYONIC DEVELOPMENT.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE FEMALE FAT BODY ON DAY-
CC 2 OF SPINNING STAGE, REACHING MAXIMAL LEVELS AT LARVAL-PUPAL.
CC ECDYSIS AND DECLINING THEREAFTER. NOT FOUND IN THE MALE TISSUES.
CC -1- INDUCTION: BY ECDYSTEROID AND JUVENILE HORMONE.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO HEAVY AND TWO LIGHT CHAINS.
CC -1- TISSUE SPECIFICITY: PRODUCED BY THE FAT BODY, WHERE IT IS CLEAVED
CC BEFORE BEING SECRETED INTO HEMOLYMPH. SEQUESTERED THEN BY A SINGLE

```

```

CC CLASS OF RECEPTOR MEDIATED ENDOCYTOSIS IN THE OVARY.
CC -1- PTM: GLYCOSYLATED AND PHOSPHORYLATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13160; G217296; -
CC DR EMBL: D30733; G871834; -
CC DR EMBL: D30732; G871834; JOINED.
CC KW GLYCOPROTEIN; PHOSPHORYLATION; STORAGE PROTEIN; SIGNAL.
CC FT SIGNAL 1 15
CC FT CHAIN 16 1782 VITELLOGENIN.
CC FT CHAIN 16 370 VITELLIN LIGHT CHAIN.
CC FT CHAIN 16 366 VITELLIN HEAVY CHAIN (RARE).
CC FT CHAIN 371 1782 VITELLIN HEAVY CHAIN.
CC FT CHAIN 367 1782 VITELLIN HEAVY CHAIN (RARE).
CC FT DOMAIN 336 345 POLY-SER.
CC FT DOMAIN 385 395 POLY-SER.
CC FT CARBOHYD 569 569 POTENTIAL.
CC FT CARBOHYD 587 587 POTENTIAL.
CC FT CARBOHYD 1357 1357 POTENTIAL.
CC FT CARBOHYD 1463 1463 POTENTIAL.
CC FT CARBOHYD 1596 1596 POTENTIAL.
CC SQ SEQUENCE 1782 AA; 203053 MW; 6AEFCB1 CRC32;

Query Match 64.9%: Score 48; DB 1; Length 1782;
Best Local Similarity 54.5%: Pred. No. 4.84e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1536 TTKKIDDD 1546
OY 1 TTKKVTAEELD 11

```

Search completed: Tue Aug 31 19:03:25 1999
Job time : 9 secs.

(a) (b) (c) (d) (e) (f)

CC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, AND MGAS500;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61556; G47292; -.
DR EMBL; X61557; G47320; -.
DR EMBL; X61560; G47288; -.
DR EMBL; X61555; G47310; -.
DR EMBL; X61558; G47332; -.
DR EMBL; X61559; G47284; -.
DR EMBL; X61554; G47328; -.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 81A0C2FE CRC32;

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 1.48e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKKMTA0E1D 168
QY 1 TNKKMTA0E1D 12
||||:|||||||

RESULT 3
ID 054779 PRELIMINARY; PRT; 236 AA.
AC 054779: 054613: 054736: 054740: 054741:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
KW STREPTOCOCCUS PYOGENES.
OS BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61569; G47314; -.
DR EMBL; X61572; G47334; -.
DR EMBL; X61568; G47290; -.
DR EMBL; X61570; G47316; -.
DR EMBL; X61571; G47324; -.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; E902D6D CRC32;

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 1.48e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKKMTA0E1D 168
QY 1 TNKKMTA0E1D 12
||||:|||||||

RESULT 4
ID 057453 PRELIMINARY; PRT; 236 AA.
AC 057453:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
KW STREPTOCOCCUS PYOGENES.
OS BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS496;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61562; G47300; -.
DR EMBL; X61563; G47302; -.
DR EMBL; X61567; G47326; -.
DR EMBL; X61564; G47298; -.
DR EMBL; X61564; G47306; -.
DR EMBL; X61565; G47312; -.
DR EMBL; X61566; G47318; -.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; A5B1EED CRC32;

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 1.48e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKKMTA0E1D 168
QY 1 TNKKMTA0E1D 12
||||:|||||||

RESULT 5
ID 054696 PRELIMINARY; PRT; 236 AA.
AC 054696:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
KW STREPTOCOCCUS PYOGENES.
OS BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. EXP. MED. 174:1271-1274(1991).

DR EMBL: X61573; G47304; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27575 MW; A799A5F3 CRC32;
Query Match 86.5%; Score 64; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 157 TSKKVTAEELD 168
QY 1 TNKKKVTAEELD 12
RESULT 6
ID 006531 PRELIMINARY; PRT; 239 AA.
AC 006531;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=4446;
RC MEDLINE; 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
PYROGENIC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC EMBL: L13374; G295141; -
DR PFAM: PF01123; Staph_Strep_toxin; 1.
DR ENTEROTOXIN; TOXIN; SUPERANTIGEN.
KW NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; 52B18853 CRC32;
Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 149 TDKRSVTAQELD 160
QY 1 TNKKKVTAEELD 12
RESULT 7
ID 005157 PRELIMINARY; PRT; 239 AA.
AC 005157;
DT 01-JUL-1997 (TREMBREL. 04, CREATED)
DT 01-JUL-1997 (TREMBREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE TYPE C ENTEROTOXIN (FRAGMENT).
OS STAPHYLOCOCCUS INTERMEDIUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA EDWARDS V.M., DERINGER J.R., CALLANTINE S.D., DEOBALD C.F.,
BERGER P.H., KAPOR V., STAUFACHER C.V., BOHACH G.A.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U91526; G1906052; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 239 AA; 27536 MW; 390EB227 CRC32;
Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 149 TDKRSVTAQELD 160
QY 1 TNKKKVTAEELD 12
RESULT 8
ID 053678 PRELIMINARY; PRT; 239 AA.
AC 053678;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
DR EMBL: L13376; G295145; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN.
KW NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; 0810BB9D CRC32;
Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 149 TDKRSVTAQELD 160
QY 1 TNKKKVTAEELD 12
RESULT 9
ID 006535 PRELIMINARY; PRT; 239 AA.
AC 006535;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRI 909;
RC MEDLINE; 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
PYROGENIC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC EMBL: L13377; G295147; -

MUSSER J.M., R.R.
superantigen SSA allelic
transfer of ssa within

Query Local 101
 Best Matches
 172 INK
 1/2 01, CREATED
 1/2 01, LAST SEQUENCE UPDATE
 1 REL. 08, LAST ANNOTATION UPDATE
 DP
 QN

DM N.A.

4222556. LAMPHEAR J.G., MUSSEK J.M.
MOLLIK J.A.,

Characterization and phylogenetic distribution of *Streptococcus pyogenes*.

ccal superantigen gene (S

565; G476764; -
strp toxin; 1.

1123; Step_out= GEN. 30797 MW: FE391C2B CRC32:

| AA | Score | DB | Length |
|-----|-------|----|--------|
| 260 | 63 | 2 | 260 |

| Similarity | Pred. No. | Indels | Gaps |
|------------|-----------|--------|------|
| 85.18% | 2,906 | 0 | 0 |
| 83.38% | 2 | 2 | 0 |
| 0.00% | 0 | 0 | 0 |

10; Conservative

183 KONTVOELD

KKKVTAELO 12

260 AA
ppm:

PRELIMINARY;

| | 01, | CREATED, |
|------------------|-----|-------------------------|
| 1996 (TREMBLREL. | 01, | LAST SEQUENCE UPDATE) |
| 1996 (TREMBLREL. | 01, | LAST ANNOTATION UPDATE) |

-1998 (TREMBLREL.
-1998

STREPTOCOCCACEAE

OCOCOCUS PROGEN-
IA; FIRMICUTES; B

COCCUS.

----- I G. MUSSER J.M.

NAME: 942222556. LAMPHEAR O.C.,
K.B. KAPUR V., MOLLICK J.A.,
distribution of the

characterization and ph

superantigen gene
62.1867-1874(1994) -
TMUN

| | | |
|----|-----|---|
| RN | [2] | SEQUENCE FROM N.A. |
| RP | | STRAIN-MGAS 1842; |
| RC | | STR-96178602. |
| | | MUSSEY J.M., R.R.; |
| | | LAMPHEAR J.G., MOUNTAINVIEW SSA allelic |

RA MEDLINE, KAPUR V., GOEL D., for horizontal transfer of ssa within

"phylogenetic evidence for the
variants provides evidence."
RT RT (1996)

```

RT      Streptococcus 64:1161-1165(1950).
INFECT. IMMUN. 64:1161-1165(1950).
RL      INFECT. IMMUN. 64:1161-1165(1950).

```

```
DR      048753;  stap_strip-toxin;  3069EAB4 CRC32;  
DR      PF01123;  EF01123;  29836 MW;  3069EAB4 CRC32;  
PEAM:   29836 AA;  29836 MW;  3069EAB4 CRC32;
```

| SEQUENCE | 200 | DB 2; | Length 200; | Gaps |
|----------|-----------|-------|-------------|--------|
| 85.18; | score 63; | DB 2; | Length 200; | Gaps 0 |
| 85.18; | score 63; | DB 2; | Length 200; | Gaps 0 |

```

Query Match      83.38;      Pred. No. 2;      Index
Query Similarity 0;          Mismatches 2;
Best Local Similarity
Best Local Conservative

```

10; Conserve
Matches

Db 172 T N K K O V T V Q E L D 103
| | | | | | | |
| | | | | | | |

1 TNNKKVTAQELD 12
QY

Completed: Tue Aug 31 19:04:41 1998

Search completed
Job time : 57 secs

THIS PAGE BLANK (USPTO)

M P E S E R E H
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:08:18 1999; Maspar time 3.50 Seconds
Tabular output not generated.

Title: >US-09-150-947-2
(1-12) from US09150947.pep
Description: 81
Perfect Score: 1 YNKKKATVQELD 12
Sequence: 1 YNKKKATVQELD 12

Scoring table:
PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.360; Variance 49.153; scale 0.353

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 81 | 100.0 | 12 34 | W64637 | Synthetic SEB peptide | 1.54e-02 |
| 2 | 81 | 100.0 | 13 34 | W64641 | Synthetic SEB peptide | 1.54e-02 |
| 3 | 81 | 100.0 | 13 34 | W64646 | Synthetic SEB peptide | 1.54e-02 |
| 4 | 81 | 100.0 | 14 34 | W64644 | Synthetic SEB peptide | 1.54e-02 |
| 5 | 81 | 100.0 | 14 34 | W64645 | Synthetic SEB peptide | 1.54e-02 |
| 6 | 81 | 100.0 | 24 34 | W64642 | Synthetic SEB peptide | 1.54e-02 |
| 7 | 81 | 100.0 | 35 34 | W64643 | Synthetic SEB peptide | 1.54e-02 |
| 8 | 64 | 79.0 | 10 34 | W64638 | Synthetic SEB peptide | 1.54e-02 |
| 9 | 59 | 72.8 | 28 19 | W04494 | Staphylococcal entero | 7.72e+00 |
| 10 | 59 | 72.8 | 36 35 | W72426 | Peptide #5 for reduci | 7.72e+00 |
| 11 | 59 | 72.8 | 38 36 | W72427 | Peptide #6 for reduci | 7.72e+00 |
| 12 | 59 | 72.8 | 91 27 | W24299 | Staphylococcus aureus | 7.72e+00 |
| 13 | 59 | 72.8 | 233 3 | R13203 | Staphylococcal entero | 7.72e+00 |
| 14 | 59 | 72.8 | 233 8 | R45011 | Staphylococcal entero | 7.72e+00 |
| 15 | 59 | 72.8 | 233 27 | W35373 | Staphylococcus entero | 7.72e+00 |
| 16 | 59 | 72.8 | 233 20 | W06738 | Staphylococcus entero | 7.72e+00 |

| | | | | | | |
|----|----|------|--------|--------|-----------------------|----------|
| 17 | 58 | 71.6 | 12 34 | W64636 | Synthetic SEB peptide | 1.01e+01 |
| 18 | 58 | 71.6 | 13 34 | W64640 | Synthetic SEB peptide | 1.01e+01 |
| 19 | 58 | 71.6 | 239 34 | W64647 | Synthetic SEB protein | 1.01e+01 |
| 20 | 58 | 71.6 | 239 8 | R45014 | Staphylococcal entero | 1.01e+01 |
| 21 | 58 | 71.6 | 239 3 | R13206 | Staphylococcal entero | 1.01e+01 |
| 22 | 58 | 71.6 | 255 20 | W06737 | Staphylococcal entero | 1.01e+01 |
| 23 | 57 | 70.4 | 228 3 | R13205 | Staphylococcal entero | 1.32e+01 |
| 24 | 57 | 70.4 | 228 8 | R45013 | Staphylococcal entero | 1.32e+01 |
| 25 | 54 | 66.7 | 24 36 | W72423 | Peptide #2 for reduci | 2.94e+01 |
| 26 | 54 | 66.7 | 28 36 | W72425 | Peptide #4 for reduci | 2.94e+01 |
| 27 | 53 | 65.4 | 10 34 | W64639 | Synthetic SEB peptide | 3.82e+01 |
| 28 | 53 | 65.4 | 230 3 | R13204 | Staphylococcal entero | 3.82e+01 |
| 29 | 53 | 65.4 | 230 8 | R45012 | Staphylococcal entero | 3.82e+01 |
| 30 | 53 | 65.4 | 245 27 | W53374 | Staphylococcus entero | 3.82e+01 |
| 31 | 53 | 65.4 | 245 27 | W53375 | Staphylococcus entero | 3.82e+01 |
| 32 | 52 | 64.2 | 221 3 | R13209 | Staphylococcus entero | 4.97e+01 |
| 33 | 52 | 64.2 | 221 8 | R45017 | Staphylococcal entero | 4.97e+01 |
| 34 | 52 | 64.2 | 250 24 | W12145 | Streptococcus pyogene | 4.97e+01 |
| 35 | 52 | 64.2 | 251 24 | W12147 | Streptococcus pyogene | 4.97e+01 |
| 36 | 52 | 64.2 | 251 24 | W12153 | Streptococcus pyogene | 4.97e+01 |
| 37 | 52 | 64.2 | 251 24 | W12097 | Streptococcus pyogene | 4.97e+01 |
| 38 | 52 | 64.2 | 251 33 | W59781 | Streptococcus pyogene | 4.97e+01 |
| 39 | 52 | 64.2 | 251 33 | W59780 | Amino acid sequence o | 4.97e+01 |
| 40 | 52 | 64.2 | 251 24 | W12151 | Streptococcus pyogene | 4.97e+01 |
| 41 | 52 | 64.2 | 251 24 | W12150 | Streptococcus pyogene | 4.97e+01 |
| 42 | 52 | 64.2 | 251 24 | W12152 | Streptococcus pyogene | 4.97e+01 |
| 43 | 52 | 64.2 | 251 24 | W12146 | Streptococcus pyogene | 4.97e+01 |
| 44 | 52 | 64.2 | 251 24 | W12149 | Streptococcus pyogene | 4.97e+01 |
| 45 | 52 | 64.2 | 401 36 | W22779 | Human sepiin-2 protol | 4.97e+01 |

ALIGNMENTS

RESULT 1
ID W64637 standard: peptide: 12 AA.
AC W64637:

DE 23-OCT-1998 (first entry)
KW Synthetic SEB peptide p12(151-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-11938.
PA (YISS) YISSUM RES. & DEV CO.
PI Atad G, Kaempfer R.
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)

PS Claim 8: Page 41: 68pp: English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PERT or by a mixture of PERTs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PERTs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PERT.
SQ Sequence 12 AA:

Query Match 100.0%; Score 81; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ynkktatvqeld 12

```

Oy      1 YNKKRATVOELD 12
      |||||||
RESULT  2
ID      W64641 standard; peptide: 13 AA.
AC      W64641;
DE      23-OCT-1998 (first entry)
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
FH      Staphylococcus aureus.
FT      Key
        Modified_site 1 Location/Qualifiers
        /note="N-terminal Tyr modified by presence of
        N-lauryl-cysteyl"
PN      WO9829444-A1.
PD      09-JUL-1998.
PE      30-DEC-1997: IL0438.
PR      30-DEC-1996: IL-119938.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
DR      WPI; 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 16; Page 41; 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PET or by a mixture of PETs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PETs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PET. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PET.
        Sequence 13 AA.
SQ
Query Match      100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 ynkktatvgeld 13
      |||||||
Oy      1 YNKKRATVOELD 12
      |||||||
RESULT  3
ID      W64646 standard; peptide: 13 AA.
AC      W64646;
DE      23-OCT-1998 (first entry)
KW      Synthetic SEB peptide AC-p12(150-161).
        Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
FH      Staphylococcus aureus.
FT      Key
        Modified_site 1 Location/Qualifiers
        /note="N-terminal Tyr modified by N-acetyl group"
        /note="D-form residue"
PN      WO9829444-A1.
PD      09-JUL-1998.
PE      30-DEC-1997: IL0438.
PR      30-DEC-1996: IL-119938.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;

```

```

DR      WPI; 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 24; Page 41; 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PET or by a mixture of PETs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PETs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PET. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PET.
        Sequence 13 AA.
SQ
Query Match      100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 ynkktatvgeld 12
      |||||||
Oy      1 YNKKRATVOELD 12
      |||||||
RESULT  4
ID      W64644 standard; peptide: 14 AA.
AC      W64644;
DE      23-OCT-1998 (first entry)
KW      Synthetic SEB peptide Cys-p12(150-161).
        Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
FH      Staphylococcus aureus.
FT      Key
        Modified_site 1 Location/Qualifiers
        /note="N-terminal Tyr modified by N-acetyl group"
        /note="D-form residue"
PN      WO9829444-A1.
PD      09-JUL-1998.
PE      30-DEC-1997: IL0438.
PR      30-DEC-1996: IL-119938.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
DR      WPI; 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 21; Page 41; 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PET or by a mixture of PETs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PETs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PET. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PET.
        Sequence 14 AA.
SQ
Query Match      100.0%; Score 81; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 ynkktatvgeld 13
      |||||||
Oy      1 YNKKRATVOELD 12
      |||||||
RESULT  5

```


ID W64645 standard; peptide: 14 AA.
AC W64645;
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide D-Ala.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
FH Key
FT Misc_difference 1 Location/Qualifiers
FT Misc_difference 1 /note= "D-form residue"
FT Matches 12; Conservative 14 /note= "D-form residue"
PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 23; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 14 AA.

Query Match 100.0%; Score 81; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ynkkratvgeld 13
|||
Qy 1 YNKKRATVQELD 12

RESULT 6
ID W64642 standard; peptide: 24 AA.
AC W64642;
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide dimer.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 18; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 24 AA.

Query Match 100.0%; Score 81; DB 34; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ynkkratvgeld 12
|||
Qy 1 YNKKRATVQELD 12

RESULT 7
ID W64643 standard; peptide: 35 AA.
AC W64643;
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide trimer.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 19; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 35 AA.

Query Match 100.0%; Score 81; DB 34; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ynkkratvgeld 12
|||
Qy 1 YNKKRATVQELD 12

RESULT 8
ID W64638 standard; peptide: 10 AA.
AC W64638;
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide SEB(152-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.

PN W09829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PK 30-DEC-1996; IL-119938.
 PK (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention of
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 10; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 10 AA;

Query Match 79.0%; Score 64; DB 34; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.96e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KKATVGEID 10
 |||||
 OY 3 NKKATVGEID 12

RESULT 9
 ID W04494 standard; peptide: 28 AA.
 AC W04494;
 DE 10-DEC-1996 (first entry)
 DE Staphylococcal enterotoxin A residues 146-173, T-cell agonist.
 KW Staphylococcal enterotoxin A; agonist; T-cell proliferation;
 KW treatment; immunodeficiency; autoimmune disease; TNF-alpha;
 KW tumour necrosis factor alpha.
 OS Staphylococcus spp.
 PN US5545716-A.
 PD 13-AUG-1996.
 PF 08-SEP-1992; 941497.
 PR 08-SEP-1992; US-941497.
 PR 29-MAR-1994; US-220378.
 PA (UYFL) UNIV FLORIDA.
 PI Griggs ND, Johnson HM, Pontzer CH;
 DR WPI: 96-383718/38.
 PT Peptide fragments of Staphylococcal enterotoxin A (SEA) - useful as
 PT SEA agonists for stimulating T-cell proliferation, e.g. in treatment
 PT of immunodeficiency and autoimmune diseases
 PS Example 1: Columns 15-16; 17pp; English.
 CC The present peptide, comprising residues 146-173 of Staphylococcal
 CC enterotoxin A (SEA), is useful as an SEA agonist for stimulating
 CC T-cell proliferation, e.g. in the treatment of immunodeficiency and
 CC autoimmune diseases. Supernatant from PBMC stimulated with
 CC 100 microm of the peptide for 18 hrs., was collected and assayed
 CC for TNF-alpha activity by cytotoxicity on L-929 cells. The result
 CC given as units/ml of TNF-alpha activity was 1.85, compared to 24.1
 CC for the most effective agonist, comprising SEA residues 121-149.
 SQ Sequence 28 AA;

Query Match 72.8%; Score 59; DB 19; Length 28;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 nknvtvgeid 11
 |||: |||||
 OY 2 NKKATVGEID 12

RESULT 10
 ID W72426 standard; peptide: 36 AA.
 AC W72426;
 DE 22-DEC-1998 (first entry)
 DE Peptide #5 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PF 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX17X2X34X5N #1,
 CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SE or SEA, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit biogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 SQ Sequence 36 AA;

Query Match 72.8%; Score 59; DB 36; Length 36;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 12 nknvtvgeid 22
 |||: |||||
 OY 2 NKKATVGEID 12

RESULT 11
 ID W72427 standard; peptide: 38 AA.
 AC W72427;
 DE 22-DEC-1998 (first entry)
 DE Peptide #6 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PF 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC where consensus sequence #1 and #2 are: X25X26GXIYX23X4X5N #1,
 CC KX6X7X8X9X10X11X12X13DX14X15X16X17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.

CC Sequence 38 AA;

Query Match 72.8%; Score 59; DB 36; Length 38;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvteqeld 22
 |||: |||||

QY 2 NKKKATVQELD 12

RESULT 12
 ID W24299 standard; Protein: 91 AA.

AC W24299;
 DT 14-APR-1998 (first entry)

DE Staphylococcus aureus Gene #5 polypeptide sequence 2.

KM Staphylococcus aureus MCHH 29; antagonist; antibacterial; immunogen;

KW vaccine; disease; protection; isolation.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT MISC-difference 29 /note= "Unspecified amino acid"

PN MO9731114-A2.

PD 28-AUG-1997; G00524.

PF 23-FEB-1997; G00524.

PR 26-FEB-1996; GB-004045.

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Hodgson JE;

DR WPI: 97-435166/40.

DR N-PSDB; V01865.

PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for

PS Isolating antagonist of the polypeptide(s) useful as anti-bacterials

CC Claim 11: Page 33; 117pp; English.

CC The present sequence represents a novel polypeptide, which is optionally

CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding

CC it, are derived from Staphylococcus aureus. Cells expressing ligands

CC binding the polypeptide can be used to isolated candidate compounds

CC that bind and inhibit the activity of the polypeptide. Such compounds

CC can be used as anti-bacterial compounds. The polypeptide may also be

CC used as an immunogen to vaccinate an animal for protection against

CC Staphylococcus aureus caused disease.

CC Sequence 91 AA;

Query Match 72.8%; Score 59; DB 27; Length 91;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 40 nkknvteqeld 50
 |||: |||||

QY 2 NKKKATVQELD 12

RESULT 13
 ID R13203 standard; Protein: 233 AA.

AC R13203;
 DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin A.
 KM SEA; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.

PN MO9110680-A.

PD 25-JUL-1991.

PF 17-JAN-1991; U00342.

PR 17-JAN-1990; US-466577.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI: 91-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -

PS administered by IV injection, having same tumoricidal activity

CC as Staphylococcal protein A without potential toxic reactions

CC Disclosure; Fig 1; 74pp; English.

CC SEA was isolated and purified from S. aureus. It can be used for

CC treating cancer, activating cytokine mediators and procoagulant

CC systems, augmenting natural killer cell cytotoxicity, etc. The

CC enterotoxin can be administered intravenously, optionally with

CC ibuprofen to attenuate toxic reaction to SEA. Synthetic

CC polypeptides having structural homology to Staphylococcal exotoxins

CC are claimed, provided the homology includes statistically

CC significant sequence homology, alignment of Cysteine residues and

CC similar hydrophathy profiles.

CC See also R13204-R13211.

CC Sequence 233 AA;

Query Match 72.8%; Score 59; DB 3; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvteqeld 156
 |||: |||||

QY 2 NKKKATVQELD 12

RESULT 14
 ID R45011 standard; Protein: 233 AA.

AC R45011;

DT 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SEA.

KM Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;

OS autoimmune disease; toxicity; Protein A; perfusion system.

FH Key Location/Qualifiers

FT MISC-difference 49 /note= "Given in the specification as O, no further

PN details given"

PD WO9324136-A.

PF 09-DEC-1993.

PR 01-JUN-1993; U05213.

CC 01-JUN-1992; US-891718.

CC (STON/) STONE J L.

CC (TERM/) TERMAN D S.

CC Stone JL, Terman DS;

CC WPI: 93-405418/50.

CC Use of staphylococcal enterotoxin(s) and homologues - for

CC treating cancer in a patient or for the treatment of auto-immune

CC diseases

CC Disclosure; Fig 1; 90pp; English.

CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)

CC which may be used in the methods of the invention for treating cancer

CC in a patient. These SEs, and homologues of them, can be used as

CC tumouricidal agents for treating cancers and autoimmune disease

CC They exhibit tumouricidal activity and toxicity identical to that

CC observed for the Protein A perfusion system. They may be administered

CC by i.v. injection.

CC Sequence 233 AA;

Query Match 72.8%; Score 59; DB 8; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvteqeld 156
 |||: |||||

QY 2 NKKKATVQELD 12

RESULT 15

ID W35373 standard: peptide; 233 AA.
 AC W35373;
 DT 20-APR-1998 (first entry)
 DE Staphylococcus enterotoxin SEA wild-type superantigen.
 KM SEI: SEA; Staphylococcus enterotoxin; superantigen; conjugate;
 KW treatment: cancer; infection; autoimmune disease; antibody.
 OS Staphylococcus sp.
 PN W09736932-A1.
 PD 09-OCT-1997.
 PF 26-MAR-1997; SE0537.
 PR 12-AUG-1996: US-695692.
 PR 29-MAR-1996: SE-001245.
 PA (PHAA) PHARMACIA & UPJOHN AB.
 PI Aarhaugen L, Antonsson P, Bjoerk P, Dohlsten M,
 Forsberg G, Hansson J, Kalland T;
 DR WPI; 97-503052/46.
 PT Conjugate of target seeking moiety and modified superantigen -
 PT useful for activating the immune system to treat cancer, viral
 PT infections, parasitic infestations and autoimmune diseases
 PS Claim 8; Pages 36-37; 58pp; English.
 CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
 CC SEA superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to
 CC T cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 SU Sequence 233 AA;

Query Match 72.8%; Score 59; DB 27; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 146 nkknvtvgeld 156
 |||: |||||
 QY 2 NKKKATVQELD 12

Search completed: Tue Aug 31 19:08:35 1999
 Job time : 17 secs.

(74)

```
##experimental_source strain FR1337
SUMMARY #length 257 #molecular-weight 29669 #checksum 2543

Query Match 72.8%; Score 59; DB 2; Length 257;
Best Local Similarity 81.8%; Pred. No. 2.55e-01;
Matches 9; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

Db 170 NKKNTVQELD 180
|||:|||||
QY 2 NKKKATVQELD 12

RESULT 3
ENTRY #type complete
TITLE sporulation protein - Clostridium acetobutylicum
ORGANISM #formal_name Clostridium acetobutylicum
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
09-Sep-1997
ACCESSIONS S27530
REFERENCE S27530
#authors Reid, S.J.; Hancock, K.; Santangelo, J.D.; Woods, D.R.
#submitted to the EMBL Data Library, March 1992
#description Cloning and sequencing of a spoIID gene from Clostridium
acetobutylicum.
#accession S27530
#status preliminary
#molecule_type DNA
##residues 1-362 #label REI
##cross-references EMBL:M87835; NID:g144914; PID:g144915
SUMMARY #length 362 #molecular-weight 40998 #checksum 3634

Query Match 72.8%; Score 59; DB 2; Length 362;
Best Local Similarity 58.3%; Pred. No. 2.55e-01;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKRDSVYELD 78
|||:|||||
QY 1 YNKKKATVQELD 12

RESULT 4
ENTRY #type complete
TITLE enterotoxin B precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change
11-Sep-1998
ACCESSIONS S27360; A92065; S27240; A01815
REFERENCE S27360
#authors Jones, C.L.; Khan, S.A.
#journal J. Bacteriol. (1986) 166:29-33
#title Nucleotide sequence of the enterotoxin B gene from
Staphylococcus aureus.
#accession S27360
#cross-references M01D:86168029
#molecule_type DNA
##residues 1-266 #label JON
##cross-references EMBL:M1118; NID:g152999; PID:g153000
REFERENCE A92065
#experimental_source strain S6
#journal Huang, I.Y.; Bergdoll, M.S.
#title J. Biol. Chem. (1970) 245:3518-3525
The primary structure of staphylococcal enterotoxin B. II.
The cyanogen bromide peptides of reduced and aminoethylated
enterotoxin B, and the complete amino acid sequence.
#cross-references M01D:71007902
#accession A92065
#molecule_type protein
##residues 28-55; 'NMD', '59-68', 'NE', '71', 'FDLIVL', '78-117', '119-127', 'N',
129, 'D', '131-132', 'ENT', '136-148', 'GN', '151-156', 'Y',
157-184, 'EO', '187-232', 'N', '234-245', 'ND', '248-266' #label
HUA
#experimental_source strain S-6
REFERENCE A92064
```

```
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3511-3517
#title The primary structure of staphylococcal enterotoxin B. II.
Isolation, composition, and sequence of chymotryptic
peptides.
#cross-references M01D:71007901
#contents annotation: chymotryptic peptides
REFERENCE A92063
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3493-3510
#title The primary structure of staphylococcal enterotoxin B. I.
Isolation, composition, and sequence of tryptic peptides
from oxidized entero-toxin B.
#cross-references M01D:71007900
#contents annotation: tryptic peptides
REFERENCE A90548
#authors Schantz, E.J.; Roessler, W.G.; Wegman, J.; Spero, L.;
Dunnehy, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin B.
#cross-references M01D:66035792
#contents annotation: biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.;
Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of
staphylococcal enterotoxin B.
#accession S27240
#molecule_type protein
##residues 28-42; 128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin; extracellular protein; toxin
FEATURE 1-27
28-266
120-140
SUMMARY #length 266 #molecular-weight 31436 #checksum 4249

Query Match 71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 4.14e-01;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 178 NKKRVTAQELD 188
|||:|||||
QY 2 NKKKATVQELD 12

RESULT 5
ENTRY #type complete
TITLE enterotoxin D precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
09-Sep-1997
ACCESSIONS A33953
REFERENCE A33953
#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of the gene encoding
staphylococcal enterotoxin D.
#cross-references M01D:89359112
#accession A33953
#status preliminary
#molecule_type DNA
##residues 1-258 #label BAY
##cross-references GB:M28521; NID:g1492109; PID:g758691
SUMMARY #length 258 #molecular-weight 29746 #checksum 39

Query Match 70.4%; Score 57; DB 2; Length 258;
Best Local Similarity 72.7%; Pred. No. 6.68e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

Db 171 DKRNVTQELD 181
:|:|:|:|:|:|
QY 2 NKKKATVQELD 12

RESULT 6
ENTRY A28179 #type complete
TITLE enterotoxin E precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Sep-1997

ACCESSIONS
REFERENCE A28179
#authors J. L.; Solitis, M.T.; Betley, M.J.
#journal J. Bacteriol. (1988) 170:2954-2960
#title Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
#cross-references MUID:88257005
#accession A28179
#molecule_type DNA
#residues 1-257 #label COU
SUMMARY #cross-references GB:M21319; NID:g153001; PID:g153002
#length 257 #molecular_weight 29358 #checksum 2562

Query Match 65.4%; Score 53; DB 2; Length 257;
Best Local Similarity 72.7%; Pred. No. 4.30e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 170 SKKEVTQELD 180
:|:|:|:|:|:|
QY 2 NKKKATVQELD 12

RESULT 7
ENTRY A40692 #type complete
TITLE signal recognition particle 72k chain - dog
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997

ACCESSIONS
REFERENCE A40692
#authors Lutcke, H.; Prehn, S.; Ashford, A.J.; Remus, M.; Frank, R.; Dobberstein, B.
#journal J. Cell Biol. (1993) 121:977-985
#title Assembly of the 68- and 72-kD proteins of signal recognition particle with 7S RNA.
#cross-references MUID:93273803
#accession A40692
#status preliminary
#molecule_type mRNA; protein
#residues 1-671 #label LUT
SUMMARY #cross-references EMBL:x67813; NID:g297767; PID:g297768
#note Sequence extracted from NCBI backbone (NCBIP:132901)
#length 671 #molecular_weight 74493 #checksum 6622

Query Match 65.4%; Score 53; DB 2; Length 671;
Best Local Similarity 33.3%; Pred. No. 4.30e+00;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 450 YGRKKAISDL 471
|:|:|:|:|:|:|
QY 1 YNKKATVQELD 12

RESULT 8
ENTRY S51473 #type complete
TITLE probable membrane protein YLR386w - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Nov-1997
ACCESSIONS S51473.

REFERENCE S51466
#authors Du, Z.
#submission submitted to the EMBL Data Library, December 1994
#description The sequence of S. cerevisiae cosmid L3502.
#accession S51473
#molecule_type DNA
#residues 1-880 #label DUZ
SUMMARY #cross-references EMBL:U019104; NID:g609423; PID:g609424; MIPS:YLR386w

GENETICS
#map_position 12R
KEYWORDS transmembrane protein
FEATURES
426-442
SUMMARY #domain transmembrane #status Predicted #label TMM
#length 880 #molecular_weight 99771 #checksum 5546

Query Match 65.4%; Score 53; DB 2; Length 880;
Best Local Similarity 50.0%; Pred. No. 4.30e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 14 YEKRAALELE 25
|:|:|:|:|:|:|
QY 1 YNKKATVQELD 12

RESULT 9
ENTRY I54383 #type complete
TITLE gene SBI.8/DXS423E protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 28-Feb-1997

ACCESSIONS
REFERENCE I54383
#authors Rocques, P.J.; Clark, J.; Ball, S.; Crew, J.; Gill, S.; Christodoulou, Z.; Borts, R.H.; Louis, E.J.; Davies, K.E.; Cooper, C.S.
#journal Hum. Mol. Genet. (1995) 4:243-249
#title The human SBI.8 gene (DXS423E) encodes a putative chromosome segregation protein conserved in lower eukaryotes and prokaryotes.
#cross-references MUID:95276737
#accession I54383
#status preliminary; translated from GB/EMBL/DBJ
SUMMARY #molecule_type mRNA
#residues 1-1233 #label RES
#cross-references GB:S78271; NID:g999379; PID:g999380

GENETICS
#length 1233 #molecular_weight 143204 #checksum 7067

Query Match 65.4%; Score 53; DB 2; Length 1233;
Best Local Similarity 41.7%; Pred. No. 4.30e+00;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKRRKGMDELE 337
|:|:|:|:|:|:|
QY 1 YNKKATVQELD 12

RESULT 10
ENTRY B69767 #type complete
TITLE conserved hypothetical protein yzcC - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998

ACCESSIONS
REFERENCE B69767
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertello, M.G.; Bessières, P.; Bolotin, A.; Borchert, S.; Bortiss, R.; Boursier, L.; Brans, A.; Braun, M.; Brigue, S.C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Conerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;

Erlich, S.D.; Emerson, P.T.; Ertan, K.D.; Ertugun, J.; Fabre, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Gusep, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kaahara, Y.; Klier-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Labber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle, D.; Porvillik, S.; Prescott, A.M.; Pressecan, E.; Pulic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serron, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassaret, A.; Viari, A.; Wambuit, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zanchin, A.

#journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
#cross-references MUID:98044033
#accession B69767
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-127 #label KUN
#cross-references GB:299105; GB:AL009126; NID:g2632457; PID:el182223;
#experimental_source strain 168

GENETICS
#gene yzcC
SUMMARY
#length 127 #molecular-weight 13950 #checksum 9937

Query Match 64.2%; Score 52; DB 2; Length 127;
Best Local Similarity 45.5%; Pred. No. 6.76e+00;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 107 FTKKQTVHDM 117
: ||| |||:
Qy 1 YNKKATVOEL 11

RESULT 11
ENTRY 549746 #type complete
TITLE Probable membrane protein YML033w - yeast (*Saccharomyces cerevisiae*)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 21-Nov-1997

ACCESSIONS
#residues 549746
#authors Badcock, K.; Churcher, C.
#submission submitted to the EMBL Data Library, November 1994
#accession S49746
#molecule_type DNA
#residues 1-146 #label BAD
#cross-references EMBL:246659; NID:g575680; PID:g575686; MIPS:YML033w

GENETICS
#map_position 13L
KEYWORDS Transmembrane protein
FEATURE
19-35 #domain transmembrane #status predicted #label TMW

SUMMARY
#length 146 #molecular-weight 17729 #checksum 5607

Query Match 64.2%; Score 52; DB 2; Length 146;
Best Local Similarity 54.5%; Pred. No. 6.76e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 40 YNKKARIEEL 50
: ||| |||:
Qy 1 YNKKATVOEL 11

RESULT 12
ENTRY 518786 #type fragment
TITLE exotoxin type A precursor (allele 2) - *Streptococcus pyogenes* (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage strain MGA5250 isolate California; strain MGA5251 isolate California; strain MGA5256 isolate California; strain MGA5285 isolate Colorado; strain MGA5480 isolate Yugoslavia; strain MGA5492 isolate United Kingdom; strain MGA5496 isolate Germany
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998

ACCESSIONS
#residues 518786
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in *Streptococcus pyogenes*.
#cross-references MUID:92044323
#accession 518786
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEU
#cross-references EMBL:X61561; NID:g47297; PID:g47298
#experimental_source strain MGA5250 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession 518787
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEA
#cross-references EMBL:X61562; NID:g47299; PID:g47300
#experimental_source strain MGA5251 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession 518788
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEZ
#cross-references EMBL:X61563; NID:g47301; PID:g47302
#experimental_source strain MGA5256 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession 518790
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEY
#cross-references EMBL:X61564; NID:g47305; PID:g47306
#experimental_source strain MGA5285 isolate Colorado unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession 518792
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEO
#cross-references EMBL:X61565; NID:g47311; PID:g47312
#experimental_source strain MGA5480 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18795
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61566; NID:947317; PID:947318
##experimental_source strain MGAS492 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18799
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NES
##cross-references EMBL:X61567; NID:947325; PID:947326
##experimental_source strain MGAS496 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
23-236 #domain signal sequence (fragment) #status predicted
#label sig
#product exotoxin type A (fragment) #status predicted
#label MAT

SUMMARY
#length 236 #checksum 1685

Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATVOELD 168
|||:| ||||
Qy 2 NKKKATVOELD 12

RESULT 13
ENTRY S18783
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS624 isolate Germany; strain MGAS495 isolate Germany 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998
DATE S18783; S18793; S18794; S18801; S18798
ACCESSIONS S18782
REFERENCE Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#authors J. Exp. Med. (1991) 174:1271-1274
#journal Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#title
#cross-references MUID:92044323
#accession S18783
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEU
##cross-references EMBL:X61568; NID:947289; PID:947290
##experimental_source strain MGAS158 isolate Nebraska unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18793
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61569; NID:947313; PID:947314
##experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18794
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEZ
##cross-references EMBL:X61570; NID:947315; PID:947316
##experimental_source strain MGAS491 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18801
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61571; NID:947323; PID:947324
##experimental_source strain MGAS624 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
23-236 #domain signal sequence (fragment) #status predicted
#label sig
#product exotoxin type A (fragment) #status predicted
#label MAT

SUMMARY
#length 236 #checksum 612

Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATVOELD 168
|||:| ||||
Qy 2 NKKKATVOELD 12

RESULT 14
ENTRY S29659
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes (fragment)
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage T12 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change 25-Mar-1998
DATE S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
ACCESSIONS S29659
REFERENCE Weeks, C.R.; Ferretti, J.J.
#authors Infect. Immun. (1986) 52:144-150
#journal Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#title
#cross-references MUID:86166804
#accession S29659
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-251 ##label WPE
##cross-references GB:U04453; EMBL:M19350; NID:91877426; PID:91877430
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323

```
#accession  S18782
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-244 ##label NE1
#cross-references EMBL:X61560; NID:q47287; PID:q47288
#experimental_source Streptococcus pyogenes strain MGAS156 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18784
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-244 ##label NEA
#cross-references EMBL:X61556; NID:q47291; PID:q47292
#experimental_source Streptococcus pyogenes strain MGAS165 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18785
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-244 ##label NE2
#cross-references EMBL:X61559; NID:q47293; PID:q47294
#experimental_source Streptococcus pyogenes strain MGAS167 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18791
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-244 ##label NEY
#cross-references EMBL:X61555; NID:q47309; PID:q47310
#experimental_source Streptococcus pyogenes strain MGAS327 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18796
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-244 ##label NEO
#cross-references EMBL:X61557; NID:q47319; PID:q47320
#experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18797
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-244 ##label NEH
#cross-references EMBL:X61558; NID:q47321; PID:q47322
#experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18800
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    9-228 ##label NES
#cross-references EMBL:X61554; NID:q47327; PID:q47328
#experimental_source Streptococcus pyogenes strain MGAS500 isolate New
              Zealand unassigned phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

GENETICS
#gene        speA1
CLASSIFICATION #superfamily enterotoxin B
FEATURE
1-30          #domain signal sequence #status predicted #label SIG
31-251        #product exotoxin type A #status predicted #label MAT
SUMMARY
length 251 #molecular-weight 29246 #checksum 1475

Query Match      64.2%; Score 52; DB 2; Length 251;
```

```
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Db      166 NKKMTVAQELD 176
      111 : 11111
Oy      2 NKKMTVAQELD 12

RESULT      15
ENTRY      558590 #type complete
TITLE      ribosomal protein S3 - maize chloroplast
ORGANISM   #formal_name chloroplast Zea mays #common_name maize
DATE       29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change
              17-Mar-1999
ACCESSIONS 558590
REFERENCE   558531
#authors    Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
#journal     J. Mol. Biol. (1995) 251:614-628
#title       Complete sequence of the maize chloroplast genome: gene
              content, hotspots of divergence and fine tuning of genetic
              information by transcript editing.
#cross-references MUID:9535841
#accession   S58590
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues    1-224 ##label MAI
#cross-references EMBL:X86563; NID:g902200; PID:g902260
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, April 1995

GENETICS
#gene        rps3
#gene        chloroplast
CLASSIFICATION #superfamily Escherichia coli ribosomal protein S3
KEYWORDS     chloroplast; protein biosynthesis; ribosome
SUMMARY      #length 224 #molecular-weight 25916 #checksum 3426

Query Match      63.0%; Score 51; DB 2; Length 224;
Best Local Similarity 50.0%; Pred. No. 1,05e+01;
Matches      5; Conservative      5; Mismatches      0; Indels      0; Gaps      0;

Db      93 KKGAIIELE 102
      111:::111
Oy      3 KKGATVQELD 12

Search completed: Tue Aug 31 19:08:01 1999
Job time : 22 secs.
```

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (C) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:06:16 1999; MasPar time 2.30 Seconds

Tabular output not generated. 147.506 Million cell updates/sec

Title: >US-09-150-947-2

Description: (1-12) from US09150947.pap

Perfect Score: 81

Sequence: 1 YNKKKATVQELD 12

Scoring table: PAM 150

Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot37

1:swissprot

Statistics: Mean 24.929; Variance 27.412; scale 0.909

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|------------------------------------|-----------|
| 1 | 59 | 72.8 | 257 | 1 | ETXA_STAAU ENTEROTOXIN TYPE A PRE | 4.80e-02 |
| 2 | 58 | 71.6 | 266 | 1 | ETXB_STAAU ENTEROTOXIN TYPE B PRE | 8.32e-02 |
| 3 | 57 | 70.4 | 258 | 1 | ETXD_STAAU ENTEROTOXIN TYPE D PRE | 1.43e-01 |
| 4 | 53 | 65.4 | 257 | 1 | ETXE_STAAU ENTEROTOXIN TYPE E PRE | 1.18e+00 |
| 5 | 53 | 65.4 | 670 | 1 | SR72_CANFA SIGNAL RECOGNITION PAR | 1.18e+00 |
| 6 | 52 | 64.2 | 146 | 1 | YMD3_YEAST HYPOHETICAL 17.7 KD P | 1.97e+00 |
| 7 | 52 | 64.2 | 251 | 1 | SPEA_STRPY EXOTOXIN TYPE A PRECUR | 1.97e+00 |
| 8 | 51 | 63.0 | 187 | 1 | YCF4_CAPPA HYPOHETICAL 21.2 KD P | 3.26e+00 |
| 9 | 51 | 63.0 | 224 | 1 | RR3_ORYSA CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 10 | 51 | 63.0 | 239 | 1 | RR3_MAIZE CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 11 | 51 | 63.0 | 412 | 1 | PT56_YEAST RIBOSE METHYLTRANSFERA | 3.26e+00 |
| 12 | 51 | 63.0 | 566 | 1 | LIGA_MOUSE LIGATIN (FRAGMENT). 2 S | 3.26e+00 |
| 13 | 51 | 63.0 | 3418 | 1 | BRC2_HUMAN BREAST CANCER TYPE 2 S | 5.36e+00 |
| 14 | 50 | 61.7 | 268 | 1 | NO20_MEDTR EARLY NODULIN 20 PRECU | 5.36e+00 |
| 15 | 50 | 61.7 | 274 | 1 | HEL_HABIN LIPOPROTEIN E PRECURSO | 5.36e+00 |
| 16 | 50 | 61.7 | 386 | 1 | YAMH_SCHPO HYPOHETICAL 44.5 KD P | 5.36e+00 |
| 17 | 50 | 61.7 | 1072 | 1 | HSEB_RAT HEAT-STABLE ENTEROTOXI | 5.36e+00 |
| 18 | 50 | 61.7 | 1223 | 1 | KPBL_HUMAN PHOSPHORILASE B KINASE | 5.36e+00 |
| 19 | 50 | 61.7 | 3685 | 1 | DMD_HUMAN DYSTROPHIN. | 5.36e+00 |
| 20 | 49 | 60.5 | 290 | 1 | YABG_BACSU HYPOHETICAL 33.3 KD P | 8.72e+00 |
| 21 | 49 | 60.5 | 455 | 1 | MAD_DROME MOTHERS AGAINST DPP PR | 8.72e+00 |
| 22 | 49 | 60.5 | 559 | 1 | KIEF2_XENLA KINESIN-LIKE PROTEIN K | 8.72e+00 |
| 23 | 49 | 60.5 | 670 | 1 | SR72_HUMAN SIGNAL RECOGNITION PAR | 8.72e+00 |

| RESULT ID | 1 | ETXA_STAAU | STANDARD: | PRT: | 257 AA. |
|-----------|---|------------|-----------|------|---------|
| AC | P13163: | | | | |
| DT | 01-JAN-1990 (REL. 13, CREATED) | | | | |
| DT | 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) | | | | |
| DT | 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN TYPE A PRECURSOR (SEA). | | | | |
| GN | ENTX. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | |
| CC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-FRI337. | | | | |
| RX | MEDLINE; 88068892. | | | | |
| RA | BETLEY M.J., MEKALANOS J.J.; | | | | |
| RT | "Nucleotide sequence of the type A staphylococcal enterotoxin gene.;" | | | | |
| RL | J. BACTERIOL. 170:34-41(1988). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 25-257. | | | | |
| RX | MEDLINE; 87222293. | | | | |
| RA | HUANG I.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J.; | | | | |
| RT | "Complete amino acid sequence of staphylococcal enterotoxin A.;" | | | | |
| RL | J. BIOL. CHEM. 262:7006-7013(1987). | | | | |
| RN | [3] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). | | | | |
| RX | MEDLINE; 95354648. | | | | |
| RA | SCHAD E.M., ZAITSEVA I., ZAITSEV V.N., DOHLSTEN M., KALLAND T., | | | | |
| RT | SCHLIEVERT P.M., OHENDORF D.H., SVENSSON L.A.; | | | | |
| RL | "Crystal structure of the superantigen staphylococcal enterotoxin type A.;" | | | | |
| EMBO | J. 14:3292-3301(1995). | | | | |
| RN | [4] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). | | | | |
| RX | MEDLINE; 97113025. | | | | |
| RA | SUNDSTROM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEN M., | | | | |
| RT | ABRAHMSSEN L.; | | | | |
| RT | "The Co-crystal structure of staphylococcal enterotoxin type A with zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.;" | | | | |
| RL | J. BIOL. CHEM. 271:32212-32216(1996). | | | | |
| RN | [5] | | | | |
| RP | 3D-STRUCTURE MODELING. | | | | |
| RX | MEDLINE; 96022987. | | | | |
| RA | SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.; | | | | |
| RT | "Residues defining V beta specificity in staphylococcal enterotoxins.;" | | | | |

ALIGNMENTS

| | | | | | | | |
|----|----|------|------|---|------------|------------------------|----------|
| 24 | 49 | 60.5 | 859 | 1 | DPP6_RAT | DIPETIDYL PEPTIDASE I | 8.72e+00 |
| 25 | 49 | 60.5 | 863 | 1 | DPP6_BOVIN | DIPETIDYL PEPTIDASE I | 8.72e+00 |
| 26 | 49 | 60.5 | 865 | 1 | DPP6_HUMAN | DIPETIDYL PEPTIDASE I | 8.72e+00 |
| 27 | 49 | 60.5 | 1164 | 1 | BAG_STRAG | IGA FC RECEPTOR PRECUR | 8.72e+00 |
| 28 | 49 | 60.5 | 3678 | 1 | DMD_MOUSE | DYSTROPHIN. | 8.72e+00 |
| 29 | 48 | 59.3 | 130 | 1 | VC67_BPPH5 | EARLY PROTEIN GP16.7. | 1.41e+01 |
| 30 | 48 | 59.3 | 261 | 1 | HCD2_MOUSE | 3-HYDROXYACYL-COA DEHY | 1.41e+01 |
| 31 | 48 | 59.3 | 266 | 1 | ETC1_STAAU | ENTEROTOXIN TYPE C-1 P | 1.41e+01 |
| 32 | 48 | 59.3 | 266 | 1 | ETC2_STAAU | ENTEROTOXIN TYPE C-2 P | 1.41e+01 |
| 33 | 48 | 59.3 | 266 | 1 | ETC3_STAAU | ENTEROTOXIN TYPE C-3 P | 1.41e+01 |
| 34 | 48 | 59.3 | 269 | 1 | YD54_SCHPO | HYPOHETICAL 31.2 KD P | 1.41e+01 |
| 35 | 48 | 59.3 | 293 | 1 | RL5_CAEL | PROBABLE 60S RIBOSOMAL | 1.41e+01 |
| 36 | 48 | 59.3 | 302 | 1 | CAN1_RABIT | CALPAIN 1, LARGE [CAT | 1.41e+01 |
| 37 | 48 | 59.3 | 330 | 1 | HBPA_ARATH | TRANSCRIPTION FACTOR H | 1.41e+01 |
| 38 | 48 | 59.3 | 332 | 1 | HBPA_WHEAT | TRANSCRIPTION FACTOR H | 1.41e+01 |
| 39 | 48 | 59.3 | 346 | 1 | VGLM_HSVJ | GLYCOPROTEIN M. | 1.41e+01 |
| 40 | 48 | 59.3 | 359 | 1 | TGAA_TOBAC | TGAGC-SEQUENCE SPECIFI | 1.41e+01 |
| 41 | 48 | 59.3 | 560 | 1 | G6P1_ARATH | GLUCOSE-6-PHOSPHATE IS | 1.41e+01 |
| 42 | 48 | 59.3 | 634 | 1 | DNK2_SYNPF | DNK PROTEIN 2 (HEAT S | 1.41e+01 |
| 43 | 47 | 58.0 | 383 | 1 | YAGN_RHISN | HYPOHETICAL 45.0 KD P | 2.26e+01 |
| 44 | 47 | 58.0 | 433 | 1 | PR12_CAEL | PROBABLE DNA PRIMASE L | 2.26e+01 |
| 45 | 47 | 58.0 | 556 | 1 | STR_BACSU | ARGINYL-TRNA SYNTHETAS | 2.26e+01 |

```

RL NAT. STRUCT. BIOL. 2:680-686(1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE: 97334373.
KA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. MOL. BIOL. 269:270-280(1997).
CC -1- SUBUNIT: MONOMER.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18970; G153121; -.
DR PIR: A28664; A28664.
DR PIR: A29566; A29566.
DR PDB: 1SEF; 1JUL-96.
DR PDB: 1SEA; 15-OCT-95.
DR PDB: 1SXT; 19-NOV-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
KM ENTEROTOXIN: TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
FT SIGNAL 1 24
FT CHAIN 25 257 ENTEROTOXIN A.
FT DISULFID 120 130
FT METAL 25 25 ZINC.
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT METAL 242 242 T -> S (IN REF. 2).
SQ SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;

Query Match 72.84; Score 59; DB 1; Length 257;
Best Local Similarity 81.88; Pred. No. 4.80e-02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 170 NKKKATVQELD 180
QY 2 NKKKATVQELD 12

RESULT 2
ID ETVB-STAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN ENTB.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 86168029.
KA JONES C.L., KHAN S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus."
RL J. BACTERIOL. 166:29-33(1986).
RN [2]
RX SEQUENCE OF 40-91 FROM N.A.

```

```

RX MEDLINE: 85298255.
RA RANELLI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.;
RT Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and staphylococcus aureus."
RL PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985).
RN [3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE: 71007902.
RA HUANG I.-Y., BERGDOLL M.S.;
RT "The primary structure of staphylococcal enterotoxin B. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence."
RL J. BIOL. CHEM. 245:3518-3525(1970).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP MEDLINE: 93063291.
RA SWAMINATHAN S., FUREY W.F., JR., PLETCHER J., SAX M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen."
RL NATURE 359:801-806(1992).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RP MEDLINE: 94203282.
RA JARETZKY T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G.,
RT CHI Y.I., STAUFACHER C., SPROMINGER J.L., WILEY D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen."
RL NATURE 368:711-718(1994).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RP MEDLINE: 98181012.
RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: Implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors."
RL J. MOL. BIOL. 277:61-79(1998).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M1118; G153000; -.
DR PIR: A01815; ENSAB6.
DR PIR: S27360; S27360.
DR PDB: 1SEB; 20-JUN-96.
DR PDB: 2SEB; 28-JAN-98.
DR PDB: 3SEB; 27-MAY-98.
DR PDB: 1SER3; 16-JUN-97.
DR PDB: 1SEA; 15-OCT-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
KM ENTEROTOXIN: TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN B.
FT DISULFID 120 140
FT METAL 56 58
FT METAL 69 77 DOFLYEDI -> NEFLDIYL (IN REF. 3).
FT METAL 118 118 MISSING (IN REF. 3).
FT METAL 128 128 DIN -> NID (IN REF. 3).
FT METAL 133 135 QTD -> ENT (IN REF. 3).
FT METAL 149 150 NG -> GN (IN REF. 3).
FT METAL 156 156 Y -> YY (IN REF. 3).
FT METAL 185 186 OE -> EO (IN REF. 3).
FT METAL 233 233 D -> N (IN REF. 3).
FT METAL 246 247 DN -> ND (IN REF. 3).

```

SQ SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
Query Match 71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 8.32e-02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 178 NKKKATVQELD 188
1111111111
QY 2 NKKKATVQELD 12

RESULT 3
ID ETXD_STAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE D PRECURSOR (SED).
GN ENTD.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89359112.
RA BAYLES K.W., IANDOLO J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";
RT J. BACTERIOL. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE: 97157473.
RA SUNDSTROM M., ABRAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W., DOHUSTEN M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn²⁺-mediated homodimerization.";
RT EMBO J. 15:6832-6840(1996).
CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M28521; G758691; -
DR PIR: A33953; A33953.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph_strep_toxin; 1.
KW HSP; P13163; ISXT.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 2D1AA120 CRC32;
Query Match 70.4%; Score 57; DB 1; Length 258;
Best Local Similarity 72.7%; Pred. No. 1.43e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 171 DKKNTVQELD 181
1111111111

QY 2 NKKKATVQELD 12

RESULT 4
ID ETXD_STAU STANDARD; PRT; 257 AA.
AC P12993;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN ENTE.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC STRAIN-MJB265;
RX MEDLINE: 88257005.
RA COUCH J.L., SOLTIS M.T., BETLEY M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.";
RT J. BACTERIOL. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELLING.
RX MEDLINE: 96022987.
RA SWAMINATHAN S., FUREY W.F. JR., FLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal enterotoxins.";
RT NAT. STRUCT. BIOL. 2:680-686(1995).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M21319; G153002; -
DR PIR: A28179; A28179.
DR PDB: 1SEB; 15-OCT-95.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph_strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 257 ENTEROTOXIN E.
SQ SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;
Query Match 65.4%; Score 53; DB 1; Length 257;
Best Local Similarity 72.7%; Pred. No. 1.18e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 170 SKKEVTVQELD 180
1111111111
QY 2 NKKKATVQELD 12

RESULT 5
ID SR72_CANFA STANDARD; PRT; 670 AA.
AC P33731;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).
GN SRP72.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.

RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE: 93273803.
 RA LUETTICH H., PREHN S., ASHFORD A.J., REMUS M., FRANK R.,
 RA DOBBERSTEIN B.,
 RT "Assembly of the 68- and 72-kD proteins of signal recognition
 RT particle with 7S RNA."
 RL J. CELL BIOL. 121:977-985(1993).
 CC -1- FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE
 CC IN TARGETING SECRETORY PROTEINS TO THE ROUGH ENDOPLASMIC
 CC RETICULUM MEMBRANE. SRP72 BINDS THE 7S RNA ONLY IN PRESENCE OF
 CC SRP68. THIS RIBONUCLEOPROTEIN COMPLEX MIGHT INTERACT DIRECTLY WITH
 CC THE DOCKING PROTEIN IN THE ER MEMBRANE AND POSSIBLY PARTICIPATE
 CC IN THE ELONGATION ARREST FUNCTION.
 CC -1- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE
 CC OF 300 NUCLEOTIDES AND SIX PROTEIN SUBUNITS: SRP72, SRP68, SRP54,
 CC SRP19, SRP14 AND SRP9.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- DOMAIN: THE C-TERMINAL IS ESSENTIAL FOR THE INTERACTION WITH THE
 CC SRP68/7S RNA COMPLEX.
 CC -1- SIMILARITY: BELONGS TO THE SRP72 FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X67813; G297768; -
 DR PIR: S32167; S32167;
 DR PIR: A40692; A40692.
 KM SIGNAL RECOGNITION PARTICLE; RIBONUCLEOPROTEIN.
 FT INIT_MET 0 0 PROBABLE.
 FT MOD_RES 1 1 BLOCKED.
 FT DOMAIN 551 560 POLY-LYS.
 FT DOMAIN 661 664 POLY-LYS.
 SQ SEQUENCE 670 AA; 74362 MW; 9CB38962 CRC32;
 SO
 Query Match 65.4%; Score 53; DB 1; Length 670;
 Best Local Similarity 33.3%; Pred. No. 1.18e+00;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Eb 459 YGRKKRAISIDE 470
 Oy 1 YNKKRAIVQELD 12
 RESULT 6
 ID YMD3 YEAST STANDARD; PRT; 146 AA.
 AC 003712;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 17.7 KD PROTEIN IN AMD1-RAD52 INTERGENIC REGION.
 GN YMD033W.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA BADCOCK K., CHURCHER C., BARRELL B.G., RAUNDREEM M.A., WALSH S.V.;
 RL SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST YDR4458C.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z46659; G575686; -
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 146 AA; 17729 MW; 9A378D91 CRC32;
 Query Match 64.2%; Score 52; DB 1; Length 146;
 Best Local Similarity 54.5%; Pred. No. 1.97e+00;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 40 YNKKRAIVQEL 50
 Oy 1 YNKKRAIVQEL 11
 RESULT 7
 ID SPEA_STREP STANDARD; PRT; 251 AA.
 AC P08095;
 DT 01-AUG-1988 (REL. 08, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
 DE (SPE A).
 GN SPEA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86166804.
 RA WEEKS C.R., FERRETTI J.J.;
 RT "Nucleotide sequence of the type A streptococcal exotoxin
 RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 RT t12."
 RL INFECT. IMMUN. 52:144-150(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86284313.
 RA JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 RT related to Staphylococcus aureus enterotoxin B."
 RL MOL. GEN. GENET. 203:354-356(1986).
 CC -1- DISEASE: THE STREPTOCOCCAL PYOGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U40453; G1877430; -
 DR EMBL: X03929; G47442; -
 DR PIR: A26152; A26152.
 DR PIR: S29659; S29659.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 DR HSSP: P01552; 1SEB.
 KW TOXIN; STGNAL.
 FT SIGNAL 1 30
 FT CHAIN 31 251
 FT CHAIN 6 6
 FT CONFLICT 17 18
 FT CONFLICT 25 35
 EXOTOXIN TYPE A.
 K -> E (IN REF. 2).
 VT -> MK (IN REF. 2).
 SOEVFAQDDPD -> LPKGICSTRPK (IN REF. 2).

```

FT CONFLICT 40 40 H -> Q (IN REF. 2).
FT CONFLICT 43 43 S -> N (IN REF. 2).
FT CONFLICT 47 59 NLOINFLYEGDP -> TFKIYIFPMAYTL (IN
FT CONFLICT 129 129 REF. 2).
FT CONFLICT 165 178 I -> L (IN REF. 2).
FT CONFLICT 165 178 TNKMTVAOELDYK -> QIKNGNCSRIXYT (IN
FT SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;
REF. 2).

Query Match
Best Local Similarity 64.2%; Score 52; DB 1; Length 251;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

155 NKMTVAOELD 176
111:11111
2 NKMTVAOELD 12

RESULT 8
ID YCF4-CYAPA STANDARD; PRT; 187 AA.
AC P48192;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 21.2 KD PROTEIN YCF4.
GN YCF4.
OS CYANOPHORA PARADOXA.
OC CYANELLE.
OC EUKARYOTA: GLAUCOCYSTOPHYCEAE: CYANOPHORACEAE: CYANOPHORA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LB555 / PRINGSHEIM;
RA STIREWALT V.L., MICHALOWSKI C.B., LUFFELHARDT W., BOHNET H.J.,
RA BRYANT D.A.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: BELONGS TO THE YCF4 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U30821; G1016091; -
CC DR MENDEL; 7950; CYAPA:ycf4.1.
CC CYANELLE: HYPOTHETICAL PROTEIN.
CC SEQUENCE 187 AA; 21207 MW; B5D7E756 CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 187;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

97 YNKKKGV 104
11111111
1 YNKKKATV 8

RESULT 9
ID R33-MAIZE STANDARD; PRT; 224 AA.
AC P06586;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ZEA MAYS (MAIZE).
OC CHLOROPLAST.
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;
OC POACEAE: ZEA.
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 87231045.
RA MCLAUGHLIN W.E., LARRINUA I.M.;
RT "The sequence of the maize plastid encoded rps3 locus.";
RL NUCLEIC ACIDS RES. 15:4689-4689(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95395841.
RA MAIER R.M., NECKERMANN K., IGLOI G.L., KOESSSEL H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. MOL. BIOL. 251:614-628(1995).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y00340; G12469; -
CC DR EMBL; M31336; G552741; -
CC DR EMBL; X86563; G902260; -
CC DR MAIZEDB; 66303; -
CC DR PROSITE; P500548; RIBOSOMAL_S3; 1.
CC DR PFAM; PF00189; S3_C; 1.
CC DR PFAM; PF00417; S3_N; 1.
CC DR MENDEL; 13473; ZEMA:rps3.1.
CC KW RIBOSOMAL PROTEIN: CHLOROPLAST.
CC SEQUENCE 224 AA; 25916 MW; 3ED95CFE CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 224;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;




93 KKKATVELE 102
11111111
3 KKKATVEELD 12


RESULT 10
ID R33-ORYZA STANDARD; PRT; 239 AA.
AC P12146;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ORYZA SATIVA (RICE).
OC CHLOROPLAST.
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;
OC POACEAE: ORYZA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA SUGIURA M.;
RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP COMPLETE GENOME.
RX MEDLINE: 89364698.
RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,
RA MORI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-Q.,
RA KANNO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct trna genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL MOL. GEN. GENET. 217:185-194(1989).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----

```


GN BRCA2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96172838.
 RA TAVTIGIAN S.V., ROMMENS J.M., COUCH F.J., NEUHAUSEN S., BELL R.,
 BERRY S., BOGDEN R., CHEN Q., DAVIS T., FRYE C., HATTEIR T.,
 JAMULAPATI S., JANECKI T., JIANG P., KEHRER R., SCHROEDER M.,
 SNYDER S., STRINGFELLOW M., STROUP C., SWEDLUND B., TENG D.,
 THOMAS A., TRAN T., WEAVER-FELDAUS J., WONG A., LEBLANC J.-F.,
 BELANGER C., TRANCHANT M., SAMSON C., DUMONT M.,
 MCARTHUR-MORRISON J., MCSMEENEY D., PENG Y., SHIZUYA H.,
 SLEPKE T., SIMON M.I., LABRIE F., SHATTUCK-EIDENS D., SKOLNICK M.,
 RA GOLDGAR D., WEBER B.L., SIMARD J., KAMB A.;
 RT "The complete BRCA2 gene and mutations in chromosome 13q-linked
 kindreds.";
 RL NAT. GENET. 12:333-337(1996).
 RN [2]
 RP VARIANTS ASN-372; ASP-991; SER-1147; MET-1915 AND CYS-2034.
 RX MEDLINE: 96241588.
 RA COUCH F.J., FARID L.M., DESHANO M.L., TAVTIGIAN S.V., CALZONE K.,
 RA CAMPEAU L., PENG Y., BOGDEN B., CHEN Q., NEUHAUSEN S.,
 RA SHATTUCK-EIDENS D., GODWIN A.K., DALY M., RADFORD D.M., SEDLACEK S.,
 RA ROMMENS J., SIMARD J., GARBER J., MERAJVER S., WEBER B.L.;
 RT "BRCA2 germline mutations in male breast cancer cases and breast
 cancer families.";
 RL NAT. GENET. 13:123-125(1996).
 RN [3]
 RP VARIANT GLU-3095.
 RX MEDLINE: 96225456.
 RA LANCASTER J.M., WOOSTER R., MANGION J., PHELAN C.M., COCHRAN C.,
 RA GUMBS C., SEAL S., BARFOOT R., COLLINS N., BIGNELL G., PAEL S.,
 RA HAMODI R., LARSSON C., WISEMAN R.W., BERCHUCK A., IGLEHART J.D.,
 RA MARKS J.R., ASHMORETH A., STRATTON M.R., FUTRELL P.A.;
 RT "BRCA2 mutations in primary breast and ovarian cancers.";
 RL NAT. GENET. 13:238-240(1996).
 RN [4]
 RP VARIANTS.
 RX MEDLINE: 96225457.
 RA TENG D.H.-F., BOGDEN R., MITCHELL J., BAUGMARD M., BELL R., BERRY S.,
 RA DAVIS T., HA P.C., KEHRER R., JAMULAPATI S., CHEN Q., OFERT K.,
 RA SKOLNICK M.H., TAVTIGIAN S.V., JHANNAR S., SWEDLUND B., WONG A.K.C.,
 RA KAMB A.;
 RT "Low incidence of BRCA2 mutations in breast carcinoma and other
 cancers.";
 RL NAT. GENET. 13:241-244(1996).
 RN [5]
 RP VARIANT ASN-2415.
 RX MEDLINE: 96225458.
 RA MIKI Y., KATAGIRI T., KASUMI F., YOSHIMOTO T., NAKAMURA Y.;
 RT "Mutation analysis in the BRCA2 gene in primary breast cancers.";
 RL NAT. GENET. 13:245-247(1996).
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS OF EXPRESSION IN BREAST AND
 THYMS, WITH SLIGHTLY LOWER LEVELS IN LUNG, OVARY, AND SPLEEN.
 CC -1- DISEASE: BREAST CANCER (BC) IS AN EXTREMELY COMMON MALIGNANCY,
 AFFECTING ONE IN EIGHT WOMEN DURING THEIR LIFETIME. A POSITIVE
 FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OF
 DEVELOPMENT OF THE DISEASE, AND THIS LINK IS STRIKING FOR EARLY-
 ONSET BREAST CANCER. MUTATIONS IN BRCA2 ARE THOUGHT TO BE
 RESPONSIBLE FOR SOME INHERITED BREAST CANCER. IT IS LINKED WITH
 MALE BREAST CANCER.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U43746; G1161384; -

DR MIM: 600185; -
 DR PRAM: PR00634; BRCA2.repeat; 8.
 KW DISEASE MUTATION: POLYMORPHISM: REPEAT.
 FT NE_BIND 262
 FT DOMAIN 1009 2082
 FT REPEAT 1009 1033
 FT REPEAT 1009 1033
 FT REPEAT 1219 1243
 FT REPEAT 1428 1452
 FT REPEAT 1524 1548
 FT REPEAT 1671 1695
 FT REPEAT 1844 1868
 FT REPEAT 1978 2002
 FT REPEAT 2058 2082
 FT REPEAT 75 75
 FT VARIANT 289 289
 FT VARIANT 355 355
 FT VARIANT 372 372
 FT VARIANT 630 630
 FT VARIANT 728 728
 FT VARIANT 991 991
 FT VARIANT 1147 1147
 FT VARIANT 1302 1302
 FT VARIANT 1529 1529
 FT VARIANT 1880 1880
 FT VARIANT 1915 1915
 FT VARIANT 2034 2034
 FT VARIANT 2274 2274
 FT VARIANT 2415 2415
 FT VARIANT 2421 2421
 FT VARIANT 3095 3095
 FT VARIANT 3103 3103
 FT VARIANT 3357 3357
 FT VARIANT 3412 3412
 SQ SEQUENCE 3418 AA; 384280 MW; F5785BCB CRC32;
 Query Match 63.0%; Score 51; DB 1; Length 3418;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Db 3159 FNKKMTVENID 3170
 QY 1 YNKKKATVQELD 12
 ID NO20_MEDTR STANDARD; PRT; 268 AA.
 AC P93329;
 DT 15-DEC-1998 (REL. 37, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE ENOD20.
 GN ENOD20.
 OS MEDICAGO TRUNCATULA (BARREL MEDIC).
 OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:
 OC EUPHYLLIPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. JEMALONG;
 RA GREENE E.A., ERARD M., DEDIEU A., BARKER D.G.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X99467; E258656; -
 KW NODULATION; SIGNAL.



| | |
|--|---|
| OC | SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE; |
| OC | SCHIZOSACCHAROMYCES. |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-972H- |
| RA | LIVE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.; |
| RL | SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBD DATA BANKS. |
| DR | EMBL; AL022305; E1285407; - |
| KM | HYPOTHETICAL PROTEIN. |
| SO | SEQUENCE 460 AA; 52670 MW; 835D7303 CRC32; |
| Query March 74.1%; Score 60; DB 3; length 460; | |
| Best Local Similarity 50.0%; Pred. No. 8.4e-02; | |
| Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0; | |
| Dd | 105 YKKRKGKIEELN 116 :: : :: : y 1 YNKRKATVQELD 12 |

| | | | | |
|-----------------------|---|------------------|-------------------------|---------------|
| RESULT | 3 | | | |
| ID | 045833 | PRELIMINARY: | PRT: | 362 AA. |
| AC | Q45833; | | | |
| DT | 01-NOV-1996 | (TREMBL.REL. 01, | CREATED) | |
| DT | 01-NOV-1996 | (TREMBL.REL. 01, | LAST SEQUENCE UPDATE) | |
| DT | 01-NOV-1996 | (TREMBL.REL. 01, | LAST ANNOTATION UPDATE) | |
| DE | SPOULATION | PROTEIN. | | |
| GN | SPOID. | | | |
| OS | CLOSTRIDIUM ACETOBUTYLICUM. | | | |
| BACTERIA: | FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE; | | | |
| OC | CLOSTRIDIUM. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | REID S.J., HANCOCK K., SANTANGELO J.D., WOODS D.R.; | | | |
| RL | SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS. | | | |
| RN | EMBL: M87835; G144915; -. | | | |
| KM | SPOULATION. | | | |
| SC | SEQUENCE 362 AA; 40998 MW; 75E3556E CRC32; | | | |
| Query Match | | 72.8%; Score 59; | DB 2; | Length 362; |
| Best Local Similarity | | 58.3%; | Pred. NO. 1.44e-01; | |
| Matches | 7; | Conservative | 3; | Mismatches 2; |
| | | | Indels | 0; |
| | | | Gaps | 0; |
| Dd | 67 YHKRDSYVEELD 78 | * | | |
| | : : : : : : : : : | | | |
| y | 1 YNKRRATVOELD 12 | | | |

| ID | RESULT | 4 | PRELIMINARY: | PRT: | 260 AA. |
|----------|---|---|--------------|------|---------|
| AC | Q54971; | | | | |
| DT | 01-NOV-1996 (TREMBLREL_01, CREATED) | | | | |
| DT | 01-NOV-1996 (TREMBLREL_01, LAST SEQUENCE UPDATE) | | | | |
| DT | 01-NOV-1998 (TREMBLREL_08, LAST ANNOTATION UPDATE) | | | | |
| DE | SUPERANTIGEN. | | | | |
| GN | SSA | | | | |
| OS | STREPTOCOCCUS PYOGENES. | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; | | | | |
| OC | STREPTOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN:WELLER: | | | | |
| RX | MEDLINE: 94222556. | | | | |
| RA | REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M., | | | | |
| RA | RICH R.R.; | | | | |
| RT | "Molecular characterization and phylogenetic distribution of the | | | | |
| RT | streptococcal superantigen gene (ssa) from Streptococcus pyogenes." | | | | |
| RL | INFECT. IMMUN. 62:1867-1874(1994). | | | | |
| DR | EMBL: L29565: G476766; | | | | |
| DR | PFAM: PF01123; Strep_Strep_toxin: 1. | | | | |
| Q | SUPERANTIGEN. | | | | |
| SEQUENCE | 260 AA: 29797 MW; FE391C2B CRC32; | | | | |

| | | | | |
|-----------------------|---------------------|---------------------|---------------|-------------|
| Query Match | 71.6%; | Score 58; | DB 2; | Length 260; |
| Best Local Similarity | 81.8%; | Pred. No. 2.39e-01; | | |
| Matches 9; | Conservative | 0; | Mismatches 2; | Indels 0; |
| Db | 173 NKKOVTOEELD 183 | | | |
| | | | | |
| 0y | 2 NKKRATVOEELD 12 | | | |

| RESULT | 5 | PRELIMINARY; | PRT; | 260 AA. |
|-----------------------|--|---|--------|---------------|
| ID | 054738 | | | |
| AC | 054738; | | | |
| DT | 01-NOV-1996 | (TREMBLREL, 01, CREATED) | | |
| DT | 01-NOV-1996 | (TREMBLREL, 01, LAST SEQUENCE UPDATE) | | |
| DT | 01-NOV-1998 | (TREMBLREL, 08, LAST ANNOTATION UPDATE) | | |
| DE | SUPERANTIGEN SSA. | | | |
| DE | SSA. | | | |
| GN | STREPTOCOCCUS PYOGENES. | | | |
| OS | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; | | | |
| OC | STREPTOCOCCUS. | | | |
| OC | [1] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RP | STRAIN-MGAS 1842; | | | |
| RX | MEDLINE: 94222556. | | | |
| RA | REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M., | | | |
| RA | RICH R.R.; | | | |
| RT | "Molecular characterization and phylogenetic distribution of the | | | |
| RT | streptococcal superantigen gene (ssa) from Streptococcus pyogenes."; | | | |
| RL | INECT. IMMUN. 62:1867-1874(1994). | | | |
| RL | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RP | STRAIN-MGAS 1842; | | | |
| RX | MEDLINE: 96178602. | | | |
| RA | REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.; | | | |
| RT | "Phylogenetic distribution of streptococcal superantigen ssa allelic | | | |
| RT | variants provides evidence for horizontal transfer of ssa within | | | |
| RT | Streptococcus pyogenes."; | | | |
| RL | INECT. IMMUN. 64:1161-1165(1996). | | | |
| DR | EMBL: U48793; GI245174; | | | |
| DR | PRIM; PF01123; Stap-Scrp_coxin; 1. | | | |
| DR | SEQUENCE 260 AA; 29836 MW; 3069EAB4 CRC32; | | | |
| Query Match | 71.6%; | Score 58; | DB 2; | Length 260; |
| Best Local Similarity | 81.8%; | Pred. No. 2,39e-01; | | |
| Matches | 9; | Conservative | 0; | Mismatches 2; |
| | | | Indels | 0; |
| | | | Gaps | 0; |
| Db | 173 NKKQVTVELD 183 | | | |
| | | | | |
| | | | | |
| cy | 2 NKKKATVQELD 12 | | | |

| | | | | |
|--------|--|--------------|------|---------|
| RESULT | 6 | PRELIMINARY: | PRT: | 260 AA. |
| ID | 054739 | | | |
| AC | 054739; 054737; | | | |
| DT | 01-NOV-1996 (TREMBLREL, 01, CREATED) | | | |
| DT | 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE) | | | |
| DT | 01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE) | | | |
| DE | SUPERANTIGEN SSA. | | | |
| GN | SSA. | | | |
| OS | STREPTOCOCCUS PYOGENES. | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE; 94422356. | | | |
| RA | REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M., | | | |
| RA | RICH R.R.; | | | |
| RT | "Molecular characterization and phylogenetic distribution of the streptococcal superantigen gene (ssa) from Streptococcus pyogenes." | | | |
| RL | INFECT. IMMUN. 62:1867-1874(1994). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE; 96178602. | | | |

RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
 RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
 RT variants provides evidence for horizontal transfer of ssa within
 RT Streptococcus pyogenes."

RL INFECT. IMMUN. 64:1161-1165(1996).

DR EMBL: U48794; G1245176; -

DR EMBL: U48792; G1245172; -

DR PFAM: PF01123; Staph-Staph-toxin; 1.

SO SEQUENCE 260 AA; 29767 MW; C81448C1 CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;
 Best Local Similarity 81.8%; Pred. No. 2,39e-01;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NRKQVVOELD 183

QY 2 NRKQVVOELD 12

RESULT 7

ID 077384 PRELIMINARY; PRT; 3394 AA.

AC 077384;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE MAL3P6.11 PROTEIN.

GN MAL3P6.11.

OS PLASMODIUM FALCIPARUM.

OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDIA; PLASMODIUM.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-3D7;

RA MORPHY L., LAMSON D., BARRELL B.;

RL SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: Z98551; E1331922; -

SO SEQUENCE 3394 AA; 402947 MW; 4C3F2778 CRC32;

Query Match 71.6%; Score 58; DB 5; Length 3394;
 Best Local Similarity 50.0%; Pred. No. 2,39e-01;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 373 YNKSNTIOOLN 384

QY 1 YNKSNTIOOLN 12

RESULT 8

ID 091693 PRELIMINARY; PRT; 464 AA.

AC 091693;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE MOTHERS AGAINST DPP.

GN XMAD.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOATRAACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96312915.

RA THOMSEN G.H.;

RT "Xenopus mothers against decapentaplegic is an embryonic ventralizing
 RT agent that acts downstream of the BMP-2/4 receptor."

RL DEVELOPMENT 122:2359-2366(1996).

DR EMBL: U58834; G1381671; -

DR PFAM: PF00968; Dwarf1; 1.

SO SEQUENCE 464 AA; 52346 MW; 4017799F CRC32;

Query Match 69.1%; Score 56; DB 13; Length 464;
 Best Local Similarity 54.5%; Pred. No. 6,64e-01;
 Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 42 KKKKGAIOELE 52

QY 42 KKKKGAIOELE 52

RESULT 9

ID P91308 PRELIMINARY; PRT; 760 AA.

AC P91308;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE COSMID F46F11.

GN F46F11.8.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA.

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKES M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RITKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans."

RL NATURE 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA PAULEY A., GATUNG S.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA WATERSTON R.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U88173; G1825648; -

SO SEQUENCE 760 AA; 88595 MW; D1020BBA CRC32;

QY 2 NRKQVVOELD 12

RESULT 9

ID P91308 PRELIMINARY; PRT; 760 AA.

AC P91308;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE COSMID F46F11.

GN F46F11.8.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA.

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKES M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RITKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans."

RL NATURE 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA PAULEY A., GATUNG S.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA WATERSTON R.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U88173; G1825648; -

SO SEQUENCE 760 AA; 88595 MW; D1020BBA CRC32;

Query Match 69.1%; Score 56; DB 5; Length 760;
 Best Local Similarity 33.3%; Pred. No. 6,64e-01;
 Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 569 YDSKNSIDOLE 580

QY 1 YNKSNTIOOLN 12

RESULT 10

ID 093308 PRELIMINARY; PRT; 1232 AA.

AC 093308;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE 14S COHESIN SMC1 SUBUNIT.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOATRAACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 98315077.

RA LOSADA A., HIRANO M., HIRANO T.;

RT "Identification of Xenopus SMC protein complexes required for sister
 RT chromatid cohesion."

RL GENES DEV. 12:1986-1997(1998).

DR EMBL: AF051784; G3328231; -

SO SEQUENCE 1232 AA; 142627 MW; FDE55B84 CRC32;

Query Match . 69.1%; Score 56; DB 13; Length 1232;
 Best Local Similarity 50.0%; Pred. No. 6.64e+01;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRKMDELE 337
 1 YNKKRATVQELD 12

RESULT 11
 ID P87145; PRELIMINARY; PRT; 811 AA.
 AC P87145;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE HYPOTHEICAL 92.5 KD PROTEIN C25H2.03 IN CHROMOSOME II.
 GN SPCC25H2.03.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 CC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
 CC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 CC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9712;
 RA DURSIO G., LYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,
 RA RAJANDREAN M.A., CONNOR R.E.;
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 DR EMBL: 295397; E316120; -
 KW HYPOTHEICAL PROTEIN; TRANSMEMBRANE.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT TRANSMEM 362 382 POTENTIAL.
 FT TRANSMEM 602 622 POTENTIAL.
 FT TRANSMEM 630 650 POTENTIAL.
 SO SEQUENCE 811 AA; 92452 MW; ELE2FB77 CRC32;

Query Match . 67.9%; Score 55; DB 3; Length 811;
 Best Local Similarity 58.3%; Pred. No. 1.10e+00;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 14 YDKRKATVELE 25
 1 YNKKRATVQELD 12

RESULT 12
 ID 007382; PRELIMINARY; PRT; 490 AA.
 AC 007382;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HISTIDINE KINASE LKINA.
 GN LKINA.
 OS LACTOCOCCUS LACTIS CREMORIS.
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 CC LACTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MG1363;
 RA KENNEDY, 97316457.
 RL "Cloning and sequence analysis of putative histidine protein kinases isolated from Lactococcus lactis MG1363."
 RL APPL. ENVIRON. MICROBIOL. 63:2454-2459(1997).
 DR EMBL: U81166; G2182835; -
 DR PFAM: PF00512; signal; 1.
 SO SEQUENCE 490 AA; 55884 MW; 05197910 CRC32;

Query Match . 66.7%; Score 54; DB 2; Length 490;
 Best Local Similarity 70.0%; Pred. No. 1.80e+00;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 7 FNKKETVEE 16
 1 YNKKRATVQELD 10

RESULT 13
 ID 073696; PRELIMINARY; PRT; 1233 AA.
 AC 073696;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE MITOSIS-SPECIFIC CHROMOSOME SEGREGATION PROTEIN SMC1 HOMOLOG.
 GN SMC1.
 OS FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 CC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
 CC TETRAODONTIFORMES; TETRAODONTIOIDEI; TETRAODONTIDAE; FUGU.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RIBOLDI TUNNICLIFFE G.R., PLATZER M., NYAKATURA G., ELGAR G.S.,
 RA BRENNER S., ROSENTHAL A.;
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF026198; G3098266; -
 SO SEQUENCE 1233 AA; 143100 MW; FBD2F859 CRC32;

Query Match . 66.7%; Score 54; DB 13; Length 1233;
 Best Local Similarity 50.0%; Pred. No. 1.80e+00;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRKMDELE 337
 1 YNKKRATVQELD 12

RESULT 14
 ID 053585; PRELIMINARY; PRT; 241 AA.
 AC 053585;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN H PRECURSOR.
 GN SEH.
 OS STAPHYLOCOCCUS AUREUS.
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D4508;
 RA REN K., BANNAN J.D., PANCHOLI V., CHEUNG A.L., ROBBINS J.C.,
 RA FISCHETTI V.A., ZABRISKIE J.B.;
 RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U11702; G510692; -
 DR PFAM: PF01123; Strep_toxin; 1.
 KW SIGNAL.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 241 ENTEROTOXIN H.
 SO SEQUENCE 241 AA; 27858 MW; AE5AB04A CRC32;

Query Match . 65.4%; Score 53; DB 2; Length 241;
 Best Local Similarity 72.7%; Pred. No. 2.94e+00;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 153 NKKNTVQELD 163
 2 NKKRATVQELD 12

RESULT 15
 ID 065075; PRELIMINARY; PRT; 271 AA.
 AC 065075;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 30.9 KD PROTEIN (FRAGMENT).
GN S850.
OS PICEA MARIANA.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC PICEA.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.;
RL GENETICS 0:0-0(1998).
DR EMBL; AF051236; G2982303; .
KW HYPOTHETICAL PROTEIN.
FT NON_TER 1
ST SEQUENCE 271 AA; 30897 MW; IDEA85B1 CRC32;

Query Match 65.4%; Score 53; DB 10; Length 271;
Best local Similarity 54.5%; Pred.No. 2.94e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 115 YSKTKAMVEDL 125
|:| | |:
QY 1 YNKKKATVQEL 11

Search completed: Tue Aug 31 19:07:21 1999
Job time : 39 secs.

THIS PAGE BLANK (USPTO)

(TM)

ID W64644 standard: peptide: 14 AA.
AC W64644:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide Cys-p12(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM Enterotoxin B; SEB; pyrogenic exotoxin; T-cell; antagonist; inhibitor;
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997: IL0438.
PR 30-DEC-1996: IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PS treatment of toxic shock caused by exotoxin(s)
PS Claim 21: Page 41: 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 14 AA:

Query Match 100.0%; Score 64; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.34e+00;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 kkatvgeid 13
1 kkratvgeid 10

RESULT 6
ID W64645 standard: peptide: 14 AA.
AC W64645:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide D-Ala.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM Enterotoxin B; SEB; pyrogenic exotoxin; T-cell; antagonist; inhibitor;
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997: IL0438.
PR 30-DEC-1996: IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PS treatment of toxic shock caused by exotoxin(s)
PS Claim 23: Page 41: 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 14 AA:

Query Match 100.0%; Score 64; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.34e+00;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 kkatvgeid 13
1 kkratvgeid 10

RESULT 7
ID W64642 standard: peptide: 24 AA.
AC W64642:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide dimer.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM Enterotoxin B; SEB; pyrogenic exotoxin; T-cell; antagonist; inhibitor;
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997: IL0438.
PR 30-DEC-1996: IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PS treatment of toxic shock caused by exotoxin(s)
PS Claim 18: Page 41: 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 24 AA:

Query Match 100.0%; Score 64; DB 34; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.34e+00;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 kkatvgeid 12
1 kkratvgeid 10

RESULT 8
ID W64643 standard: peptide: 35 AA.
AC W64643:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide trimer.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM Enterotoxin B; SEB; pyrogenic exotoxin; T-cell; antagonist; inhibitor;
OS Synthetic.
OS Staphylococcus aureus.

PN M0982944-A1.
 PD 09-JUL-1998.
 PE 30-DEC-1997: IL0438.
 PR 30-DEC-1996: IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Atad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 19; Page 41; 68pp: English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 capable of eliciting protective immunity against toxic shock induced by
 PET or by a mixture of PETs. Such peptides are also capable of
 antagonising toxin mediated activation of T-cells, inhibiting expression
 of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 TNF-beta genes. The peptides may be used to prepare therapeutics or
 vaccines for the treatment of prophylaxis of toxin-mediated activation
 of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 35 AA;

Query Match 100.0%; Score 64; DB 34; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.34e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 kkatvgeid 12
 |||||
 QY 1 KKRATVQELD 10

RESULT 9
 ID W72423 standard; peptide; 24 AA.
 AC W72423;
 DT 22-DEC-1998 (first entry)
 DE Peptide #2 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN M09845325-A1.
 PD 15-OCT-1998.
 PE 01-APR-1998: U06663.
 PR 07-APR-1997: US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases.
 PS Claim 4; Page 54; 69pp: English.
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 KD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1Y2X3X4X5N #1,
 CC K6X7X8X9X10X11X12X13DX14X15X16RX17X18X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SEP). Ab
 CC are used: (1) for diagnostic detection of SPEA or SEA, SEB and SED, in
 CC usual immunoassays; (11) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (111) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 SQ Sequence 24 AA;

Query Match 84.4%; Score 54; DB 36; Length 24;
 Best Local Similarity 80.0%; Pred. No. 1.95e+01;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 kkatvgeid 10
 |||||
 QY 1 KKRATVQELD 10

RESULT 10
 ID W04494 standard; peptide; 28 AA.
 AC W04494;
 DT 10-DEC-1996 (first entry)
 DE Staphylococcal enterotoxin A residues 146-173, T-cell agonist.
 KW Staphylococcal enterotoxin A; agonist; T-cell proliferation;
 KW treatment; immunodeficiency; autoimmune disease; TNF-alpha;
 KW tumour necrosis factor alpha.
 OS Staphylococcus spp.
 PN US5545716-A.
 PD 13-AUG-1996.
 PE 08-SEP-1992: 941497.
 PR 08-SEP-1992: US-941497.
 PR 29-MAR-1994: US-220378.
 PA (UYFL) UNIV FLORIDA.
 PI Griggs ND, Johnson HM, Pontzer CH;
 DR WPI: 96-383718/38.
 PT Peptide fragments of Staphylococcal enterotoxin A (SEA) - useful as
 PT SEA agonists for stimulating T-cell proliferation, e.g. in treatment
 PT of immunodeficiency and autoimmune diseases
 PS Example 1: Columns 15-16; 17pp: English.
 CC The present peptide, comprising residues 146-173 of Staphylococcal
 CC enterotoxin A (SEA), is useful as an SEA agonist for stimulating
 CC T-cell proliferation, e.g. in the treatment of immunodeficiency and
 CC autoimmune diseases. Supernatant from PBMC stimulated with
 CC 100 microm of the peptide for 18 hrs., was collected and assayed
 CC for TNF-alpha activity by cytotoxicity on L-929 cells. The result
 CC given as units/ml of TNF-alpha activity was 1.85, compared to 24.1
 CC for the most effective agonist, comprising SEA residues 121-149.
 SQ Sequence 28 AA;

Query Match 84.4%; Score 54; DB 19; Length 28;
 Best Local Similarity 80.0%; Pred. No. 1.95e+01;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2 kkatvgeid 11
 |||||
 QY 1 KKRATVQELD 10

RESULT 11
 ID W72425 standard; peptide; 28 AA.
 AC W72425;
 DT 22-DEC-1998 (first entry)
 DE Peptide #4 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN M09845325-A1.
 PD 15-OCT-1998.
 PE 01-APR-1998: U06663.
 PR 07-APR-1997: US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp: English.
 CC The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGX1TX3X4X5N #1,
CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
S0 Sequence 28 AA;

Query Match 84.4%; Score 54; DB 36; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.95e+01;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 3 knnvtvgeld 12
||: |||||
Qy 1 KKKATVQELD 10

RESULT 12
ID W72426 standard; peptide: 36 AA.
AC W72426;
DR 22-DEC-1998 (first entry)
DE Peptide #5 for reducing symptoms of toxic shock syndrome.
KM Toxic shock syndrome; immunogenic response; bacterial infection;
KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KM autoimmune disease.
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
PN MO9845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
PS Claim 4; Page 54; 69pp; English.
CC The present invention describes peptides having consensus sequences #1
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGX1TX3X4X5N #1,
CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
S0 Sequence 36 AA;

Query Match 84.4%; Score 54; DB 36; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.95e+01;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 13 knnvtvgeld 22
||: |||||
Qy 1 KKKATVQELD 10

RESULT 13
ID W72427 standard; peptide: 38 AA.
AC W72427;
DR 22-DEC-1998 (first entry)
DE Peptide #6 for reducing symptoms of toxic shock syndrome.
KM Toxic shock syndrome; immunogenic response; bacterial infection;
KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KM autoimmune disease.
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
PN MO9845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
PS Claim 4; Page 54; 69pp; English.
CC The present invention describes peptides having consensus sequences #1
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGX1TX3X4X5N #1,
CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
S0 Sequence 38 AA;

Query Match 84.4%; Score 54; DB 36; Length 38;
Best Local Similarity 80.0%; Pred. No. 1.95e+01;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 13 knnvtvgeld 22
||: |||||
Qy 1 KKKATVQELD 10

RESULT 14
ID W24299 standard; Protein: 91 AA.
AC W24299;
DR 14-APR-1998 (first entry)
DE Staphylococcus aureus gene #5 polypeptide sequence 2.
KM Staphylococcus aureus MCHN 29; antagonist; antibacterial; immunogen;
KM vaccine; disease; protection; isolation.
OS Staphylococcus aureus.
FH Key location/Qualifiers
FT Misc-difference 29 /note="Unspecified amino acid"
FT W09731114-A2.
PN 28-AUG-1997.
PD 25-FEB-1997; G00524.
PF 26-FEB-1996; GB-004045.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Hodgson JE;
DR WPI: 97-435166/40.
DR N-PSDB; V01865.
PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for
PT isolating antagonist of the polypeptide(s) useful as anti-bacterials
PS Claim 11; Page 33; 117pp; English.

CC The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIM 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from *Staphylococcus aureus*. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds
 CC that bind and inhibit the activity of the polypeptide. Such compounds
 CC can be used as anti-bacterial compounds. The polypeptide may also be
 CC used as an immunogen to vaccinate an animal for protection against
 CC *Staphylococcus aureus* caused disease.
 SQ Sequence 91 AA;

Query Match 84.4%; Score 54; DB 27; Length 91;
 Best Local Similarity 80.0%; Pred. No. 1.95e+01;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 41 knvtvgeid 50
 ||:|||||
 QY 1 KKKATVQELD 10

RESULT 15
 ID R13205 standard; Protein: 228 AA.

AC R13205:
 DT 15-OCT-1991 (first entry)
 DE *Staphylococcal enterotoxin D*.
 KW SED; cancer treatment; pyrogen; tumouricide.
 OS *Staphylococcus aureus*.
 PN MO9110680-A.
 PD 25-JUL-1991.
 PF 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumoricidal activity
 PT as *Staphylococcal* protein A without potential toxic reactions
 PS Disclosure; Fig 1; 74pp; English.
 CC SED was isolated and purified from *S. aureus*. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SED. Synthetic
 CC polypeptides having structural homology to *Staphylococcal* exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophathy profiles.
 CC See R13203-R13211.
 SQ Sequence 228 AA;

Query Match 84.4%; Score 54; DB 3; Length 228;
 Best Local Similarity 80.0%; Pred. No. 1.95e+01;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 142 knvtvgeid 151
 ||:|||||
 QY 1 KKKATVQELD 10

Search completed: Tue Aug 31 19:11:03 1999
 Job time : 18 secs.


```

##experimental_source strain FR137
SUMMARY      #length 257 #molecular_weight 29669 #checksum 2543
Query Match  84.4% Score 54: DB 2: Length 257:
Best Local Similarity 80.0%: Pred. No. 4.56e-01:
Matches      8: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

Db 171 KKNVTVQELD 180
||:|||||
QY 1 KKRATVQELD 10

RESULT 3
ENTRY      A33953 #type complete
TITLE      enterotoxin D precursor - Staphylococcus aureus
ORGANISM   #formal_name Staphylococcus aureus
DATE       09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
ACCESSIONS A33953
REFERENCE   A33953
#authors    Bayles, K.W.; Iandolo, J.J.
#journal     J. Bacteriol. (1989) 171:4799-4806
#title       Genetic and molecular analyses of the gene encoding
             staphylococcal enterotoxin D.
#cross-references MUID:89359112
#accession   A33953
#status      Preliminary
#molecule_type DNA
#residues    1-258 #label BAY
#cross-references GB:M28521; NID:91492109; PID:9758691
SUMMARY      #length 258 #molecular_weight 29746 #checksum 39

Query Match  84.4% Score 54: DB 2: Length 258:
Best Local Similarity 80.0%: Pred. No. 4.56e-01:
Matches      8: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

Db 172 KKNVTVQELD 181
||:|||||
QY 1 KKRATVQELD 10

RESULT 4
ENTRY      ENSAB6 #type complete
TITLE      enterotoxin B precursor - Staphylococcus aureus
ORGANISM   #formal_name Staphylococcus aureus
DATE       24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change
ACCESSIONS S27360; A92065; S27240; A01815
REFERENCE   S27360
#authors    Jones, C.L.; Khan, S.A.
#journal     J. Bacteriol. (1986) 166:29-33
#title       Nucleotide sequence of the enterotoxin B gene from
             Staphylococcus aureus.
#cross-references MUID:86168029
#accession   S27360
#molecule_type DNA
#residues    1-266 #label JON
#cross-references EMBL:M1118; NID:9152999; PID:9153000
REFERENCE     A92065
#authors    Huang, I.Y.; Bergdoll, M.S.
#journal     J. Biol. Chem. (1970) 245:3518-3525
#title       The primary structure of staphylococcal enterotoxin B. III.
             The cyanogen bromide peptides of reduced and aminoethylated
             enterotoxin B, and the complete amino acid sequence.
#cross-references MUID:71007902
#accession   A92065
#molecule_type protein
#residues    28-55, 'NND', 59-68, 'NE', 71, 'FDLIV', 78-117, 119-127, 'N',
             129, 'D', 131-132, 'ENT', 136-148, 'GN', 151-156, 'Y',
             157-184, 'EQ', 187-232, 'N', 234-245, 'ND', 248-266 #label
             HUA
##experimental_source strain S-6

```

```

REFERENCE     A92064
#authors      Huang, I.Y.; Bergdoll, M.S.
#journal      J. Biol. Chem. (1970) 245:3511-3517
#title        The primary structure of staphylococcal enterotoxin B. II.
             Isolation, composition, and sequence of chymotryptic
             peptides.
#cross-references MUID:71007901
#contents     annotation: chymotryptic peptides
REFERENCE     A92063
#authors      Huang, I.Y.; Bergdoll, M.S.
#journal      J. Biol. Chem. (1970) 245:3493-3510
#title        The primary structure of staphylococcal enterotoxin B. I.
             Isolation, composition, and sequence of tryptic peptides
             from oxidized enterotoxin B.
#cross-references MUID:71007900
#contents     annotation: tryptic peptides
REFERENCE     A90548
#authors      Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
             Dunnehy, D.A.; Bergdoll, M.S.
#journal      Biochemistry (1965) 4:1011-1016
#title        Purification of staphylococcal enterotoxin B.
#cross-references MUID:66035792
#contents     annotation: biological source of protein
REFERENCE     S27240
#authors      Alakhov, V.Y.; Klinsky, E.Y.; Kojosov, M.I.; Maurer-Pogoy, I.;
             Moskalava, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
             Shemchukova, O.B.; Severin, E.S.
#journal      Eur. J. Biochem. (1992) 209:823-828
#title        Identification of functionally active fragments of
             staphylococcal enterotoxin B.
#accession    S27240
#molecule_type protein
#residues     28-42;128-148 #label ALA
#cross-references superfamily enterotoxin B
KEYWORDS      enterotoxin; extracellular protein; toxin
FEATURES
1-27
28-266
120-140
#domain signal sequence #status predicted #label SIG\
#product enterotoxin B #status experimental #label MATV\
#disulfide_bonds #status experimental
SUMMARY      #length 266 #molecular_weight 31436 #checksum 4249

Query Match  82.8% Score 53: DB 1: Length 266:
Best Local Similarity 80.0%: Pred. No. 7.60e-01:
Matches      8: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

Db 179 KKNVTVQELD 188
||| | |||
QY 1 KKRATVQELD 10

RESULT 5
ENTRY      A28179 #type complete
TITLE      enterotoxin E precursor - Staphylococcus aureus
ORGANISM   #formal_name Staphylococcus aureus
DATE       30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
ACCESSIONS A28179
REFERENCE   A28179
#authors    Couch, J.L.; Soltis, M.T.; Betley, M.J.
#journal     J. Bacteriol. (1988) 170:2954-2960
#title       Cloning and nucleotide sequence of the type E staphylococcal
             enterotoxin gene.
#cross-references MUID:88257005
#accession   A28179
#molecule_type DNA
#residues    1-257 #label COU
#cross-references GB:M21319; NID:9153001; PID:9153002
SUMMARY      #length 257 #molecular_weight 29358 #checksum 2562

Query Match  81.3% Score 52: DB 2: Length 257:
Best Local Similarity 80.0%: Pred. No. 1.26e+00:
Matches      8: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

```


Db 171 KKEVTVQELD 180
|||
Oy 1 KKKATVQELD 10

RESULT 6
ENTRY S58590 #type complete
TITLE ribosomal protein S3 - maize chloroplast
ORGANISM #formal_name chloroplast Zea mays #common_name maize
DATE 29-Nov-1998 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999

ACCESSIONS S58590
REFERENCE S58531
#authors Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
#journal J. Mol. Biol. (1995) 251:614-628
#title Complete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by transcript editing.

#cross-references MUID:95395841
#accession S58590
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-224 #label MA1
#cross-references EMBL:X86563; NID:9902200; PID:9902260
#note the nucleotide sequence was submitted to the EMBL Data Library, April 1995

GENETICS
#gene rps3
#genome chloroplast
#CLASSIFICATION #superfamily Escherichia coli ribosomal protein S3
#KEYWORDS chloroplast; protein biosynthesis; ribosome
#SUMMARY #length 224 #molecular_weight 25916 #checksum 3426

Query Match
Best Local Similarity 79.7%; Score 51; DB 2; Length 224;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKKGAIEELE 102
|||
Oy 1 KKKATVQELD 10

RESULT 7
ENTRY R3RZ3 #type complete
TITLE ribosomal protein S3 - rice chloroplast
ORGANISM #formal_name chloroplast Oryza sativa #common_name rice
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Mar-1998
ACCESSIONS J00265; S05145
REFERENCE J00200
#authors Shimada, H.; Whittier, R.F.; Hiratsuka, J.; Maeda, Y.; Hirai, A.; Sugita, M.
#submission submitted to JIPID, December 1989
#accession J00265
#molecule_type DNA
#residues 1-239 #label SHI
#experimental_source cv. Nihonbare
#REFERENCE S05080
#authors Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kondo, C.; Honji, Y.; Sun, C.R.; Meng, B.Y.; Li, Y.Q.; Kanno, A.; Nishizawa, Y.; Hirai, A.; Shinzaki, K.; Sugita, M.
#journal Mol. Gen. Genet. (1989) 217:185-194
#title The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.

#cross-references MUID:89364698
#accession S05145
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-239 #label HIR
#cross-references GB:X15901; NID:g11957; PID:g12025

##experimental_source cv. Nihonbare
##note this sequence was submitted to EMBL, July 1989

GENETICS
#gene rps3
#genome chloroplast
#CLASSIFICATION #superfamily Escherichia coli ribosomal protein S3
#KEYWORDS chloroplast; protein biosynthesis; ribosome
#SUMMARY #length 239 #molecular_weight 27518 #checksum 5969

Query Match
Best Local Similarity 79.7%; Score 51; DB 1; Length 239;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 108 KKKGAIEELE 117
|||
Oy 1 KKKATVQELD 10

RESULT 8
ENTRY B64087 #type complete
TITLE outer membrane protein p4 precursor - Haemophilus influenzae (strain Rd KW20)
ALTERNATE_NAMES lipoprotein e
ORGANISM #formal_name Haemophilus influenzae
DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997

ACCESSIONS B64087; A43604
REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervatage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Uterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

#cross-references MUID:95350630
#accession B64087
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-274 #label TIGR
#cross-references GB:U3752; GB:LA2023; NID:g1573692; PID:g1573696;
#experimental_source strain Rd KW20
#REFERENCE A43604
#authors Green, B.A.; Farley, J.E.; Quinn-Dey, T.; Delch, R.A.; Zlotnick, G.W.
#journal Infect. Immun. (1991) 59:3191-3198
#title The e (P4) outer membrane protein of Haemophilus influenzae: biologic activity of anti-e serum and cloning and sequencing of the structural gene.

#cross-references MUID:91348867
#accession A43604
#molecule_type DNA
#residues 1-229, 'E', 31-274 #label GRE
#cross-references GB:M68502; NID:g148895; PID:g148896
#experimental_source strain KW20b
#accession B43604
#molecule_type protein
#residues 263-274 #label GRE2

GENETICS
#gene hel
#KEYWORDS lipoprotein; membrane protein
FEATURE
1-20 #domain signal sequence #status predicted #label SIG
21-274 #product outer membrane protein P4 #status predicted #label MAT
#SUMMARY #length 274 #molecular_weight 30431 #checksum 2814


```

#cross-references MUID:88067745
#accession      S09071
#molecule_type DNA
#residues       'SGHSWTHCSLIYRLPLTII',218-277 ##label HEI
#cross-references EMBL:X06293; EMBL:Y00494
#note           sequence N-terminal of residue 218 correspond to a
                putative exon
REFERENCE
#authors        154186
#journal        Roberts, R.G.; Coffey, A.J.; Bobrow, M.; Bentley, D.R.
#title          Genomics (1993) 16:536-538
#cross-references MUID:93300536
#accession      154186
#status         nucleic acid sequence not shown; translation not shown;
                translated from GB/EMBL/DBJ
#molecule_type DNA
#residues       984-1411 ##label RE3
#cross-references GB:I05642; NID:g181892; PID:g950344
#accession      168509
#status         nucleic acid sequence not shown; translation not shown;
                translated from GB/EMBL/DBJ
#molecule_type DNA
#residues       1776-1913 ##label RE2
#cross-references GB:I05646; NID:g181896; PID:g950345
#accession      168510
#status         nucleic acid sequence not shown; translation not shown;
                translated from GB/EMBL/DBJ
#molecule_type DNA
#residues       2850-2979 ##label ROB
#cross-references GB:I05649; NID:g181899; PID:g950346
#accession      154175
#authors        Roberts, R.G.; Coffey, A.J.; Bobrow, M.; Bentley, D.R.
#journal        Genomics (1992) 13:942-950
#title          Determination of the exon structure of the distal portion of
                the dystrophin gene by vectorette PCR.
#cross-references MUID:92372062
#accession      154175
#status         nucleic acid sequence not shown; translation not shown;
                translated from GB/EMBL/DBJ
#molecule_type DNA
#residues       2980-3685 ##label RES
#cross-references GB:M86903; NID:g181881; PID:g457519
#accession      154166
#authors        Ehrenspreis, J.; Hillers, M.; Junkes, B.; Pfordt, M.;
                Schindler, E.; Vosberg, H.P.
#journal        Genomics (1991) 10:551-557
#title          Analysis of a dystrophin gene deletion by amplification of
                mRNA isolated from DMD myotubes cultured in vitro.
#cross-references MUID:91365360
#accession      154166
#status         translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues       2250-2254 ##label RE4
#cross-references GB:S54699; NID:g235303; PID:g235304
#accession      S03902
#authors        Feener, C.A.; Koenig, M.; Kunkel, L.M.
#journal        Nature (1989) 338:509-511
#title          Alternative splicing of human dystrophin mRNA generates
                isoforms at the carboxy terminus.
#cross-references MUID:89181947
#accession      S03902
#molecule_type mRNA
#residues       'MED',12-32;3377-3408 ##label FEE
#cross-references EMBL:X15148
COMMENT         Dystrophin is proposed to play a role in anchoring the cytoskeleton
                ...
                Note: remainder of annotations omitted.
Query Match      78.1%; Score 50; DB 1; Length 3685;
Best Local Similarity 60.0%; Pred. No. 3.38e+00;
Matches          6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db              2512 KOKATMODULE 2521

```

```

OY              1 KKKATVQELD 10
RESULT          10
ENTRY           S46523 #type complete
TITLE           transcription factor TGA3 - Arabidopsis thaliana
ALTERNATE_NAMES TGA3-related bZIP transcription factor
ORGANISM        #formal_name Arabidopsis thaliana #common_name mouse-ear
                cress
DATE            27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
                16-Dec-1998
ACCESSIONS      S46523
REFERENCE       S46523
#authors        Miao, Z.H.; Liu, X.; Lam, E.
#journal        Plant Mol. Biol. (1994) 25:1-11
#title          TGA3 is a distinct member of the TGA family of bZIP
                transcription factors in Arabidopsis thaliana.
#cross-references MUID:94272006
#accession      S46523
#status         nucleic acid sequence not shown
#molecule_type mRNA
#residues       1-384 ##label M1A
#cross-references EMBL:L10209; NID:g304112; PID:g304113
GENETICS
#gene           TGA3
CLASSIFICATION #superfamily fos/jun DNA-binding domain homology
KEYWORDS        DNA binding; leucine zipper; transcription factor
FEATURE         91-134
SUMMARY         #domain fos/jun DNA-binding domain homology #label FUD
                #length 384 #molecular-weight 43755 #checksum 6158
Query Match      76.6%; Score 49; DB 2; Length 384;
Best Local Similarity 60.0%; Pred. No. 5.49e+00;
Matches          6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db              116 KKKATVQELD 125
OY              1 KKKATVQELD 10
RESULT          11
ENTRY           A41793 #type complete
TITLE           dipeptidyl aminopeptidase-like protein (EC 3.4.14.-) short
                form, DPPX-S - bovine
ORGANISM        #formal_name Bos primigenius taurus #common_name cattle
                04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                29-Jan-1999
ACCESSIONS      A41793
REFERENCE       A41793
#authors        Wada, K.; Yokotani, N.; Hunter, C.; Dol, K.; Wenthold, R.J.;
                Shimasaki, S.
#journal        Proc. Natl. Acad. Sci. U.S.A. (1992) 89:197-201
#title          Differential expression of two distinct forms of mRNA
                encoding members of a dipeptidyl aminopeptidase family.
#cross-references MUID:92108018
#accession      A41793
#status         preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues       1-803 ##label WAD
#cross-references GB:M76429; NID:g408719; PID:g408720
#note           sequence extracted from NCBI backbone (NCBI:75138)
KEYWORDS        dipeptidylpeptide hydrolase; glycoprotein
FEATURE         257,342
SUMMARY         #binding-site carbohydrate (Asn) (covalent) #status
                predicted
                #length 803 #molecular-weight 90459 #checksum 9315
Query Match      76.6%; Score 49; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 5.49e+00;
Matches          6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db              66 KKKATVQELD 74

```

```

OY      1 KKKATVOEL 9
      ||| |||:|
RESULT  12
ENTRY   168600 #type complete
TITLE   dipeptidyl aminopeptidase like protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996

ACCESSIONS
REFERENCE
#authors Yokotani, N.; Doi, K.; Wentholt, R.J.; Wada, K.
#journal Hum. Mol. Genet. (1993) 2:1037-1039
#title Non-conservation of a catalytic residue in a dipeptidyl
aminopeptidase IV-related protein encoded by a gene on
human chromosome 7.
#cross-references M01D:93372805
#accession 168600
#status Preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-803 ##label RES
#cross-references GB:M6860; NID:9306707; PID:9306708
#length 803 #molecular_weight 91355 #checksum 814

SUMMARY
Query Match
Best Local Similarity 66.7%; Pred. No. 5.49e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      66 KKKATVOEL 74
      ||| |||:|
OY      1 KKKATVOEL 9
      ||| |||:|

RESULT  13
ENTRY   154331 #type complete
TITLE   dipeptidyl aminopeptidase like protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996

ACCESSIONS
REFERENCE
#authors Yokotani, N.; Doi, K.; Wentholt, R.J.; Wada, K.
#journal Hum. Mol. Genet. (1993) 2:1037-1039
#title Non-conservation of a catalytic residue in a dipeptidyl
aminopeptidase IV-related protein encoded by a gene on
human chromosome 7.
#cross-references M01D:93372805
#accession 154331
#status Preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-865 ##label RES
#cross-references GB:M6860; NID:9306705; PID:9306706
#length 865 #molecular_weight 97587. #checksum 6089

SUMMARY
Query Match
Best Local Similarity 66.7%; Pred. No. 5.49e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      128 KKKATVOEL 136
      ||| |||:|
OY      1 KKKATVOEL 9
      ||| |||:|

RESULT  14
ENTRY   S28916 #type complete
TITLE   dystrophin - mouse
ALTERNATE_NAMES
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     22-Nov-1995 #sequence_revision 03-Nov-1995 #text_change
12-Feb-1999

ACCESSIONS
REFERENCE
S28916; B27162; S10922; C43837; B40134
S28916

```

```

#authors Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey,
C.T.; Chamberlain, J.S.
#journal Nucleic Acids Res. (1992) 20:1725-1731
#title Human and murine dystrophin mRNA transcripts are
differentially expressed during skeletal muscle, heart, and
brain development.
#cross-references M01D:9225376
#accession S28916
#status Preliminary: nucleic acid sequence not shown;
translation not shown
#molecule_type mRNA
#residues 1-3678 ##label BIE
#cross-references EMBL:M6860
#note the nucleotide sequence was submitted to the EMBL Data
Library, October 1991

REFERENCE
#authors A90897
Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.;
Feener, C.; Kunkel, L.M.
#journal Cell (1987) 50:509-517
#title Complete cloning of the Duchenne muscular dystrophy (DMD)
cDNA and preliminary genomic organization of the DMD gene
in normal and affected individuals.
#cross-references M01D:87273512
#accession B27162
#status not compared with conceptual translation
#molecule_type mRNA
#residues 1-201 ##label KOE

REFERENCE
#authors S06461
Nudel, D.; Zuk, D.; Eilat, P.; Zeelon, E.; Levy, Z.; Neuman,
S.; Yaffe, D.
#journal Nature (1989) 337:76-78
#title Duchenne muscular dystrophy gene product is not identical in
muscle and brain.
#cross-references M01D:89082658
#accession S10922
#status translation not shown
#molecule_type mRNA
#residues 1-106 ##label NUD
#cross-references EMBL:X14183

REFERENCE
#authors A43837
Rapaport, D.; Lederfein, D.; den Dunnen, J.T.; Grootsoorten,
P.M.; Van Ommen, G.J.; Fuchs, O.; Nudel, U.; Yaffe, D.
#journal Characterization and cell type distribution of a novel, major
transcript of the Duchenne muscular dystrophy gene.
#cross-references M01D:92316332
#accession C43837
#status Preliminary
#molecule_type mRNA
#residues 'MREHLKG', 3069-3181 ##label RAP
#note Sequence extracted from NCBI backbone

REFERENCE
#authors A40134
Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.
#journal Science (1987) 238:347-350
#title Conservation of the Duchenne muscular dystrophy gene in mice
and humans.
#cross-references M01D:88018015
#accession B40134
#status Preliminary
#molecule_type mRNA
#residues 300-676, 'F', 678-1390 ##label HOF
#cross-references GB:M18025

GENETICS
#introns 11/1
#note the list of introns may be incomplete
CLASSIFICATION
#superfamily dystrophin: alpha-actinin actin-binding domain
homology; spectrin/dystrophin repeat homology; WW repeat
homology; actin binding; alternative splicing
KEYWORDS
FEATURE
14-233
#domain alpha-actinin actin-binding domain homology
#label AAH\
340-449
#domain spectrin/dystrophin repeat homology #label SNI\

```


THIS PAGE BLANK (USPTO)

MUSKIE
(TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:08:53 1999; Maspar time 2.54 Seconds
111.150 Million cell updates/sec
Tabular output not generated.

Title: >US-09-150-947-3
Description: (1-10) from US09150947.pep
Perfect Score: 64
Sequence: 1 KKKATVDELD 10

Scoring table:
PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 23.236; Variance 23.757; scale 0.978

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|------------------------|-----------|
| 1 | 54 | 84.4 | 257 | 1 | ETXA_STAU | ENTEROTOXIN TYPE A PRE | 8.39e+02 |
| 2 | 54 | 84.4 | 258 | 1 | ETXD_STAU | ENTEROTOXIN TYPE D PRE | 8.39e+02 |
| 3 | 53 | 82.8 | 266 | 1 | ETXB_STAU | ENTEROTOXIN TYPE B PRE | 1.50e+01 |
| 4 | 52 | 81.3 | 257 | 1 | ETXE_STAU | ENTEROTOXIN TYPE E PRE | 2.68e+01 |
| 5 | 51 | 79.7 | 224 | 1 | RR3_MAIZE | CHLOROPLAST 30S RIBOSO | 4.73e+01 |
| 6 | 51 | 79.7 | 229 | 1 | RR3_ORISA | CHLOROPLAST 30S RIBOSO | 4.73e+01 |
| 7 | 50 | 78.1 | 274 | 1 | HEL_HAEIN | LIPOPROTEIN E PRECURSO | 8.30e+01 |
| 8 | 50 | 78.1 | 3685 | 1 | DMD_HUMAN | DYSTROPHIN. | 8.30e+01 |
| 9 | 49 | 76.6 | 386 | 1 | YAMH_SCHPO | HYPOTHETICAL 44.5 KD P | 1.44e+00 |
| 10 | 49 | 76.6 | 859 | 1 | DPP6_RAT | DIPEPTIDYL PEPTIDASE I | 1.44e+00 |
| 11 | 49 | 76.6 | 863 | 1 | DPP6_BOVIN | DIPEPTIDYL PEPTIDASE I | 1.44e+00 |
| 12 | 49 | 76.6 | 865 | 1 | DPP6_HUMAN | DIPEPTIDYL PEPTIDASE I | 1.44e+00 |
| 13 | 49 | 76.6 | 865 | 1 | DMD_MOUSE | DYSTROPHIN. | 1.44e+00 |
| 14 | 48 | 75.0 | 330 | 1 | HBPB_ARATH | TRANSCRIPTION FACTOR H | 2.49e+00 |
| 15 | 48 | 75.0 | 332 | 1 | HBPA_WHEAT | TRANSCRIPTION FACTOR H | 2.49e+00 |
| 16 | 48 | 75.0 | 359 | 1 | TGACG_TOBAC | TMGC-SEQUENCE SPECIFI | 2.49e+00 |
| 17 | 48 | 75.0 | 455 | 1 | MAD_DROME | MOTHERS AGAINST DPP PR | 2.49e+00 |
| 18 | 47 | 73.4 | 265 | 1 | SPEA_STRPY | EXOTOXIN TYPE A PRECUR | 4.26e+00 |
| 19 | 47 | 73.4 | 269 | 1 | YD54_SCHPO | HYPOTHETICAL 31.2 KD P | 4.26e+00 |
| 20 | 46 | 71.9 | 916 | 1 | PMAL1_AJUCA | PLASMA MEMBRANE ATPASE | 7.23e+00 |
| 21 | 46 | 71.9 | 920 | 1 | PMAL1_NEUCR | PLASMA MEMBRANE ATPASE | 7.23e+00 |
| 22 | 46 | 71.9 | 1010 | 1 | PMAL2_SCHPO | PLASMA MEMBRANE ATPASE | 7.23e+00 |
| 23 | 45 | 70.3 | 221 | 1 | RL10_YEAST | 60S RIBOSOMAL PROTEIN | 1.21e+01 |

| RESULT | ID | ETXA_STAU | STANDARD: | PRT: | 257 AA. |
|--------|--|-----------|-----------|------|---------|
| AC | P13163; | | | | |
| DT | 01-JAN-1990 (REL. 13, CREATED) | | | | |
| DT | 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) | | | | |
| DT | 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN TYPE A PRECURSOR (SEA). | | | | |
| GN | ENTA. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE. | | | | |
| OC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RC | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-FRI337; | | | | |
| RX | MEDLINE: 88086892. | | | | |
| RA | BETLEY M.J., MEKALANOS J.J.: | | | | |
| RT | "Nucleotide sequence of the type A staphylococcal enterotoxin gene." | | | | |
| RL | J. BACTERIOL. 170:34-41(1986). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 25-257. | | | | |
| RX | MEDLINE: 87222293. | | | | |
| RA | HUANG I.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J.: | | | | |
| RT | "Complete amino acid sequence of staphylococcal enterotoxin A." | | | | |
| RL | J. BIOL. CHEM. 262:7006-7013(1987). | | | | |
| RN | [3] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). | | | | |
| RX | MEDLINE: 95354648. | | | | |
| RA | SCHAD E.M., ZAITSEVA I., ZAITSEV V.N., DOHLSTEN M., KALLAND T., | | | | |
| RT | SCHLEIFERT P.M., OHLENDORF D.H., SVENSSON L.A.: | | | | |
| RL | "Crystal structure of the superantigen staphylococcal enterotoxin | | | | |
| RL | type A."; | | | | |
| RL | EMBO J. 14:3292-3301(1995). | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). | | | | |
| RX | MEDLINE: 97113025. | | | | |
| RA | SUNDSTROM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEN M., | | | | |
| RT | ABRAMSEN L.: | | | | |
| RL | "The Co-crystal structure of staphylococcal enterotoxin type A with | | | | |
| RT | Zn2+ at 2.7-A resolution. Implications for major histocompatibility | | | | |
| RL | complex class II binding." | | | | |
| RL | J. BIOL. CHEM. 271:32212-32216(1996). | | | | |
| RN | [5] | | | | |
| RP | 3D-STRUCTURE MODELLING. | | | | |
| RX | MEDLINE: 96022987. | | | | |
| RA | SWAMINATHAN S., FUREY W.F., JR., PLETCHER J., SAX M.: | | | | |
| RT | "Residues defining V beta specificity in staphylococcal | | | | |
| RT | enterotoxins." | | | | |

RL NAT. STRUCT. BIOL. 2:680-686(1995).
 RN [6]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE: 97334373.
 RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., AGHARRA K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity."
 RL J. MOL. BIOL. 269:270-280(1997).
 CC -1- SUBUNIT: MONOMER.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M18970; G153121; -
 DR PIR: A28664; A28664.
 DR PIR: A29566; A29566.
 DR PDB: 1ESF; 11-JUL-96.
 DR PDB: 1SEA; 15-OCT-95.
 DR PDB: 1SXT; 19-NOV-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PRAM: PF01123; Staph_strep_toxin; 1.
 DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN A.
 FT DISULFID 120 130
 FT METAL 25 25 ZINC.
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 2).
 FT SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;
 SQ
 Query Match 84.4%; Score 54; DB 1; Length 257;
 Best Local Similarity 80.0%; Pred. No. 8.39e-02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 171 KKNATVOELD 180
 Oy 1 KKNATVOELD 10
 RESULT 2
 ID ETYD_STAU STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE D PRECURSOR (SED).
 GN ENTJ.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 89359112.
 RA BAYLES K.W., IANDOLO J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal
 enterotoxin D."
 RL J. BACTERIOL. 171:4799-4806(1989).
 RN [2]
 RN SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RC STRAIN=ATCC 23235;
 RX MEDLINE: 97157473.
 RA SUNDSTROM M., ABRAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,
 RA DOHLSTEN M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals
 RT Zn2+-mediated homodimerization."
 RL EMBO J. 15:6832-6840(1996).
 CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M28521; G758691; -
 DR PIR: A33953; A33953.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PRAM: PF01123; Staph_strep_toxin; 1.
 DR HSP: P13163; 1SXT.
 DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
 FT SIGNAL 1 25
 FT CHAIN 26 258 ENTEROTOXIN D.
 FT METAL 212 212 ZINC.
 FT METAL 250 250 ZINC.
 FT METAL 252 252 ZINC.
 FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
 FT SEQUENCE 258 AA; 29746 MW; 2D1A120 CRC32;
 SQ
 Query Match 84.4%; Score 54; DB 1; Length 258;
 Best Local Similarity 80.0%; Pred. No. 8.39e-02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 172 KKNATVOELD 181
 Oy 1 KKNATVOELD 10
 RESULT 3
 ID ETYB_STAU STANDARD; PRT; 266 AA.
 AC P01552;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
 GN ENTB.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 86168029.
 RA JONES C.L., KHAN S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
 RT aureus."
 RL J. BACTERIOL. 166:29-33(1986).
 RN [2]
 RN SEQUENCE OF 40-91 FROM N.A.
 RX MEDLINE: 85298255.
 RA RANELLI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in
 RT Escherichia coli and Staphylococcus aureus."
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985).
 RN [3]
 RN SEQUENCE OF 28-266 (S-6).
 RP MEDLINE: 71007902.

PA HUANG I.-Y., BERGDOLL M.S.:
 PT "The primary structure of staphylococcal enterotoxin B. 3. The
 PT Cytogen bromide peptides of reduced and aminoethylated enterotoxin
 RT B, and the complete amino acid sequence.";
 RL J. BIOL. CHEM. 245:3518-3525(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE: 93063291.
 RA SAMIATIAN S., FUREY W.F. JR., PLETCHER J., SAX M.:
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
 RL NATURE 359:801-806(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RX MEDLINE: 94203282.
 RA JARDEZKY T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G.,
 RT CHI Y.I., STRAUFRACHER C., STROMINGER J.L., WILEY D.C.:
 RT "Three-dimensional structure of a human class II histocompatibility
 RT molecule complexed with superantigen.";
 RL NATURE 368:711-718(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE: 98181012.
 RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.:
 RT "Crystal structure of microbial superantigen staphylococcal
 RT enterotoxin B at 1.5-A resolution: implications for superantigen
 RT recognition by MHC class II molecules and T-cell receptors.";
 RL J. MOL. BIOL. 277:61-79(1998).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M1118; G153000; -.
 DR PIR: A01815; ENSAB6.
 DR PIR: S27360; S27360.
 DR PDB: 1SEB: 20-JUN-96.
 DR PDB: 3SEB: 28-JAN-98.
 DR PDB: 3SEB: 27-MAY-98.
 DR PDB: 1SE3: 16-JUN-97.
 DR PDB: 1SE4: 15-OCT-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph-Strep-Toxin; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 266
 FT DISULFID 120 140
 FT CONFLICT 56 58
 FT CONFLICT 69 77
 FT CONFLICT 118 118
 FT CONFLICT 128 130
 FT CONFLICT 133 135
 FT CONFLICT 149 150
 FT CONFLICT 156 156
 FT CONFLICT 185 186
 FT CONFLICT 233 233
 FT CONFLICT 246 247
 SO SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
 Query Match 82.8%; Score 53; DB 1; Length 266;
 Best Local Similarity 80.0%; Pred. No. 1,50e-01;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KKATVOELD 10
 RESULT 4
 ID ETYPE:STAAU STANDARD; PRT; 257 AA.
 AC P12993;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
 GN ENTE.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-74.
 RC STRAIN-MJB265;
 RX MEDLINE: 88257005.
 RA COUCH J.L., SOLTIS M.T., BETLEY M.J.:
 RT "Cloning and nucleotide sequence of the type E staphylococcal
 RT enterotoxin gene.";
 RL J. BACTERIOL. 170:2954-2960(1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE: 96022987.
 RA SAMIATIAN S., FUREY W.F. JR., PLETCHER J., SAX M.:
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL NAT. STRUCT. BIOL. 2:680-686(1995).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M21319; G153002; -.
 DR PIR: A28179; A28179.
 DR PDB: 1SEB: 15-OCT-95.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph-Strep-Toxin; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 257
 FT SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;
 SO SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;
 Query Match 81.3%; Score 52; DB 1; Length 257;
 Best Local Similarity 80.0%; Pred. No. 2.66e-01;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 171 KKATVOELD 180
 ||| |||||
 OY 1 KKATVOELD 10
 RESULT 5
 ID R3 MAIZE STANDARD; PRT; 224 AA.
 AC P06586;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
 GN RPS3.
 OS ZEA MAYS (MAIZE).
 OC CHLOROPLAST.
 OC EUKARYOTA: VIRIDIPANTAE; STREPTOPHYTA; EMBRIOPHYTA; TRACHEOPHYTA;

CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
CC POACEAE; ZEA.
RN [1]
CC SEQUENCE FROM N.A.
RX MEDLINE: 87231045.
RA MCLAUGHLIN W.E., LARRINDA I.M.;
RT "The sequence of the maize plastid encoded rps3 locus";
RL NUCLEIC ACIDS RES. 15:4689-4689(1987).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE: 95395841.
RA MAIER R.M., NECKERMANN K., IGOI G.L., KOESSEL H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing";
RT J. MOL. BIOL. 251:614-628(1995).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: Y00340; G12469; -
DR EMBL: M31336; G552741; -
DR EMBL: X86563; G902860; -
DR MAIZEDB: 66303; -
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
DR PFAM: PF00189; S3_C; 1.
DR PFAM: PF00417; S3_N; 1.
DR MENDEL: 13473; ZEMa:rs3.1.
KM RIBOSOMAL PROTEIN; CHLOROPLAST.
SQ SEQUENCE 224 AA; 25916 MW; 3ED95CFF CRC32;
Query Match 79.7%; Score 51; DB 1; Length 224;
Best Local Similarity 50.0%; Pred. No. 4.73e-01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
DB 93 KKGAIIELE 102
OY 1 KKGATVOELD 10
RESULT 6
ID R3_ORYSA STANDARD; PRT; 239 AA.
AC P12146;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ORYZA SATIVA (RICE).
OC CHLOROPLAST.
CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
CC POACEAE; ORYZA.
RN [1]
RX SEQUENCE FROM N.A.
RX STRAIN-CV. NIPONBARE;
RA SUGIURA M.;
RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RX COMPLETE GENOME.
RX MEDLINE: 89364698.
RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,
RA MOJI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-Q.,
RA KANNO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct tRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";

RL MOL. GEN. GENET. 217:185-194(1989).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: X15901; G12025; -
DR PIR: J00265; R3R23
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
DR PFAM: PF00189; S3_C; 1.
DR PFAM: PF00417; S3_N; 1.
DR MENDEL: 13258; Orysa:rs3.1.
KM RIBOSOMAL PROTEIN; CHLOROPLAST.
SQ SEQUENCE 239 AA; 27518 MW; 38E916EE CRC32;
Query Match 79.7%; Score 51; DB 1; Length 239;
Best Local Similarity 50.0%; Pred. No. 4.73e-01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
DB 108 KKGAIIELE 117
OY 1 KKGATVOELD 10
RESULT 7
ID HEL_HAEIN STANDARD; PRT; 274 AA.
AC P26093;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LIPOPROTEIN E PRECURSOR (OUTER MEMBRANE PROTEIN P4) (OMP P4).
GN HEL OR OMP4 OR H10693.
OS HAEMOPHILUS INFLUENZAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURACEAE;
OC HAEMOPHILUS.
RN [1]
RX SEQUENCE FROM N.A., AND SEQUENCE OF 263-274.
RX STRAIN-RD / KW20B;
RX MEDLINE: 91348867.
RA GREEN B.A., FARLEY J.E., QUINN-DEY T., DEICH R.A., ZLOTNICK G.M.;
RT "The e (P4) outer membrane protein of Haemophilus influenzae:
RT biologic activity of anti-e serum and cloning and sequencing of the
RT structural gene";
RT INFECT. IMMUN. 59:3191-3198(1991).
RN [2]
RX SEQUENCE FROM N.A.
RX STRAIN-RD / KW20;
RX MEDLINE: 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA MCKENNAVE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., CORTON M.D.,
RA UETTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RT SCIENCE 269:496-512(1995).
RL -1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
CC ANCHOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

CC -1- THE DMD GENE IS THE LARGEST KNOWN GENE IN HUMANS. IT IS 2.4
 CC MILLION BASE-PAIRS IN SIZE AND COMPRISES 79 EXONS.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING; THE 3 SHORTER VARIANTS ARE CALLED
 CC DYSTROPHIN-1, -2 AND -3.
 CC -1- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY
 CC ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIBRININ,
 CC ABP-120, ABP-180, OR BETA-FODRIN).
 CC -1- SIMILARITY: CONTAINS 1 WW DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X06179; G30840; ALT_SEQ.
 DR EMBL: X06178; G30837; -.
 DR EMBL: X14298; G30846; ALT_SEQ.
 DR EMBL: X15495; E20865; -.
 DR EMBL: X54820; G30842; -.
 DR EMBL: X13045; E3996; -.
 DR EMBL: X13046; G809549; -.
 DR EMBL: X13047; E15313; -.
 DR EMBL: X13048; E15311; -.
 DR EMBL: U27203; G1171132; -.
 DR EMBL: U27203; G1171133; -.
 DR EMBL: X15148; G30939; -.
 DR PIR: A27605; A27605.
 DR PIR: A27162; A27162.
 DR PIR: S05291; S05291.
 DR MIM: 310200; -.
 DR MIM: 302045; -.
 DR PROSITE: PS00019; ACTININ_1; 1.
 DR PROSITE: PS00020; ACTININ_2; 1.
 DR PROSITE: PS01159; WW_DOMAIN_1; 1.
 DR PROSITE: PS50020; WW_DOMAIN_2; 1.
 DR PFAM: PF00307; actinin-binding; 1.
 DR PFAM: PF00397; ww_rps_mwp; 1.
 DR PFAM: PF00435; spectrin; 21.
 DR PFAM: PF00569; 22; 1.
 DR HSSP: 001082; 1AA2.
 KW STRUCTURAL PROTEIN; ACTIN-BINDING; CALCIUM-BINDING; CYTOSKELETON;
 KM REPEAT; DISEASE MUTATION; ALTERNATIVE SPLICING.
 FT DOMAIN 1 240
 FT DOMAIN 300 3000
 FT DOMAIN 3055 3088
 FT DOMAIN 3089 3360
 FT VARIANT 32 62
 FT VARIANT 54 54
 FT VARIANT 133 133
 FT VARIANT 168 168
 FT VARIANT 231 231
 FT VARIANT 231 231
 FT VARIANT 365 365
 FT VARIANT 495 534
 FT VARIANT 623 623
 FT VARIANT 773 773
 FT VARIANT 784 784
 FT VARIANT 882 882
 FT VARIANT 1197 1197
 FT VARIANT 1245 1245
 FT VARIANT 1278 1278
 FT VARIANT 1377 1377
 FT VARIANT 1469 1469
 FT VARIANT 1745 1745
 FT VARIANT 1844 1844
 FT VARIANT 2155 2155
 FT VARIANT 2191 2191
 FT VARIANT 2305 2366
 FT VARIANT 2366 2366
 FT VARIANT 2910 2910
 E -> V (IN DMD).

FT VARIANT 2912 2912 N -> D (IN DMD).
 FT VARIANT 2921 2921 H -> R (IN BMD).
 FT VARIANT 2937 2937 Q -> R.
 FT VARIANT 3421 3421 A -> V (IN BMD).
 FT VARSPLIC 1 1 M -> MTEILLIFFEPAFLN (IN DYSTROPHIN-1).
 FT VARSPLIC 2 1357 MISSING (IN DYSTROPHIN-1).
 Note: remainder of annotations omitted.
 Query Match 78.18; Score 50; DB 1; Length 3685;
 Best Local Similarity 60.08; Pred. No. 8.30e-01;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 2512 KOKATMODEL 2521
 Qy 1 KKKATVOELD 10
 RESULT 9
 ID VAMH SCHPO STANDARD; PRT; 386 AA.
 AC Q101S1;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 44.5 KD PROTEIN C3P10.17 IN CHROMOSOME I.
 GN SPAC3P10.17
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 OC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA MURPHY E., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: TO YEAST LTV1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z69369; E22121; -.
 DR HYPOTHETICAL PROTEIN; ATP-BINDING.
 KW NP_BIND 216 223 ATP (POTENTIAL).
 SQ SEQUENCE 386 AA; 44480 MW; 8B48AB60 CRC32;
 Query Match 76.68; Score 49; DB 1; Length 386;
 Best Local Similarity 60.08; Pred. No. 1.44e+00;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Db 366 KKKSSLEELD 375
 Qy 1 KKKATVOELD 10
 RESULT 10
 ID DPP6 RAT STANDARD; PRT; 859 AA.
 AC P46101;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
 DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
 GN DPP6
 OS RATIUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
RX MEDLINE; 92108018.
RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;
RT "Differential expression of two distinct forms of mRNA encoding
RL members of a dipeptidyl aminopeptidase family.";
PROC. NATL. ACAD. SCI. U.S.A. 89:197-201(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
CC FUNCTION. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: DPPX-S IS EXPRESSED IN BRAIN AND SOME
CC PERIPHERAL TISSUES INCLUDING KIDNEY, OVARY, AND TESTIS; IN
CC CONTRAST DPPX-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN.
CC -1- ALTERNATIVE PRODUCTS: TWO DISTINCT FORMS (DPPX-L AND -S) SHARE AN
CC IDENTICAL TRANSMEMBRANE DOMAIN AND A LONG C-TERMINAL EXTRACELLULAR
CC DOMAIN, BUT HAVE LONG AND SHORT N-TERMINAL CYTOPLASMIC DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M76426; G408714; -;
DR EMBL; M76427; G408716; -;
DR PFM; PF00326; Prolyl_oligopep; 1.
DR PFM; PF00930; DPPX_N-term; 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
FT DOMAIN 1 89
FT TRANSMEM 90 110
FT FT CYTOPLASMIC (POTENTIAL).
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 111 859
FT CARBOHYD 167 167
FT CARBOHYD 168 168
FT CARBOHYD 313 313
FT CARBOHYD 398 398
FT CARBOHYD 465 465
FT CARBOHYD 529 529
FT CARBOHYD 560 560
FT CARBOHYD 807 807
FT CARBOHYD 859 859
FT VARSPLIC 1 75
FT MASLYQRTGKINTSRSPAPPEASRLGGGPEDEAGSKP
FT LGPOAQAAPRERCGAGGRPFQYQARSDCDEED -> MTT
FT AKSPASGKSVQOQDO (IN DPPX-S).
SQ SEQUENCE 859 AA; 97301 MM; BA3COE82 CRC32;
Query Match 76.6%; Score 49; DB 1; Length 859;
Best Local Similarity 66.7%; Pred. No. 1.44e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 122 KKATVDEL 130
QY 1 KKATVDEL 9
RESULT 11
ID DPP6_BOVIN STANDARD: PRT; 863 AA.
AC P42659;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
GN DPP6.
OS BOS Taurus (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE-BRAIN;
RX MEDLINE; 92108018.
RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;
RT "Differential expression of two distinct forms of mRNA encoding
RL members of a dipeptidyl aminopeptidase family.";
PROC. NATL. ACAD. SCI. U.S.A. 89:197-201(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
CC FUNCTION. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN. DPPX-L
CC IS EXPRESSED EXCLUSIVELY IN THE BRAIN WHEREAS DPPX-S IS FOUND IN
CC BRAIN, KIDNEY, OVARY AND TESTIS.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM
CC (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE
CC SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M76428; G408718; -;
DR EMBL; M76429; G408720; -;
DR PFM; PF00326; Prolyl_oligopep; 1.
DR PFM; PF00930; DPPX_N-term; 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
FT DOMAIN 1 93
FT TRANSMEM 94 114
FT FT CYTOPLASMIC (POTENTIAL).
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 115 863
FT CARBOHYD 171 171
FT CARBOHYD 402 402
FT CARBOHYD 469 469
FT CARBOHYD 533 533
FT CARBOHYD 564 564
FT CARBOHYD 811 811
FT CARBOHYD 863 863
FT VARSPLIC 1 79
FT MASLYQRTGKINTSRSPAPPEASRLGGGPEDEAGSKP
FT PLGQAAPAAAPRERCGAGGRPFQYQARSDCDEED ->
FT MTTAKENASGKSVQOQDO (IN DPPX-S).
SQ SEQUENCE 863 AA; 96556 MM; 8DA40472 CRC32;
Query Match 76.6%; Score 49; DB 1; Length 863;
Best Local Similarity 66.7%; Pred. No. 1.44e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 126 KKATVDEL 134
QY 1 KKATVDEL 9
RESULT 12
ID DPP6_HUMAN STANDARD: PRT; 865 AA.
AC P42658;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
GN DPP6.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
SEQUENCE FROM N.A.

```

RC TISSUE-HIPPOCAMPUS;
RX MEDLINE; 93372805.
RA YOKOTANI N., DOI K., WENTHOLD R.J., WADA K.:
RT "Non-conservation of a catalytic residue in a dipeptidyl
RT aminopeptidase IV-related protein encoded by a gene on human
RT chromosome 7."
RL HUM. MOL. GENET. 2:1037-1039(1993).
CC -1- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
CC ACTIVITY. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM
CC (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE
CC SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96859; G306706; -
DR EMBL; M96860; G306708; -
DR MIM; 126141; -
DR PFAM; PF00326; Prolyl-oligopep; 1.
DR PFAM; PF00930; DPPX_N.term; 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
FT DOMAIN 1 95
FT TRANSMEM 96 116
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 117 865
FT CARBOHYD 173 173
FT CARBOHYD 319 319
FT CARBOHYD 404 404
FT CARBOHYD 471 471
FT CARBOHYD 535 535
FT CARBOHYD 566 566
FT CARBOHYD 813 813
FT CARBOHYD 813 813
FT VARSPLIC 1 81
FT FT MASKEDPORTKINTSRSPAPPPSHLIGGCGPEEDGAGA
FT FT KPLGRAGAAAPRRGGGGGAGGPRFOYGRSGDGED
FT FT -> MTTAKEPSAGSKSYOOEOE (IN DPPX-S).
SQ SEQUENCE 865 AA; 97588 MW; 514C21E2 CRC32;
Query Match 76.6%; Score 49; DB 1; Length 865;
Best Local Similarity 66.7%; Pred. No. 144e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 128 KKKVTEDEL 136
QY 1 KKKATVQEL 9

```

```

RESULT 13
ID DMD_MOUSE STANDARD; PRT; 3678 AA.
AC P11531; Q60703;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE DYSTROPHIN.
GN DMD.
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCURIONATHI; MORIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92253376.

```

```

RA BIES R.D., PHELPS S.F., CORTEZ M.D., ROBERTS R., CASKEY C.T.,
RA CHAMBERLAIN J.S.:
RT "Human and murine dystrophin mRNA transcripts are differentially
RT expressed during skeletal muscle, heart, and brain development."
RL NUCLEIC ACIDS RES. 20:1725-1731(1992).
RN [2]
RP SEQUENCE OF 1-201 FROM N.A.
RA MEDLINE; 87273512.
RA KOENIG M., HOFFMAN E.P., BERTELSON C.J., MONACO A.P., FEENER C.,
RA KUNKEL L.M.:
RT "Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and
RT preliminary genomic organization of the DMD gene in normal and
RT affected individuals."
RL CELL 50:509-517(1987).
RN [3]
RP SEQUENCE OF 300-1390 FROM N.A.
RA MEDLINE; 88018015.
RA HOFFMAN E.P., MONACO A.P., FEENER C.C., KUNKEL L.M.:
RT "Conservation of the Duchenne muscular dystrophy gene in mice and
RT humans."
RL SCIENCE 238:347-350(1987).
RN [4]
RP SEQUENCE OF 986-1056 FROM N.A.
RN STRAIN-C57BL/10; TISSUE-SKELETAL MUSCLE.
RX MEDLINE; 94154933.
RA CHAMBERLAIN J.S., PHELPS S.F., COX G.A., MAICHELE A.J.,
RA GREENWOOD A.D.:
RT "PCR analysis of muscular dystrophy in mdx mice."
RL MOL. CELL BIOL. HUM. DIS. SER. 3:167-169(1993).
RN [5]
RP ALTERNATIVE SPLICING.
RC STRAIN-C57BL/10; TISSUE-RETINA;
RX MEDLINE; 95360002.
RA D'SOUZA V.N., NGUYEN T.M., MORRIS G.E., KARGES W., PILBERS D.A.,
RA RAY P.N.:
RT "A novel dystrophin isoform is required for normal retinal
RT electrophysiology."
RL HUM. MOL. GENET. 4:837-842(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE
CC PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED DURING SKELETAL
CC MUSCLE, HEART, AND BRAIN DEVELOPMENT. ALSO EXPRESSED IN
CC RETINA.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 11 DISTINCT ISOFORMS EXIST.
CC -1- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY
CC ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FILBRIN,
CC ABP-120, ABP-180, OR BETA-FODRIN).
CC -1- SIMILARITY: CONTAINS 1 MW DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M68859; G3188028; -
DR EMBL; M18025; G192972; -
DR EMBL; U56724; G136045; -
DR EMBL; U15218; G681889; -
DR PIR; B27162; B27162.
DR MGD; MGI:94909; DMD.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS01159; MW DOMAIN_1; 1.
DR PROSITE; PS50020; MW DOMAIN_2; 1.
DR PFAM; PF00307; actinin-binding; 1.
DR PFAM; PF00435; spectrin; 1.
DR PFAM; PF00569; Z2; 1.
DR HSSP; 001082; 1AA2.
KW STRUCTURAL PROTEIN; ACTIN-BINDING; CALCIUM-BINDING; CYTOSKELETON;

```


THIS PAGE BLANK (USPTO)

 MWSELEH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

Mparc_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:09:16 1999; MasPar time 5.19 Seconds

Tabular output not generated. 105.122 Million cell updates/sec

Title: >US-09-150-947-3

Description: (1-10) from US09150947.pep

Perfect Score: 64

Sequence: 1 KKKATVOELD 10

Scoring table: PAM 150

Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl9
 1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
 5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
 9:sp.phage 10:sp.plant 11:sp.protein 12:sp.unclassified
 13:sp.invertebrate 14:sp.virus

Statistics: Mean 22.230; Variance 25.047; scale 0.888

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------|------------------------|-----------|
| 1 | 58 | 90.6 | 268 | 2 | 085217 | ENTEROTOXIN J | 2.55e-02 |
| 2 | 55 | 85.9 | 464 | 13 | 091693 | MOTHERS AGAINST DPP. | 1.39e-01 |
| 3 | 53 | 82.8 | 260 | 2 | 034971 | SUPERANTIGEN. | 4.20e-01 |
| 4 | 53 | 82.8 | 260 | 2 | 054739 | SUPERANTIGEN SSA. | 4.20e-01 |
| 5 | 53 | 82.8 | 260 | 2 | 054738 | SUPERANTIGEN SSA. | 4.20e-01 |
| 6 | 50 | 78.1 | 288 | 13 | 091491 | DYSTROPHIN (FRAGMENT). | 2.10e-00 |
| 7 | 50 | 78.1 | 368 | 4 | 014205 | DYSTROPHIN (DMD). | 2.10e-00 |
| 8 | 49 | 76.6 | 384 | 10 | 029224 | BZIP TRANSCRIPTION FAC | 3.53e+00 |
| 9 | 49 | 76.6 | 850 | 5 | 021350 | KOBF4.1 PROTEIN. | 3.53e+00 |
| 10 | 48 | 75.0 | 180 | 10 | 081265 | CAMP RESPONSIVE ELEMEN | 5.92e+00 |
| 11 | 48 | 75.0 | 241 | 2 | 053585 | ENTEROTOXIN H PRECURSO | 5.92e+00 |
| 12 | 48 | 75.0 | 324 | 10 | 039163 | OCS-ELEMENT BINDING FA | 5.92e+00 |
| 13 | 48 | 75.0 | 325 | 10 | 039140 | LEUCINE ZIPPER. | 5.92e+00 |
| 14 | 48 | 75.0 | 334 | 10 | 041237 | MAS-BINDING FACTOR MBF | 5.92e+00 |
| 15 | 48 | 75.0 | 362 | 10 | 039897 | TGACG-MOTIF-BINDING PR | 5.92e+00 |
| 16 | 48 | 75.0 | 364 | 10 | 039162 | OCS-ELEMENT BINDING FA | 5.92e+00 |
| 17 | 48 | 75.0 | 367 | 10 | 039237 | BZIP TRANSCRIPTION FAC | 5.92e+00 |
| 18 | 48 | 75.0 | 368 | 10 | 041236 | MAS-BINDING FACTOR MBF | 5.92e+00 |
| 19 | 48 | 75.0 | 370 | 10 | 043647 | LEUCINE ZIPPER TRANSCR | 5.92e+00 |
| 20 | 48 | 75.0 | 372 | 10 | 005699 | TRANSCRIPTIONAL ACTIVA | 5.92e+00 |

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------|------------------------|-----------|
| 21 | 48 | 75.0 | 374 | 10 | 041235 | MAS-BINDING FACTOR MBF | 5.92e+00 |
| 22 | 48 | 75.0 | 433 | 10 | 041650 | CEBB-LIKE PROTEIN. | 5.92e+00 |
| 23 | 48 | 75.0 | 436 | 10 | 024160 | LEUCINE ZIPPER TRANSCR | 5.92e+00 |
| 24 | 48 | 75.0 | 464 | 13 | 091913 | MAD1. | 5.92e+00 |
| 25 | 48 | 75.0 | 465 | 11 | P70442 | MAD HOMOLOG 1 (MOTHERS | 5.92e+00 |
| 26 | 48 | 75.0 | 465 | 11 | P97454 | MAD HOMOLOG 1 (SMAD5). | 5.92e+00 |
| 27 | 48 | 75.0 | 465 | 4 | 015798 | SMAD5. | 5.92e+00 |
| 28 | 48 | 75.0 | 465 | 4 | 015797 | SMAD1. | 5.92e+00 |
| 29 | 48 | 75.0 | 465 | 4 | 099717 | MAD-LIKE PROTEIN. | 5.92e+00 |
| 30 | 48 | 75.0 | 465 | 11 | P70341 | SMAD5. | 5.92e+00 |
| 31 | 48 | 75.0 | 465 | 4 | 014688 | SMAD5. | 5.92e+00 |
| 32 | 48 | 75.0 | 465 | 11 | P70340 | SMAD1. | 5.92e+00 |
| 33 | 48 | 75.0 | 465 | 13 | P79947 | SMAD1. | 5.92e+00 |
| 34 | 48 | 75.0 | 466 | 11 | P97568 | MOTHERS AGAINST DPP 1 | 5.92e+00 |
| 35 | 48 | 75.0 | 466 | 11 | P70520 | SMAD1 PROTEIN. | 5.92e+00 |
| 36 | 48 | 75.0 | 531 | 10 | 049067 | BASIC LEUCINE ZIPPER P | 5.92e+00 |
| 37 | 48 | 75.0 | 1369 | 13 | P79950 | TYROSINE KINASE RECEPT | 5.92e+00 |
| 38 | 48 | 75.0 | 1369 | 13 | P70003 | XRON. | 5.92e+00 |
| 39 | 47 | 73.4 | 236 | 2 | 054696 | TYPE A EXOTOXIN PRECUR | 9.83e+00 |
| 40 | 47 | 73.4 | 236 | 2 | 057453 | TYPE A EXOTOXIN PRECUR | 9.83e+00 |
| 41 | 47 | 73.4 | 236 | 2 | P97163 | TYPE A EXOTOXIN PRECUR | 9.83e+00 |
| 42 | 47 | 73.4 | 236 | 2 | 054779 | TYPE A EXOTOXIN PRECUR | 9.83e+00 |
| 43 | 47 | 73.4 | 334 | 2 | 052631 | GLYCERALDEHYDE-3-PHOSP | 9.83e+00 |
| 44 | 47 | 73.4 | 460 | 3 | 060095 | HYPOTHETICAL 52.7 KD P | 9.83e+00 |
| 45 | 47 | 73.4 | 656 | 5 | 017539 | COIB10.8 PROTEIN. | 9.83e+00 |

ALIGNMENTS

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|--|--------------|--------|-----|-----|-------------|-----------|
| AC | 085217 | PRELIMINARY; | PRT; | 268 | AA. | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, CREATED) | | | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) | | | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) | | | | | | |
| DE | ENTEROTOXIN J. | | | | | | |
| GN | SEQ | | | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | | | |
| OG | PLASMID PIB485. | | | | | | |
| OC | BACTERIAL FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | | | |
| OC | STAPHYLOCOCCUS. | | | | | | |
| RN | [1] | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN-KS11410. | | | | | | |
| RA | ZHANG S., IANDOLO J.J., STEWART G.C.; | | | | | | |
| RT | "The enterotoxin D plasmid of Staphylococcus aureus encodes a second | | | | | | |
| RT | enterotoxin determinant (seq)." | | | | | | |
| RL | SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS. | | | | | | |
| DR | EMBL: AF053140; G3372542;... | | | | | | |
| DR | PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1. | | | | | | |
| DR | PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1. | | | | | | |
| KM | PLASMID. | | | | | | |
| SO | SEQUENCE 268 AA; 31230 MW; 52EB1B06 CRC32; | | | | | | |

Query Match 90.6%; Score 58; DB 2; Length 268;
 Best Local Similarity 80.0%; Pred. No. 2.55e-02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|---|----------------|--------|-----|-----|-------------|-----------|
| DB | 171 | KKKATVOELD 160 | | | | | |
| QY | 1 | KKKATVOELD 10 | | | | | |
| RESULT | 2 | PRELIMINARY; | PRT; | 464 | AA. | | |
| AC | 091693 | PRELIMINARY; | PRT; | 464 | AA. | | |
| DT | 01-NOV-1996 (TREMBLREL. 01, CREATED) | | | | | | |
| DT | 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) | | | | | | |
| DT | 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) | | | | | | |
| DE | MOTHERS AGAINST DPP. | | | | | | |
| GN | XKAD. | | | | | | |
| OS | XENOPUS LAEVIS (AFRICAN CLAWED FROG). | | | | | | |
| OC | EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; | | | | | | |

```
OC MESOBATRACHIA: PIPOIDEA: PIPIDAE: XENOPODINAE: XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96312915.
RA THOMSEN G.H.;
RT "Xenopus mothers against decapentaplegic is an embryonic ventralizing
agent that acts downstream of the BMP-2/4 receptor."
RL DEVELOPMENT 122:2359-2366(1996).
DR EMBL: U58834: G1381671: -.
DR PFAM: PF00968: Dwarfin: 1.
SQ SEQUENCE 464 AA; 52346 MW; 4017799F CRC32;

Query Match      85.9%; Score 55; DB 13; Length 464;
Best Local Similarity 60.0%; Pred. No. 1.39e-01;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 43 KKGAIQELE 52
OY 1 KKKATVOELD 10

RESULT 3
ID 054971 PRELIMINARY: PRT: 260 AA.
AC 054971;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-WELER;
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL INFECT. IMMUN. 62:1867-1874(1994).
DR EMBL: L29565; G476764; -.
DR PFAM: PF01123: Strep-Strp-toxin: 1.
KW SUPERANTIGEN.
SQ SEQUENCE 260 AA; 29797 MW; FE391C2B CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 4.20e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKOYTVQELD 183
OY 1 KKKATVOELD 10

RESULT 4
ID 054739 PRELIMINARY: PRT: 260 AA.
AC 054739;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL INFECT. IMMUN. 62:1867-1874(1994).
DR EMBL: U48793; G1245174; -.
DR PFAM: PF01123: Strep-Strp-toxin: 1.
SQ SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 4.20e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKOYTVQELD 183
OY 1 KKKATVOELD 10

RESULT 6
ID 091491 PRELIMINARY: PRT: 288 AA.
AC 091491;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE DYSTROPHIN (FRAGMENT).
OS TOREPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
```

```
RL INFECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL INFECT. IMMUN. 64:1161-1165(1996).
DR EMBL: U48794; G1245176; -.
DR EMBL: U48792; G1245172; -.
DR PFAM: PF01123: Strep-Strp-toxin: 1.
SQ SEQUENCE 260 AA; 29767 MW; C81448C1 CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 4.20e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKOYTVQELD 183
OY 1 KKKATVOELD 10

RESULT 5
ID 054738 PRELIMINARY: PRT: 260 AA.
AC 054738;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-MGAS 1842;
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL INFECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-MGAS 1842;
RX MEDLINE: 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL INFECT. IMMUN. 64:1161-1165(1996).
DR EMBL: U48793; G1245174; -.
DR PFAM: PF01123: Strep-Strp-toxin: 1.
SQ SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 4.20e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKOYTVQELD 183
OY 1 KKKATVOELD 10

RESULT 6
ID 091491 PRELIMINARY: PRT: 288 AA.
AC 091491;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE DYSTROPHIN (FRAGMENT).
OS TOREPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
```

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
 OC ELASMOBRANCHII; RAJIFORMES; TORPEDINOIDEI; TORPEDINIDAE; TORPEDO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ELECTRIC ORGAN;
 RA RAVIN A.J., DYER S.M., YEADON J.E., BURDEN S.J.;
 RL J. PHYSIOL. 85:131-133(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ELECTRIC ORGAN;
 RA YEADON J.E.;
 RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U01229; G402248; -;
 FT NON_TER
 SO SEQUENCE 288 AA; 32781 MW; 6F238B53 CRC32;
 Query Match 78.1%; Score 50; DB 13; Length 288;
 Best Local Similarity 70.0%; Pred. No. 2.10e+00;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 278 KOKATQDD 287
 QY 1 KKKATVQELD 10
 RESULT 7
 ID 014205 PRELIMINARY; PRT: 3685 AA.
 AC 014205; P78452; P78450; 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE DYSTROPHIN (DMD).
 GN DMD.
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE OF 1-497 FROM N.A.
 RX MEDLINE; 87273512.
 RA KOENIG M., HOFFMAN E.P., BENTELSON C.J., MONACO A.P., FEENER C.,
 RA KUNKEL L.M.;
 RT "Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and
 RT preliminary genomic organization of the DMD gene in normal and
 RT affected individuals.";
 RL CELL 50:509-517(1987).
 RN [2]
 RP SEQUENCE OF 490-1208 FROM N.A.
 PX MEDLINE; 88018015.
 RA HOFFMAN E.P., MONACO A.P., FEENER C.C., KUNKEL L.M.;
 RT "Conservation of the Duchenne muscular dystrophy gene in mice and
 RT humans.";
 RL SCIENCE 238:347-350(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88194521.
 RA KOENIG M., MONACO A.P., KUNKEL L.M.;
 RT "The complete sequence of dystrophin predicts a rod-shaped
 RT cytoskeletal protein.";
 RL CELL 53:219-226(1988).
 RN [4]
 RP SEQUENCE OF 2980-3685 FROM N.A.
 RX MEDLINE; 92372062.
 RA ROBERTS R.G., COFFEY A.J., BOBROW M., BENTLEY D.R.;
 RT Determination of the exon structure of the distal portion of the
 RT dystrophin gene by vectorite PCR.";
 RL GENOMICS 13:942-950(1992).
 RN [5]
 RP SEQUENCE OF 3377-3408 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 89181947.
 RA FEENER C.A., KOENIG M., KUNKEL L.M.;
 RT "Alternative splicing of human dystrophin mRNA generates isoforms at
 RT the carboxy terminus.";

RL NATURE 338:509-511(1989).
 RN [6]
 RP SEQUENCE OF 218-277 FROM N.A.
 RX MEDLINE; 88067745.
 RA HEILIG R., LEMAIRE C., MANDEL J.L.;
 RT "A 230kb cosmid walk in the Duchenne muscular dystrophy gene:
 RT detection of a conserved sequence and of a possible deletion prone
 RT region.";
 RL NUCLEIC ACIDS RES. 15:9129-9142(1987).
 RN [7]
 RP SEQUENCE OF 218-276 FROM N.A.
 RX MEDLINE; 89043945.
 RA MALHOTRA S.B., HART K.A., KLAUT H.J., THOMAS N.S.T., BOBRUG S.E.,
 RA BURGESS A.H.M., BOBROW M., HARPER P.S., THOMPSON M.W., RAY P.N.,
 RA WORTON R.G.;
 RT "Frame-shift deletions in patients with Duchenne and Becker muscular
 RT dystrophy.";
 RL SCIENCE 242:755-759(1988).
 DR EMBL; M86884; G457519; JOINED.
 DR EMBL; M86885; G457519; JOINED.
 DR EMBL; M86886; G457519; JOINED.
 DR EMBL; M86887; G457519; JOINED.
 DR EMBL; M86888; G457519; JOINED.
 DR EMBL; M86889; G457519; JOINED.
 DR EMBL; M86890; G457519; JOINED.
 DR EMBL; M86891; G457519; JOINED.
 DR EMBL; M86892; G457519; JOINED.
 DR EMBL; M86893; G457519; JOINED.
 DR EMBL; M86894; G457519; JOINED.
 DR EMBL; M86895; G457519; JOINED.
 DR EMBL; M86896; G457519; JOINED.
 DR EMBL; M18533; G181857; -;
 DR EMBL; M86903; G457519; -;
 DR EMBL; M86897; G457519; JOINED.
 DR EMBL; X06293; E3995; -;
 DR EMBL; M23261; G514936; -;
 DR EMBL; M86898; G457519; JOINED.
 DR EMBL; M86899; G457519; JOINED.
 DR EMBL; M86900; G457519; JOINED.
 DR EMBL; M86901; G457519; JOINED.
 DR EMBL; M86902; G457519; JOINED.
 DR EMBL; X15149; G30931; -;
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS01159; MW_DOMAIN_1; 1.
 DR PFAM; PF00307; actinin-binding; 1.
 DR PFAM; PF00397; MW_rsp5_WWP; 1.
 DR PFAM; PF00435; spectrin; 21.
 DR PFAM; PF00569; 22; 1.
 KW MEMBRANE.
 SQ SEQUENCE 3685 AA; 426674 MW; 51981B59 CRC32;
 Query Match 78.1%; Score 50; DB 4; Length 3685;
 Best Local Similarity 60.0%; Pred. No. 2.10e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 2512 KOKATQDD 2521
 QY 1 KKKATVQELD 10
 RESULT 8
 ID 039234 PRELIMINARY; PRT: 384 AA.
 AC 039234;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE BZIP TRANSCRIPTION FACTOR.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRUALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA:
 RX MEDLINE: 94272006.
 RA MAO Z.H., LIU X., LAM E.E.L.;
 RT "TGA3 is a distinct member of the TGA family of bZIP transcription
 RL factors in Arabidopsis thaliana.";
 CC PLANT MOL. BIOL. 25:1-11(1994).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER bZIP PROTEINS.
 DR EMBL: L10208; G304113; -.
 DR PROSITE: PS00036; bZIP_BASIC; 1.
 DR PFAM: PF00170; bZIP; 1.
 DR MENDEL: 6813; ARATH:1269; 5.
 KM DNA-BINDING: NUCLEAR PROTEIN.
 SQ SEQUENCE 384 AA: 43755 MW: 8004A3B2 CRC32;

Query Match 76.6%; Score 49; DB 10; Length 384;
 Best Local Similarity 60.0%; Pred. No. 3.53e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 116 KKKATVOELD 125
 :||| ||:|:
 QY 1 KKKATVOELD 10

RESULT 9
 ID 021350 PRELIMINARY; PRT; 850 AA.
 AC 021350;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE K08F4.1 PROTEIN.
 GN K08F4.1
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HEMERY C.;
 RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSFORTH R., ANDERSON K., BAYNES C., BEERS M.,
 RA BONEFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIR M., JOHNSTON L.,
 RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIRKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL NATURE 368:32-38(1994).
 DR EMBL: Z68879; E1348045; -.
 SQ SEQUENCE 850 AA: 96892 MW: E60173F0 CRC32;

Query Match 76.6%; Score 49; DB 5; Length 850;
 Best Local Similarity 60.0%; Pred. No. 3.53e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 834 KKKATVOELD 843
 ||| ||:|:
 QY 1 KKKATVOELD 10

RESULT 10
 ID 081265 PRELIMINARY; PRT; 180 AA.
 AC 081265;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE CAMP RESPONSIVE ELEMENT BINDING PROTEIN (FRAGMENT).
 OS CICHORIUM INTIBUS (CHICORY).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 OC ASTERIDAE; ASTERALES; ASTERACEAE; CICHORIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MESSIAEN J., DRAVE M., BELLEFONTAINE F., VAN CUTSEM P.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF067187; G3249626; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 180 AA: 20262 MW: 47EE7ICE CRC32;

Query Match 75.0%; Score 48; DB 10; Length 180;
 Best Local Similarity 60.0%; Pred. No. 5.92e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 11 KKKATVOELD 20
 :||| ||:|:
 QY 1 KKKATVOELD 10

RESULT 11
 ID 053585 PRELIMINARY; PRT; 241 AA.
 AC 053585;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN H PRECURSOR.
 GN SEH.
 OS STAPHYLOCOCCUS AUREUS.
 OS BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D4508;
 RA REN K., BANNAN J.D., PANCHOLI V., CHEUNG A.L., ROBBINS J.C.,
 RA FISCHETTI V.A., ZABRISKIE J.B.;
 RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U11702; G510692; -.
 DR PFAM: PF01123; Staph_Strep_toxin; 1.
 KM SIGNAL.
 FT SIGNAL 1
 FT CHAIN 25
 SQ SEQUENCE 241 AA: 27858 MW: AE5AB04A CRC32;

Query Match 75.0%; Score 48; DB 2; Length 241;
 Best Local Similarity 70.0%; Pred. No. 5.92e+00;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 154 KKKATVOELD 163
 ||| ||:|:
 QY 1 KKKATVOELD 10

RESULT 12
 ID 039163 PRELIMINARY; PRT; 324 AA.
 AC 039163;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE OCS-ELEMENT BINDING FACTOR 5 (FRAGMENT).
 GN OBF5.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA: TISSUE-ROOT CALLUS;
 RX MEDLINE: 94073225.

RA ZHANG B., FOLEY R.C., SINGH K.B.;
 RT "Isolation and characterization of two related Arabidopsis
 AT ccs-element bzlp binding proteins.";
 RL PLANT J. 4:711-716(1993).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
 CC EMBL: X69900; G414615; .
 DR PROSITE: PS00036; BZIP_BASIC; 1.
 DR PFAM: PF00170; bzip; 1.
 DR MENDEL: 6812; ARATH; 1269;4.
 KW DNA-BINDING; NUCLEAR PROTEIN.
 FT NON_TER 1
 SQ SEQUENCE 324 AA; 36332 MW; ABA7EAFD CRC32;
 Query Match 75.0%; Score 48; DB 10; Length 324;
 Best Local Similarity 60.0%; Pred. No. 5.92e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 58 RKKAYVOOLE 67
 :||| ||:|:
 QY 1 KKKATVQELD 10

RESULT 13
 ID Q39140 PRELIMINARY; PRT; 325 AA.
 AC Q39140;
 DT 01-NOV-1996 (TREMBLERL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLERL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLERL. 09, LAST ANNOTATION UPDATE)
 DE LEOCINE ZIPPER.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 CC EURARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: TRACHEOPHYTA:
 CC EUPHYLIOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
 CC CAPRARIACE: BRASSICACEAE: ARABIDOPSIS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA: TISSUE-LEAF;
 RA VANGALA S., BAILEY-SERRES J.;
 RL PLANT PHYSIOL. 109:721-721(1995).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
 CC EMBL: L42327; G903688; .
 DR PROSITE: PS00036; BZIP_BASIC; 1.
 DR PFAM: PF00170; bzip; 1.
 DR MENDEL: 6810; ARATH; 1269;2.
 KW DNA-BINDING; NUCLEAR PROTEIN.
 SQ SEQUENCE 325 AA; 36391 MW; 93C41913 CRC32;

Query Match 75.0%; Score 48; DB 10; Length 325;
 Best Local Similarity 60.0%; Pred. No. 5.92e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 58 RKKAYVOOLE 67
 :||| ||:|:
 QY 1 KKKATVQELD 10

RESULT 14
 ID Q41237 PRELIMINARY; PRT; 334 AA.
 AC Q41237;
 DT 01-NOV-1996 (TREMBLERL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLERL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLERL. 09, LAST ANNOTATION UPDATE)
 DE MAS-BINDING FACTOR MBF1 (FRAGMENT).
 OS SOLANUM TUBEROSUM (POTATO).
 CC EURARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: TRACHEOPHYTA;
 CC EUPHYLIOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS;
 CC ASTERIDAE: SOLANACEAE: SOLANALES: SOLANACEAE: SOLANUM.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 94302169.
 RA FELTKAMP D., MASTERSON R., STARK J., ROSAHL S.;
 RT "Analysis of the involvement of ocs-1-like bzip-binding elements in the

RT differential strength of the bidirectional mas1'2' promoter.";
 RL PLANT PHYSIOL. 105:259-268(1994).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
 CC EMBL: S73828; G765201; .
 DR PROSITE: PS00036; BZIP_BASIC; 1.
 DR PFAM: PF00170; bzip; 1.
 DR MENDEL: 10645; SOLTU; 1269;3.
 KW DNA-BINDING; NUCLEAR PROTEIN.
 FT NON_TER 1
 SQ SEQUENCE 334 AA; 37796 MW; 331DC21C CRC32;
 Query Match 75.0%; Score 48; DB 10; Length 334;
 Best Local Similarity 60.0%; Pred. No. 5.92e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 67 RKKAYVOOLE 76
 :||| ||:|:
 QY 1 KKKATVQELD 10

RESULT 15
 ID Q39897 PRELIMINARY; PRT; 362 AA.
 AC Q39897;
 DT 01-NOV-1996 (TREMBLERL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLERL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLERL. 09, LAST ANNOTATION UPDATE)
 DE TGAG-MOTIF-BINDING PROTEIN.
 GN STGAL1.
 OS GLYCINE MAX (SOYBEAN).
 CC EURARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMERYOPHYTA: TRACHEOPHYTA:
 CC EUPHYLIOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
 CC FABALES: FABACEAE: PAPILIONOIDEAE: GLYCINE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-WILLIAMS;
 RA CHEONG Y.H., PARK J.M., YOO C.M., BAHK J.D., CHO M.J., HONG J.C.;
 RL MOL. CELLS 4:405-412(1994).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
 CC EMBL: L28005; G986969; .
 DR PROSITE: PS00036; BZIP_BASIC; 1.
 DR PFAM: PF00170; bzip; 1.
 DR MENDEL: 8279; GLYMA; 1269;1.
 KW DNA-BINDING; NUCLEAR PROTEIN.
 SQ SEQUENCE 362 AA; 40948 MW; 08E0A07B CRC32;

Query Match 75.0%; Score 48; DB 10; Length 362;
 Best Local Similarity 60.0%; Pred. No. 5.92e+00;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 96 RKKAYVOOLE 105
 :||| ||:|:
 QY 1 KKKATVQELD 10

Search completed: Tue Aug 31 19:09:53 1999
 Job time : 37 secs.

THIS PAGE BLANK (USPTO)


```

QY      1 KKKVTAQELD 10
      |||
RESULT  2
ID      W64636 standard; peptide: 12 AA.
AC      W64636;
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide pSEB(150-161).
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
PN      Staphylococcus aureus.
PD      W09829444-A1.
PE      09-JUL-1998.
PR      30-DEC-1997; IL0438.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
DR      WPI: 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 6; Page 41; 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PERT or by a mixture of PERTs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PERTs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PERT. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PERT.
SQ      Sequence 12 AA;

Query Match      100.0%; Score 64; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.58e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      3 KKKVtageld 12
      |||
QY      1 KKKVTAQELD 10

RESULT  3
ID      W64640 standard; peptide: 13 AA.
AC      W64640;
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide pSEB(150-161).
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
PN      Staphylococcus aureus.
PD      W09829444-A1.
PE      09-JUL-1998.
PR      30-DEC-1997; IL0438.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
DR      WPI: 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 15; Page 41; 68pp; English.

```

```

CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced
        by PERT or by a mixture of PERTs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PERTs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PERT. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PERT.
SQ      Sequence 13 AA;

Query Match      100.0%; Score 64; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.58e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      4 KKKVtageld 13
      |||
QY      1 KKKVTAQELD 10

RESULT  4
ID      W64647 standard; peptide: 239 AA.
AC      W64647;
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB protein fragment.
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
PN      Staphylococcus aureus.
PD      W09829444-A1.
PE      09-JUL-1998.
PR      30-DEC-1997; IL0438.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
DR      WPI: 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Example 8; Page 41; 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced
        by PERT or by a mixture of PERTs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PERTs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PERT. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PERT.
SQ      Sequence 239 AA;

Query Match      100.0%; Score 64; DB 34; Length 239;
Best Local Similarity 100.0%; Pred. No. 9.58e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      152 KKKVtageld 161
      |||
QY      1 KKKVTAQELD 10

RESULT  5
ID      R13206 standard; Protein: 239 AA.
AC      R13206;
DT      15-OCT-1991 (first entry)
DE      Staphylococcal enterotoxin B.
KW      SEB; cancer treatment; pyrogen; tumouricide.

```


OS Staphylococcus aureus.
 PN W09110680-A.
 PD 25-JUL-1991.
 PF 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 as Staphylococcal protein A without potential toxic reactions
 PS Disclosure: Fig 1: 74pp; English.
 CC SEB was isolated and purified from S.aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEB. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydropathy profiles.
 CC See R13203-R13211.
 SQ Sequence 239 AA;

Query Match 100.0%; Score 64; DB 3; Length 239;
 Best Local Similarity 100.0%; Pred. No. 9.58e-01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 152 kkkvtageld 161
 |||||
 QY 1 KKKVTAQELD 10

RESULT 6
 ID R45014 standard; protein: 239 AA.
 AC R45014;

DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SEB.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 OS autoimmune disease; toxicity; Protein A; perfusion system.
 PN W09324136-A.
 PD 09-DEC-1993.
 PF 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PI (TERM/) TERMAN D S.
 DR Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS Disclosure: Fig 1: 90pp; English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC Sequence 239 AA;

Query Match 100.0%; Score 64; DB 8; Length 239;
 Best Local Similarity 100.0%; Pred. No. 9.58e-01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 152 kkkvtageld 161
 |||||
 QY 1 KKKVTAQELD 10

RESULT 7
 ID W06737 standard; Protein: 255 AA.

AC W06737;
 DT 08-MAR-1997 (first entry)
 DE Staphylococcus enterotoxin B.
 KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
 KW vaccine; adjuvant.
 OS Staphylococcus sp.

FT Key Location/Qualifiers
 FT peptide 1..15
 FT /label= sig_peptide
 PN W09636366-A1.
 PD 21-NOV-1996.
 PF 20-MAY-1996; U07432.
 PR 18-MAY-1995; US-446918.
 PR 29-DEC-1995; US-580806.
 PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
 PI Dow SW, Elmslie RE, Potter TA;
 DR WPI: 97-011857/01.
 DR N-PSDB; T45698.

PT Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer
 PS Example 1: Page 96-97; 13pp; English.
 CC A cDNA clone (T45698) codes for staphylococcal enterotoxin B
 CC (W06737) superantigen. Nucleic acids encoding superantigens (see
 CC also W06738-39), esp. truncated forms of the superantigen lacking
 CC the leader peptide, can be utilised in the gene therapy of cancer,
 CC infectious diseases and immunological disorders. The nucleic acid,
 CC optionally in combination with cytokine or chemokine nucleic acids,
 CC is delivered to an animal using e.g. liposomes. It acts by
 CC controlling the activity of effector cells, such as T-cells,
 CC macrophages, monocytes and/or natural killer cells. Localised
 CC prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal.
 SQ Sequence 255 AA;

Query Match 100.0%; Score 64; DB 20; Length 255;
 Best Local Similarity 100.0%; Pred. No. 9.58e-01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 168 kkkvtageld 177
 |||||
 QY 1 KKKVTAQELD 10

RESULT 8
 ID R13209 standard; Protein: 221 AA.
 AC R13209;

DT 15-OCT-1991 (first entry)
 DE Streptococcal pyrogenic enterotoxin A.
 KW SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 OS Streptococcus NY-5 strain.
 PN W09110680-A.
 PD 25-JUL-1991.
 PF 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure: Fig 1: 74pp; English.
 CC SPE A can be used for tumouricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to Streptococcal
 CC pyrogenic exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles.
 CC See R13203-R13211.
 SQ Sequence 221 AA;

Query Match 90.6%; Score 58; DB 3; Length 221;
 Best Local Similarity 90.0%; Pred. No. 5.13e+00;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 137 kkmvtaqeld 146

Qy 1 KKKVTAQELD 10

RESULT 9

ID R45017 standard; protein; 221 AA.

AC R45017;

DT 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SPE A.

KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;

OS autoimmune disease; toxicity; Protein A; perfusion system.

PN W09324136-A.

PD 09-DEC-1993.

PF 01-JUN-1993; U05213.

PR 01-JUN-1992; US-891718.

PA (STON/) STONE J L.

PI (TERM/) TERMAN D S.

DR Stone JL, Terman DS;

WP: 93-405418/50.

PT Use of staphylococcal enterotoxin(s) and homologues - for

PS treating cancer in a patient or for the treatment of auto-immune

CC diseases

CC The sequences given in R45017-21 are Staphylococcal enterotoxins (SEs)

CC which may be used in the methods of the invention for treating cancer

CC in a patient. These SEs, and homologues of them, can be used as

CC tumouricidal agents for treating cancers and autoimmune disease.

CC They exhibit tumouricidal activity and toxicity identical to that

CC observed for the protein A perfusion system. They may be administered

CC by intravenous injection.

CC Sequence 221 AA;

Qy 1 KKKVTAQELD 10

Db 137 kkmvtaqeld 146

Qy 1 KKKVTAQELD 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

CC The present sequence is a non-lethal Streptococcus pyogenes

CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce

CC vaccines to protect animals against wild type SPE-A and to treat

CC cancer and streptococcal toxic shock syndrome (STSS). The mutant

CC SPE-A causes neutralising antibodies (Ab) to be produced, which

CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,

CC group A streptococcal infection, myositis, fasciitis and liver

CC damage. The neutralising Ab is preferably administered in

CC conjunction with antibiotic therapy. The mutant SPE-A is

CC especially useful for treating T cell lymphomas, and ovarian and

CC uterine cancer. It is thought that mutant SPE-A can be selectively

CC toxic to T cell lymphoma cells.

CC N.B. Sequence not given in the specification, but constructed

CC using the wild type SPE-A sequence given on pages 77-79.

CC Sequence 250 AA;

Qy 1 KKKVTAQELD 10

Db 166 kkmvtaqeld 175

Qy 1 KKKVTAQELD 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

Query Match 90.6%; Score 58; DB 24; Length 250;

Best Local Similarity 90.0%; Pred. No. 5.13e+00;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 166 kkmvtaqeld 175

Qy 1 KKKVTAQELD 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

Query Match 90.6%; Score 58; DB 24; Length 251;

Best Local Similarity 90.0%; Pred. No. 5.13e+00;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 166 kkmvtaqeld 175

Qy 1 KKKVTAQELD 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

FT 10

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 167 kkmvtageld 176
 ||:|||||
 1 KKKVTAQELD 10

Qy 1 KKKVTAQELD 10

RESULT 12
 ID W12152 standard; Protein: 251 AA.
 AC W12152.
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Cys98Ser.
 KW Streptococcal toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 PS Synthetic.
 FT Key
 FT peptide Location/Qualifiers
 FT /label= sig_peptide
 FT /label= mat_peptide
 FT /label= mat_peptide
 FT Misc_difference 128
 FT /note= "wild type Cys replaced by Ser"
 FT W09640930-A1.
 PN 19-DEC-1996.
 PF 07-JUN-1996; U10252.
 PR 07-JUN-1995; US-480261.
 PA (MINU) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR WPI: 97-099936/09.
 PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Example 4; Page -: 102pp; English.
 CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 SQ Sequence 251 AA;

Query Match 90.6%; Score 58; DB 24; Length 251;
 Best Local Similarity 90.0%; Pred. No. 5.13e+00;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 167 kkmvtageld 176
 ||:|||||
 1 KKKVTAQELD 10

Qy 1 KKKVTAQELD 10

RESULT 13
 ID W12149 standard; Protein: 251 AA.
 AC W12149.
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant N20D/C98S.
 KW Streptococcal toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.

OS Synthetic.
 FH Key
 FH peptide Location/Qualifiers
 FH /label= sig_peptide
 FH /label= mat_peptide
 FH /label= mat_peptide
 FH Misc_difference 50
 FH /note= "wild type Asn replaced by Asp"
 FH Misc_difference 128
 FH /note= "wild type Cys replaced by Ser"
 FT W09640930-A1.
 PN 19-DEC-1996.
 PF 07-JUN-1996; U10252.
 PR 07-JUN-1995; US-480261.
 PA (MINU) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR WPI: 97-099936/09.
 PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Claim 5; Page -: 102pp; English.
 CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 SQ Sequence 251 AA;

Query Match 90.6%; Score 58; DB 24; Length 251;
 Best Local Similarity 90.0%; Pred. No. 5.13e+00;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 167 kkmvtageld 176
 ||:|||||
 1 KKKVTAQELD 10

Qy 1 KKKVTAQELD 10

RESULT 14
 ID W59781 standard; Protein: 251 AA.
 AC W59781.
 DT 12-OCT-1998 (first entry)
 DE Amino acid sequence of mutant Streptococcus pyogenes exotoxin A.
 KW SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
 KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
 KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
 KW uterine cancer.
 OS Streptococcus pyogenes.
 PN W09824911-A2.
 PD 11-JUN-1998.
 PF 05-DEC-1997; U22228.
 PR 06-DEC-1996; US-032830.
 PA (MINU) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR WPI: 98-333330/29.
 PT New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention
 PT or treatment of streptococcal infection or toxic shock syndrome
 PS Claim 3; Page -: 95pp; English.
 CC This is the amino acid sequence of the mutant Streptococcus pyogenes
 CC exotoxin A (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin
 CC has at least 1 aa change and is nonlethal compared with a protein to
 CC wild type SPE-A toxin. The mutant SPE-A toxins are nontoxic and can
 CC produce antibodies that neutralise wild type SPE-A toxin activity. The
 CC toxins can be used in vaccines and therapeutics to generate a protective
 CC immune response against streptococcal infection. They can be used to

CC protect against the development of streptococcal toxic shock syndrome
 CC (STSS). In addition, the toxins can be used for treating animals with
 CC symptoms of streptococcal infection or STSS and in methods for
 CC stimulating T cell proliferation and in the treatment of cancer. In
 CC particular they can be used for treating T cell lymphomas, and ovarian
 CC and uterine cancer.
 CC This sequence was not present in the specification but was created
 CC using information given.
 SQ Sequence 251 AA;

Query Match 90.6%; Score 58; DB 33; Length 251;
 Best Local Similarity 90.0%; Pred. No. 5.13e+00;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 167 kkmvtaqeld 176
 ||:|||||
 QY 1 KKKVTAQELD 10

RESULT 15

ID M12147 standard; Protein: 251 AA.

DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Asn20Asp.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 OS Synthetic.

FH Key Location/Qualifiers
 FT peptide 1..30

FT peptide /label= sig_peptide
 FT peptide 31..251

FT peptide /label= mat_peptide
 FT peptide 50

FT peptide /note= "wild type Asn replaced by Asp"

PN M09640930-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; U10252.

PR 07-JUN-1995; US-480261.

PA (MINU) UNIV MINNESOTA.

PI Ohlendorf D, Roggiani M, Schlievert PM, Stroehr J;

PT WPI: 97-098936/09

PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.

PS Claim 5; Page -: 102pp; English.

CC The present sequence is a non-lethal Streptococcus pyogenes

CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce

CC vaccines to protect animals against wild type SPE-A and to treat

CC cancer and streptococcal toxic shock syndrome (STSS). The mutant

CC SPE-A causes neutralising antibodies (Ab) to be produced, which

CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,

CC group A streptococcal infection, myositis, fasciitis and liver

CC damage. The neutralising Ab is preferably administered in

CC conjunction with antibiotic therapy. The mutant SPE-A is

CC especially useful for treating T cell lymphomas, and ovarian and

CC uterine cancer. It is thought that mutant SPE-A can be selectively

CC toxic to T cell lymphoma cells.

CC N.B. Sequence not given in the specification, but constructed

CC using the wild type SPE-A sequence given on pages 77-79.

CC Sequence 251 AA;

Query Match 90.6%; Score 58; DB 24; Length 251;
 Best Local Similarity 90.0%; Pred. No. 5.13e+00;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 167 kkmvtaqeld 176
 ||:|||||
 QY 1 KKKVTAQELD 10

Search completed: Tue Aug 31 19:13:23 1999
 Job time : 16 secs.

#contents annotation: tryptic peptides
REFERENCE A90548
#authors Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
#journal Dunnehy, D.A.; Bergdoll, M.S.
#title Biochemistry (1965) 4:1011-1016
#cross-references EMBL:X61573; NID:947303; PID:947304
#contents annotation: biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinsky, E.Y.; Kolesov, M.I.; Maurer-Fogy, I.;
Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of
#accession S27240
#molecule-type protein
#residues 28-42;128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin; extracellular protein; toxin
FEATURE
#journal #domain signal sequence #status predicted #label SIG\
#title #product enterotoxin B #status experimental #label MAR\
#accession #disulfide_bonds #status experimental
SUMMARY #length 266 #molecular-weight 31436 #checksum 4249
Query Match 100.0%; Score 64; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 1,42e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 179 KKKVTAQELD 188
1 KKKVTAQELD 10
RESULT 2
ENTRY S18789 #type fragment
TITLE exotoxin A precursor (allele 4) - Streptococcus pyogenes
ALTERNATE_NAMES scarlet fever toxin
ORANISM #formal_name Streptococcus pyogenes
#variety strain MGAS262 isolate California
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
25-Mar-1998
ACCESSIONS S18789
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references EMBL:X61573
#accession S18789
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61573; NID:947303; PID:947304
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
#journal #domain signal sequence (fragment) #status predicted
#title #label SIG\
#accession #product exotoxin A (fragment) #status predicted #label
SUMMARY #length 236 #checksum 3493
Query Match 90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 4.05e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 159 KKKVTAQELD 168
1 KKKVTAQELD 10
Oy 1 KKKVTAQELD 10
RESULT 3
ENTRY S18783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes
#accession S18783
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61568; NID:947289; PID:947290
#experimental_source strain MGAS158 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
ALTERNATE_NAMES scarlet fever toxin
ORANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS158 isolate Nebraska; strain MGAS485 isolate
Yugoslavia; strain MGAS491 isolate United Kingdom; strain
MGAS624 isolate Germany; strain MGAS495 isolate Germany
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
ACCESSIONS S18783; S18793; S18794; S18801; S18798
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references EMBL:X61573
#accession S18783
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61568; NID:947289; PID:947290
#experimental_source strain MGAS158 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18793
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEA
#cross-references EMBL:X61569; NID:947313; PID:947314
#experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18794
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEZ
#cross-references EMBL:X61570; NID:947315; PID:947316
#experimental_source strain MGAS491 isolate United Kingdom unassigned
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18801
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEY
#cross-references EMBL:X61572; NID:947333; PID:947334
#experimental_source strain MGAS624 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18798
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-236 #label NEO
#cross-references EMBL:X61571; NID:947323; PID:947324
#experimental_source strain MGAS495 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
#journal #domain signal sequence (fragment) #status predicted
#title #label SIG\
#accession #product exotoxin A (fragment) #status predicted #label
SUMMARY #length 236 #checksum 3493
Query Match 90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 4.05e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
23-236      #label SIG\
#product exotoxin type A (fragment) #status predicted
SUMMARY      #length 236 #checksum 612

Query Match      90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 4.05e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 159 KKMVTAOELD 168
OY 1 KKMVTAOELD 10

RESULT 4
ENTRY  S18786 #type fragment
TITLE  exotoxin type A precursor (allele 2) - Streptococcus pyogenes
        (phage (strain MGAS250 isolate California and others)
        (fragment))
ALTERNATE_NAMES  scarlet fever toxin
ORGANISM  #formal_name Streptococcus pyogenes phage
            strain MGAS250 isolate California; strain MGAS251 isolate
            California; strain MGAS256 isolate California; strain
            MGAS285 isolate Colorado; strain MGAS480 isolate
            Yugoslavia; strain MGAS492 isolate United Kingdom; strain
            MGAS496 isolate Germany
DATE  29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
        02-Jul-1998
ACCESSIONS  S18786; S18787; S18788; S18790; S18792; S18795; S18799
REFERENCE  S18782
#authors  Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal  J. Exp. Med. (1991) 174:1271-1274
#title  Characterization and clonal distribution of four alleles of
        the speA gene encoding pyrogenic exotoxin A (scarlet fever
        toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession  S18786
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NEI
#cross-references EMBL:X61561; NID:g47297; PID:g47298
#experimental_source  strain MGAS250 isolate California unassigned phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991
#accession  S18787
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NEA
#cross-references EMBL:X61562; NID:g47299; PID:g47300
#experimental_source  strain MGAS251 isolate California unassigned phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991
#accession  S18788
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NE2
#cross-references EMBL:X61563; NID:g47301; PID:g47302
#experimental_source  strain MGAS256 isolate California unassigned phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991
#accession  S18790
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NEY
#cross-references EMBL:X61564; NID:g47305; PID:g47306
#experimental_source  strain MGAS285 isolate Colorado unassigned phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991
#accession  S18792
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NEO
#cross-references EMBL:X61565; NID:g47311; PID:g47312

#experimental_source  strain MGAS480 isolate Yugoslavia unassigned phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991
#accession  S18795
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NEH
#cross-references EMBL:X61566; NID:g47317; PID:g47318
#experimental_source  strain MGAS492 isolate United Kingdom unassigned
        phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991
#accession  S18799
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  1-236 #label NES
#cross-references EMBL:X61567; NID:g47325; PID:g47326
#experimental_source  strain MGAS496 isolate Germany unassigned phage
#note  the nucleotide sequence was submitted to the EMBL Data
        Library, September 1991

GENETICS
#gene  speA2
CLASSIFICATION  #superfamily enterotoxin B
KEYWORDS  exotoxin
FEATURE  1-22
        #domain signal sequence (fragment) #status predicted
        #label SIG\
        #product exotoxin type A (fragment) #status predicted
        #label MAT

SUMMARY  #length 236 #checksum 1685

Query Match      90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 4.05e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 159 KKMVTAOELD 168
OY 1 KKMVTAOELD 10

RESULT 5
ENTRY  S29659 #type complete
TITLE  exotoxin type A precursor (allele 1) - Streptococcus pyogenes
        phase T12
ALTERNATE_NAMES  erythrogenic toxin; scarlet fever toxin
ORGANISM  #formal_name Streptococcus pyogenes phase T12
DATE  22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change
        25-Mar-1998
ACCESSIONS  S29659; S18782; S18784; S18785; S18791; S18796; S18797;
        S18800
REFERENCE  S29659
#authors  Weeks, C.R.; Ferretti, J.J.
#journal  Infect. Immun. (1986) 52:144-150
#title  Nucleotide sequence of the type A streptococcal exotoxin
        (erythrogenic toxin) gene from Streptococcus pyogenes
        bacteriophage T12.
#cross-references GB:U04053; EMBL:M19350; NID:g1877426; PID:g1877430
#accession  S29659
#molecule_type  DNA
#residues  1-251 #label WFE
#cross-references GB:U04053; EMBL:M19350; NID:g1877426; PID:g1877430
REFERENCE  S18782
#authors  Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal  J. Exp. Med. (1991) 174:1271-1274
#title  Characterization and clonal distribution of four alleles of
        the speA gene encoding pyrogenic exotoxin A (scarlet fever
        toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession  S18782
#status  nucleic acid sequence not shown; translation not shown
#molecule_type  DNA
#residues  9-244 #label NEI
#cross-references EMBL:X61560; NID:g47287; PID:g47288
```



```

SUMMARY      #length 266 #molecular-weight 30671 #checksum 6135
Query Match  : 87.5%; Score 56; DB 2; Length 266;
Best Local Similarity 90.0%; Pred. No. 1,19e-01;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 178 KKSVAQELD 187
||| |||||
QY 1 KKKVTAQELD 10

RESULT 8      ENSAC1 #type complete
ENTRY         enterotoxin C-I precursor - Staphylococcus aureus
TITLE         #formal_name Staphylococcus aureus
ORGANISM      15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change
DATE          05-Sep-1997
ACCESSIONS    S06356; A01816
REFERENCE     S06356
#authors      Bohach, G.A.; Schlievert, P.M.
#journal      Mol. Gen. Genet. (1987) 209:15-20
#title        Nucleotide sequence of the staphylococcal enterotoxin C1 gene
              and relatedness to other pyrogenic toxins.
#cross-references M01D:88038352
#accession    S06356
#molecule_type DNA
#residues     1-266 ##label BOH
#cross-references EMBL:X05815; NID:g46566; PID:g46567
REFERENCE     A01816
#authors      Schmidt, J.J.; Spero, L.
#journal      J. Biol. Chem. (1983) 258:6300-6306
#title        The complete amino acid sequence of Staphylococcal
              enterotoxin C-1.
#cross-references M01D:83213327
#accession    A01816
#molecule_type Protein
#residues     28-75,'IL','78-176','N','178-266 ##label SCH

GENETICS
#gene          entC1
#classification #superfamily enterotoxin B
#keywords      enterotoxin
#feature       1-27
              28-266
              #domain signal sequence #status predicted #label STG\
              #product enterotoxin C-1 #status experimental #label
              MAR\
SUMMARY      #length 266 #molecular-weight 30546 #checksum 4489
Query Match  : 87.5%; Score 56; DB 1; Length 266;
Best Local Similarity 90.0%; Pred. No. 1,19e-01;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 178 KKSVAQELD 187
||| |||||
QY 1 KKKVTAQELD 10

RESULT 9      A29566 #type complete
ENTRY         enterotoxin A
TITLE         #formal_name Staphylococcus aureus
ORGANISM      05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change
DATE          18-Jun-1993
ACCESSIONS    A29566
REFERENCE     A29566
#authors      Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
#journal      J. Biol. Chem. (1987) 262:7006-7013
#title        Complete amino acid sequence of staphylococcal enterotoxin A.
#cross-references M01D:87222293
#accession    A29566
#molecule_type protein
#residues     1-233 ##label HVA

GENETICS

```

```

#gene          entA
#map_position  6
SUMMARY      #length 233 #molecular-weight 27079 #checksum 9580
Query Match  : 84.4%; Score 54; DB 2; Length 233;
Best Local Similarity 80.0%; Pred. No. 3,44e-01;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 147 KKNVTAQELD 156
||| |||||
QY 1 KKKVTAQELD 10

RESULT 10     A28664 #type complete
ENTRY         enterotoxin A precursor - Staphylococcus aureus (strain
TITLE         FRI337)
ORGANISM      #formal_name Staphylococcus aureus
DATE          30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
              20-Mar-1998
ACCESSIONS    A28664
REFERENCE     A28664
#authors      Betley, M.J.; Mekalanos, J.J.
#journal      J. Bacteriol. (1988) 170:34-41
#title        Nucleotide sequence of the type A staphylococcal enterotoxin
              gene.
#cross-references M01D:88086892
#accession    A28664
#molecule_type DNA
#residues     1-257 ##label BET
#cross-references GB:M18970; NID:g153120; PID:g153121
#experimental_source strain FRI337
SUMMARY      #length 257 #molecular-weight 29669 #checksum 2543
Query Match  : 84.4%; Score 54; DB 2; Length 257;
Best Local Similarity 80.0%; Pred. No. 3,44e-01;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 171 KKNVTAQELD 180
||| |||||
QY 1 KKKVTAQELD 10

RESULT 11     A33953 #type complete
ENTRY         enterotoxin D precursor - Staphylococcus aureus
TITLE         #formal_name Staphylococcus aureus
ORGANISM      09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
DATE          09-Sep-1997
ACCESSIONS    A33953
REFERENCE     A33953
#authors      Bayles, K.W.; Iandolo, J.J.
#journal      J. Bacteriol. (1989) 171:4799-4806
#title        Genetic and molecular analyses of the gene encoding
              staphylococcal enterotoxin D.
#cross-references M01D:89359112
#accession    A33953
#status       Preliminary
#molecule_type DNA
#residues     1-258 ##label BAY
#cross-references GB:M28521; NID:g1492109; PID:g758691
SUMMARY      #length 258 #molecular-weight 29746 #checksum 39
Query Match  : 84.4%; Score 54; DB 2; Length 258;
Best Local Similarity 80.0%; Pred. No. 3,44e-01;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 172 KKNVTAQELD 181
||| |||||
QY 1 KKKVTAQELD 10

RESULT 12

```

ENTRY A28179 #type complete
TITLE enterotoxin E precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Sep-1997

ACCESSIONS A28179
#authors A28179
#journal Couch, J.L.; Solits, M.T.; Betley, M.J.
#title J. Bacteriol. (1988) 170:2954-2960
#note Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
#cross-references MUID:88257005
#accession A28179
##molecule_type DNA
##residues 1-257 ##label COU
##cross-references GB:M21319; NID:g153001; PID:g153002
SUMMARY #length 257 #molecular_weight 29358 #checksum 2562

Query Match 81.3%; Score 52; DB 2; Length 257;
Best Local Similarity 80.0%; Pred. No. 9.68e+01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 171 KKEYVOELD 180
OY 1 KKEYVOELD 10

RESULT 13
ENTRY A64575 #type complete
TITLE virB4 homolog - Helicobacter pylori (strain 26695)
ORGANISM #formal_name Helicobacter pylori
DATE 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 10-Oct-1997

ACCESSIONS A64575
REFERENCE A64520
#authors Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Uitterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Feldman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.
#journal Nature (1997) 388:539-547
#title The complete genome sequence of the gastric pathogen Helicobacter pylori.
#cross-references MUID:97394467
#accession A64575
#status preliminary; nucleic acid sequence not shown;
##molecule_type DNA
##residues 1-807 ##label TOM
##cross-references GB:AE000559; GB:AE000511; NID:g2313536; PID:g2313543; TIGR:HP0441

SUMMARY #length 807 #molecular_weight 93383 #checksum 7147

Query Match 81.3%; Score 52; DB 2; Length 807;
Best Local Similarity 60.0%; Pred. No. 9.68e+01;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 143 KKEYTNELE 152
OY 1 KKEYTAEELD 10

RESULT 14
ENTRY A41793 #type complete
TITLE dipeptidyl aminopeptidase-like protein (EC 3.4.14.-) short form, DPPX-S - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle

DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999

ACCESSIONS A41793
REFERENCE A41793
#authors Wada, K.; Yokotani, N.; Hunter, C.; Doi, K.; Wenthold, R.J.; Shimasaki, S.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:197-201
#title Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family.
#cross-references MUID:92108018
#accession A41793
#status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-803 ##label WAD
##cross-references GB:M76429; NID:g408719; PID:g408720
#note sequence extracted from NCBI backbone (NCBIP:75138)
KEYWORDS dipeptidylpeptide hydrolase; glycoprotein
FEATURE 257,342

SUMMARY #length 803 #molecular_weight 90459 #checksum 9315

Query Match 76.6%; Score 49; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 4.37e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 66 KKEYTVEDL 74
OY 1 KKEYTAEEL 9

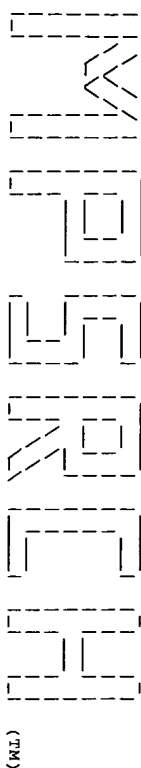
RESULT 15
ENTRY I68600 #type complete
TITLE dipeptidyl aminopeptidase like protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 06-Sep-1996

ACCESSIONS I68600
REFERENCE I54331
#authors Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K.
#journal Hum. Mol. Genet. (1993) 2:1037-1039
#title Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-related protein encoded by a gene on human chromosome 7.
#cross-references MUID:93372805
#accession I68600
#status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-803 ##label RES
##cross-references GB:M6860; NID:g306707; PID:g306708
SUMMARY #length 803 #molecular_weight 91355 #checksum 814

Query Match 76.6%; Score 49; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 4.37e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 66 KKEYTVEDL 74
OY 1 KKEYTAEEL 9

Search completed: Tue Aug 31 19:12:49 1999
Job time : 11 secs.


 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution Rights by Oxford Molecular Ltd

Mpsrch.p protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Aug 31 19:11:19 1999; Maspar time 2.26 Seconds
 Tabular output not generated. 125.221 Million cell updates/sec

Title: >US-09-150-947-4
 Description: (1-10) from US09150947.pep
 Perfect Score: 64
 Sequence: 1 KKKVTAQELD 10

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 23.143; Variance 23.315; scale 0.993

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed.
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description | Pred. No. |
|------------|-------|--------------------|--------|-----------------------------------|-----------|
| 1 | 64 | 100.0 | 266 1 | ETYB_STAAU ENTEROTOXIN TYPE B PRE | 1.21e-04 |
| 2 | 58 | 90.6 | 251 1 | SPEA_STRPY EXOTOXIN TYPE A PRECUR | 5.66e-03 |
| 3 | 56 | 87.5 | 266 1 | ETC3_STAAU ENTEROTOXIN TYPE C-3 P | 1.95e-02 |
| 4 | 56 | 87.5 | 266 1 | ETC1_STAAU ENTEROTOXIN TYPE C-1 P | 1.95e-02 |
| 5 | 56 | 87.5 | 266 1 | ETC2_STAAU ENTEROTOXIN TYPE C-2 P | 1.95e-02 |
| 6 | 54 | 84.4 | 257 1 | ETXA_STAAU ENTEROTOXIN TYPE A PRE | 6.52e-02 |
| 7 | 54 | 84.4 | 257 1 | ETXD_STAAU ENTEROTOXIN TYPE D PRE | 6.52e-02 |
| 8 | 52 | 81.3 | 257 1 | ETXE_STAAU ENTEROTOXIN TYPE E PRE | 2.12e-01 |
| 9 | 49 | 76.6 | 859 1 | DPPE_RAT DIPEPTIDYL PEPTIDASE I | 1.18e+00 |
| 10 | 49 | 76.6 | 863 1 | DPPE_BOVIN DIPEPTIDYL PEPTIDASE I | 1.18e+00 |
| 11 | 49 | 76.6 | 865 1 | DPPE_HUMAN DIPEPTIDYL PEPTIDASE I | 1.18e+00 |
| 12 | 47 | 73.4 | 649 1 | RAA2_SCHPO DNA REPAIR PROTEIN RAD | 3.54e+00 |
| 13 | 46 | 71.9 | 257 1 | RU3_MYCGE 50S RIBOSOMAL PROTEIN | 6.06e+00 |
| 14 | 46 | 71.9 | 302 1 | YDT3_SCHPO HYPOTHETICAL 35.5 KD P | 6.06e+00 |
| 15 | 46 | 71.9 | 489 1 | YN21_CAEEL PUTATIVE ATP-DEPENDENT | 6.06e+00 |
| 16 | 46 | 71.9 | 572 1 | MOES_LYTVS SODIUM- AND CHLORIDE-D | 6.06e+00 |
| 17 | 46 | 71.9 | 727 1 | NTT4_RAT HYPOTHETICAL GENE 56 P | 6.06e+00 |
| 18 | 46 | 71.9 | 1179 1 | VS64_HSV11 NONSTRUCTURAL PROTEIN | 1.03e+01 |
| 19 | 45 | 70.3 | 90 1 | VNS1_LACAO NONSTRUCTURAL PROTEIN | 1.03e+01 |
| 20 | 45 | 70.3 | 202 1 | VNS1_TAFOM 3-ISOPROPYLMALATE DEHY | 1.03e+01 |
| 21 | 45 | 70.3 | 207 1 | LEUD_BUCAP NONSTRUCTURAL PROTEIN | 1.03e+01 |
| 22 | 45 | 70.3 | 230 1 | VNS1_IALEN NONSTRUCTURAL PROTEIN | 1.03e+01 |
| 23 | 45 | 70.3 | 230 1 | VNS1_IAPUE NONSTRUCTURAL PROTEIN | 1.03e+01 |

ALIGNMENTS

| RESULT ID | 1 | ETYB_STAAU | STANDARD; | PRT; | 266 AA. |
|-----------|--|------------|-----------|------|---------|
| AC | P01552; | | | | |
| DT | 21-JUL-1986 (REL. 01, CREATED) | | | | |
| DT | 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE) | | | | |
| DT | 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN TYPE B PRECURSOR (SEB). | | | | |
| GN | ENTB. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | |
| CC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE; 86168029. | | | | |
| RA | JONES C.L., KHAN S.A.; | | | | |
| RT | "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus." | | | | |
| RL | J. BACTERIOL. 166:29-33(1986). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 40-91 FROM N.A. | | | | |
| RX | MEDLINE; 85298255. | | | | |
| RA | RAVELLI D.M., JONES C.L., JOHNS M.B., MUSSERY G.J., KHAN S.A.; | | | | |
| RT | "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus." | | | | |
| RL | PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE OF 28-266 (S-6). | | | | |
| RX | MEDLINE; 71007902. | | | | |
| RA | HDUNG I.-Y., BERGDOLL M.S.; | | | | |
| RT | "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence." | | | | |
| RL | J. BIOL. CHEM. 245:3518-3525(1970). | | | | |
| RN | [4] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS). | | | | |
| RX | MEDLINE; 93063291. | | | | |
| RA | SAMMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.; | | | | |
| RT | "Crystal structure of staphylococcal enterotoxin B, a superantigen." | | | | |
| RL | NATURE 359:801-806(1992). | | | | |
| RN | [5] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II. | | | | |
| RX | MEDLINE; 94203282. | | | | |
| RA | JARDENTZKY T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G., | | | | |
| RT | CHI Y.I., STAUFACHER C., STROMINGER J.L., WILEY D.C.; | | | | |
| RL | "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen." | | | | |
| RL | NATURE 368:711-718(1994). | | | | |

| | | | | | |
|----|----|------|--------|------------------------------------|----------|
| 24 | 45 | 70.3 | 330 1 | YDC3_SCHPO HYPOTHETICAL 36.2 KD P | 1.03e+01 |
| 25 | 45 | 70.3 | 4644 1 | DVHC_RAT DYMEIN HEAVY CHAIN, CY | 1.03e+01 |
| 26 | 44 | 68.8 | 127 1 | CU04_BACR CUTICLE PROTEIN 4 (BC | 1.73e+01 |
| 27 | 44 | 68.8 | 129 1 | Y389_MYCPN HYPOHETICAL PROTEIN M | 1.73e+01 |
| 28 | 44 | 68.8 | 153 1 | YEC8_YEAST HYPOHETICAL 17.4 KD P | 1.73e+01 |
| 29 | 44 | 68.8 | 269 1 | YD54_SCHPO HYPOHETICAL 31.2 KD P | 1.73e+01 |
| 30 | 44 | 68.8 | 417 1 | FRQC_MYXXA FRQC PROTEIN (FRIZZY | 1.73e+01 |
| 31 | 44 | 68.8 | 450 1 | INVO_LEMCA INVOLUCRIN | 1.73e+01 |
| 32 | 44 | 68.8 | 463 1 | NAOX_METJA PUTATIVE NADH OXIDASE | 1.73e+01 |
| 33 | 44 | 68.8 | 498 1 | CTB5_ARATH CYTOCHROME P450 71B5 (| 1.73e+01 |
| 34 | 44 | 68.8 | 552 1 | PEPB_RICCO PYROPHOSPHATE--FRUCTOS | 1.73e+01 |
| 35 | 44 | 68.8 | 576 1 | MOES_HUMAN MOESIN (MEMBRANE-ORGAN | 1.73e+01 |
| 36 | 44 | 68.8 | 576 1 | MOES_MOUSE MOESIN (MEMBRANE-ORGAN | 1.73e+01 |
| 37 | 44 | 68.8 | 576 1 | MOES_PIG MOESIN (MEMBRANE-ORGAN | 1.73e+01 |
| 38 | 44 | 68.8 | 767 1 | PUBL1_SCHPO UBIQUITIN--PROTEIN LIG | 1.73e+01 |
| 39 | 44 | 68.8 | 1738 1 | YCF1_EPIVI HYPOHETICAL 208 KD PR | 1.73e+01 |
| 40 | 43 | 67.2 | 264 1 | SPRC_CAEEL SPARC PRECURSOR (SECR | 2.87e+01 |
| 41 | 43 | 67.2 | 319 1 | UN30_CAEEL HOMEBOX PROTEIN UNC-3 | 2.87e+01 |
| 42 | 43 | 67.2 | 553 1 | YG55_YEAST HYPOHETICAL 62.8 KD P | 2.87e+01 |
| 43 | 43 | 67.2 | 1210 1 | YEH1_ECOLI HYPOHETICAL 138.1 KD | 2.87e+01 |
| 44 | 43 | 67.2 | 1534 1 | MTDM_ARATH DNA (CITOSINE-5)-METHY | 2.87e+01 |
| 45 | 43 | 67.2 | 1752 1 | DESP_HUMAN DESMOPLAKIN I AND II (| 2.87e+01 |

[6]
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RP MEDLINE: 98181012.
 RA PARAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal
 RT enterotoxin B at 1.5-A resolution: implications for superantigen
 RT recognition by MHC class II molecules and T-cell receptors.";
 RL J. MOL. BIOL. 277:61-79(1998).
 CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M1118; GI53000; .
 DR PIR: A01815; ENSAB6.
 DR PIR: S27360; S27360.
 DR PDB: 1SEB; 20-JUN-96.
 DR PDB: 2SEB; 28-JAN-98.
 DR PDB: 3SEB; 27-MAY-98.
 DR PDB: 1SE3; 16-JUN-97.
 DR PUB: 1SE4; 15-OCT-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 DR KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 266
 FT DISULFID 120 140
 FT FT CONFLICT 56 58 DDN -> NND (IN REF. 3).
 FT FT CONFLICT 69 77 DOFLYDLI -> NEFLYLYL (IN REF. 3).
 FT FT CONFLICT 118 118 MISSING (IN REF. 3).
 FT FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
 FT FT CONFLICT 133 135 OTD -> ENT (IN REF. 3).
 FT FT CONFLICT 149 150 NG -> GN (IN REF. 3).
 FT FT CONFLICT 156 156 Y -> YV (IN REF. 3).
 FT FT CONFLICT 185 186 OE -> EO (IN REF. 3).
 FT FT CONFLICT 233 233 D -> N (IN REF. 3).
 FT FT CONFLICT 246 247 DN -> ND (IN REF. 3).
 SO SEQUENCE 266 AA; 31436 MW; EC09D63 CRC32;
 Query Match 100.0%; Score 64; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1,21e-04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

"Nucleotide sequence of the type A streptococcal exotoxin
 (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 T12.";
 RL INFECT. IMMUN. 52:144-150(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 86284313.
 RX JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 RT related to Staphylococcus aureus enterotoxin B.";
 RL MOL. GEN. GENET. 203:354-356(1986).
 CC -I- DISEASE: THE STREPTOCOCCAL PYOGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -I- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U04053; G1877430; .
 DR EMBL: X03929; G47442; .
 DR PIR: A26152; A26152.
 DR PIR: S29659; S29659.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 DR HSSP: P01552; 1SEB.
 DR KW TOXIN; SIGNAL.
 FT SIGNAL 1 30
 FT CHAIN 31 251
 FT FT CONFLICT 6 6 EXOTOXIN TYPE A.
 FT FT CONFLICT 17 18 K -> E (IN REF. 2).
 FT FT CONFLICT 25 35 VT -> MK (IN REF. 2).
 FT FT CONFLICT 40 40 SOEYFAOQDP -> LKGLICSTRPK (IN REF. 2).
 FT FT CONFLICT 43 40 H -> O (IN REF. 2).
 FT FT CONFLICT 47 59 S -> N (IN REF. 2).
 FT FT CONFLICT 129 129 NLQNIYFLYEDP -> TFKIYIFEMRYTL (IN
 FT FT CONFLICT 165 178 REF. 2).
 FT FT CONFLICT 129 129 I -> L (IN REF. 2).
 FT FT CONFLICT 165 178 TNKKMTAAQELDYK -> QIKNGNCSRISTY (IN
 SO SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;
 Query Match 90.6%; Score 58; DB 1; Length 251;
 Best Local Similarity 90.0%; Pred. No. 5,66e-03;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05815; G46567; -.
DR PIR; A01816; ENSAC1.
DR PIR; S06356; S06356.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_strep_toxin; 1.
DR HSPSP; P34071; 1SEP2.
RW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
FT SEQUENCE 266 AA; 30546 MW; FE00255A CRC32;.
SO
Query Match 87.5%; Score 56; DB 1; Length 266;
Best Local Similarity 90.0%; Pred. No. 1,95e-02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 178 KKSVTAGELD 187
OY 1 KKKVTAGELD 10
RESULT 5
AC ETC2_STAUB STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ENT2.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
OC [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE; 89277549.
RX BOHACH G.A., SCHLIEVERT P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RL enterotoxins C1 and C2."
RL INFECT. IMMUN. 57:2249-2252(1989).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE; 96027099.
RX PAPAIOORGIOU A.C., ACHARYA K.R., SHAPIRO R., PASSALACQUA E.F.,
RA BREHM R.D., TRANTER H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RL Staphylococcus aureus reveals a zinc-binding site."
RL STRUCTURE 3:769-779(1995).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE; 96022987.
RX SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RA "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL NAT. STRUCT. BIOL. 2:680-686(1995).
RN [4]
RX COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE; 9734373.
RX SCHAD E.M., PAPAIOORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal

```

RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity."
 RL J. MOL. BIOL. 269:270-280(1997).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 DR PIR: A60114; A60114.
 DR PDB: 1STE: 23-DEC-96.
 DR PDB: 1SEF: 08-MAR-96.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_Strep_toxin; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 SO SEQUENCE 266 AA; 30604 MW; A1ISFD37 CRC32;
 Query Match 87.5%; Score 56; DB 1; Length 266;
 Best Local Similarity 90.0%; Pred. No. 1.95e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 178 KKVTAQELD 187
 QY 1 KKVTAQELD 10
 RESULT 6
 ID ETTX STAAU STANDARD; PRT; 257 AA.
 AC P13163;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE A PRECURSOR (SEA).
 GN EMTA.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRI37.
 RX MEDLINE: 88086892.
 RA BETLEY M.J.; MEKALANOS J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene."
 RL J. BACTERIOL. 170:34-41(1988).
 RN [2]
 RP SEQUENCE OF 25-257.
 RX MEDLINE: 87222293.
 RA HOANG I.-Y.; HUGHES J.L.; BERGDOLL M.S.; SCHANTZ E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A."
 RL J. BIOL. CHEM. 262:7006-7013(1987).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE: 95354648.
 RA SCHAD E.M.; ZAITSEVA I.; ZAITSEV V.N.; DOHLSTEN M.; KALLAND T.;
 RA SCHLEVERT P.M.; OHLENDORF D.H.; SVENSSON L.A.;
 RT "Crystal structure of the superantigen staphylococcal enterotoxin
 type A."
 RL EMBO J. 14:3292-3301(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE: 97113025.
 RA SUNDBSTROM M.; HALLEN D.; SVENSSON A.; SCHAD E.; DOHLSTEN M.;
 RA ABRAHMSSEN L.;
 RT "The co-crystal structure of staphylococcal enterotoxin type A with
 Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding."
 RL J. BIOL. CHEM. 271:32212-32216(1996).

RN [5]
 RP 3D-STRUCTURE MODELLING.
 RX MEDLINE: 96022987.
 RA SWAMINATHAN S.; FOREY W.F. JR.; PLETCHER J.; SAX M.;
 RT "Residues defining v beta specificity in staphylococcal
 RT enterotoxins."
 RL NAT. STRUCT. BIOL. 2:680-686(1995).
 RN [6]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE: 97334573.
 RA SCHAD E.M.; PAPAGEORGIOU A.C.; SVENSSON L.A.; ACHARYA K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity."
 RL J. MOL. BIOL. 269:270-280(1997).
 CC -1- SUBUNIT: MONOMER.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL: M18970; G153121; -
 DR PIR: A28664; A28664.
 DR PIR: A29566; A29566.
 DR PDB: 1SEF: 11-JUL-96.
 DR PDB: 1SEA: 15-OCT-95.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_Strep_toxin; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN A.
 FT DISULFID 120 130
 FT METAL 25 25 ZINC.
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 2).
 SO SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;
 Query Match 84.4%; Score 54; DB 1; Length 257;
 Best Local Similarity 80.0%; Pred. No. 6.52e-02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 171 KKVTAQELD 180
 QY 1 KKVTAQELD 10
 RESULT 7
 ID ETTX STAAU STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE D PRECURSOR (SED).
 GN EMTD.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89359112.

```

RA   BAYLES K.W., IANDOLO J.J.:
RT   "Genetic and molecular analyses of the gene encoding staphylococcal
RT   enterotoxin D."
RL   J. BACTERIOL. 171:479-486(1989).
RN   121
RP   SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC   STRAIN-ATCC 23225;
RX   MEDLINE; 97157473.
RA   SUNDSTROM M., ABRAHSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,
RT   DOHLSTEN M.;
RT   "The crystal structure of staphylococcal enterotoxin type D reveals
RT   Zn2+-mediated homodimerization."
RL   EMBO J. 15:6832-6840(1996).
CC   -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC   -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC   STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC   -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC   PYROGENIC EXOTOXINS ARE ALL RELATED.
CC   -----
CC   THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M28521; G758691; -.
DR   PIR; A33953; A33953.
DR   PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR   PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR   PFAM; PF01123; Staph_Strep_toxin; 1.
DR   HSSP; P13163; 1SXT.
KW   ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
FT   SIGNAL          1      25
FT   CHAIN           26      258
FT   METAL           212     212
FT   METAL           250     250
FT   METAL           252     252
FT   VARIANT         114     114
FT   VARIANT         258 AA; 29746 MM; 2D1AA120 CRC32;
SQ   SEQUENCE      258 AA; 29746 MM; 2D1AA120 CRC32;
      1111111111
Db   172 KKNVTQGFELD 181
QY   1 KKKVTAQELD 10

Query Match      84.4%; Score 54; DB 1; Length 258;
Best Local Similarity 80.0%; Pred. No. 6,52e-02;
Matches      8; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

RESULT      8
ID   ETXE_STAAB   STANDARD;      PRT;      257 AA.
AC   P12993;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN   ENTE.
OS   STAPHYLOCOCCUS AUREUS.
OC   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC   STAPHYLOCOCCUS.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC   STRAIN-MJ8265;
RX   MEDLINE; 88257005.
RA   COUCH J.L., SOLTIS M.T., BETLEY M.J.;
RT   "Cloning and nucleotide sequence of the type E staphylococcal
RT   enterotoxin gene."
RL   J. BACTERIOL. 170:2954-2960(1988).
RN   [2]
RP   3D-STRUCTURE MODELLING.
RX   MEDLINE; 96022987.

```

```

RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.:
RT "Residues defining V beta specificity in staphylococcal
RL enterotoxins."
RL NAT. STRUCT. BIOL. 2:680-686(1995).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M21319, G153002; -.
DR PIR, A28179; A28179.
DR PDB, 1SEE; 15-OCT-95.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
KM SIGNAL
FT 1 27
FT CHAIN
SQ SEQUENCE 257 AA; 29358 MM; 88B6A7C3 CRC32;
Query Match 81.3%; Score 52; DB 1; Length 257;
Best Local Similarity 80.0%; Pred. No. 2,12e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 171 KKEVTQELD 180
1 1 1 1 1 1 1
QY 1 KKKVTAQELD 10
RESULT 9
ID ID DPPE_RAT STANDARD; PRT; 859 AA.
AC P46101.
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPE-L/DPPE-S).
GN DPPE.
OS RATTUS NORVEGICUS (RAT).
OC EUARCHOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ROENTHIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA MEDLINE; 9218018.
RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;
RT "Differential expression of two distinct forms of mRNA encoding
RT members of a dipeptidyl aminopeptidase family."
RL PROC. NATL. ACAD. SCI. U.S.A. 89:197-201(1992).
CC -I- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
CC ACTIVITY. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -I- TISSUE SPECIFICITY: DPPE-S IS EXPRESSED IN BRAIN AND SOME
CC PERIPHERAL TISSUES INCLUDING KIDNEY, OVARY, AND TESTIS; IN
CC CONTRAST DPPE-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN.
CC -I- ALTERNATIVE PRODUCTS: TWO DISTINCT FORMS (DPPE-L AND -S) SHARE AN
CC IDENTICAL TRANSMEMBRANE DOMAIN AND A LONG C-TERMINAL EXTRACELLULAR
CC DOMAIN, BUT HAVE LONG AND SHORT N-TERMINAL CYTOPLASMIC DOMAINS.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: M76426; G408714; -
DR EMBL: M76427; G408716; -
DR PFAM: PF009326; Prolyl_oligopep: 1.
DR PFAM: PF00930; DPEPTIV_N term: 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
KW DOMAIN 1 89
FT TRANSMEM 90 110
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 111 859
FT CARBOHYD 167 167
FT CARBOHYD 168 168
FT CARBOHYD 313 313
FT CARBOHYD 398 398
FT CARBOHYD 465 465
FT CARBOHYD 529 529
FT CARBOHYD 560 560
FT CARBOHYD 807 807
FT VARSPLIC 1 75
FT MASLYQRTGKINTSRSPAPPEASRLIGGCGPEEDAGKPK
FT LCPQQAQVAPRRERGGAGGRRFYQIQRSCDDED -> MT
FT AEPSSASGKSVQ00D0 (IN DPPX-S).
SQ SEQUENCE 859 AA; 97301 MW; B43C0E82 CRC32;

Query Match 76.6%; Score 49; DB 1; Length 859;
Best Local Similarity 66.7%; Pred. No. 1,18e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 122 KKKVYEDL 130
||||| : :
QY 1 KKKVTAQEL 9

RESULT 10
ID DPP6_BOVIN STANDARD; PRT; 863 AA.
AC P42659;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
GN DPP6.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=BRIN;
RX MEDLINE: 92108018.
RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;
RT "Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family.";
RL PROC. NATL. ACAD. SCI. U.S.A. 89:197-201(1992).
RT FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN ACTIVITY. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN. DPPX-L IS EXPRESSED EXCLUSIVELY IN THE BRAIN WHEREAS DPPX-S IS FOUND IN BRAIN, KIDNEY, OVARY AND TESTIS.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: M76428; G408718; -
DR EMBL: M76429; G408720; -
DR PFAM: PF009326; Prolyl_oligopep: 1.
DR PFAM: PF00930; DPEPTIV_N term: 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
KW DOMAIN 1 93
FT TRANSMEM 94 114
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 115 863
FT CARBOHYD 171 171
FT CARBOHYD 402 402
FT CARBOHYD 469 469
FT CARBOHYD 533 533
FT CARBOHYD 564 564
FT CARBOHYD 811 811
FT VARSPLIC 1 79
FT MASLYQRTGKINTSRSPAPPEASRLIGGCGPEEDAGKPK
FT PLGAQAPAPRRERGGAGGRRFYQIQRSCDDED -> MT
FT AEPSSASGKSVQ00D0 (IN DPPX-S).
SQ SEQUENCE 863 AA; 96556 MW; 8DA40472 CRC32;

Query Match 76.6%; Score 49; DB 1; Length 863;
Best Local Similarity 66.7%; Pred. No. 1,18e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 126 KKKVYEDL 134
||||| : :
QY 1 KKKVTAQEL 9

RESULT 11
ID DPP6_HUMAN STANDARD; PRT; 865 AA.
AC P42658;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
GN DPP6.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RX MEDLINE: 93372805.
RA YOKOTANI N., DOI K., WENTHOLD R.J., WADA K.;
RT "Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-related protein encoded by a gene on human chromosome 7.";
RL HUM. MOL. GENET. 2:1037-1039(1993).
RT FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN ACTIVITY. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its


```

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96859; G306706; -.
DR EMBL; M96860; G306708; -.
DR MIM; 126141; -.
DR PFM; PF00326; Prolyl-oligopep; 1.
DR PFM; PF00930; DppIV_N_term; 1.
KW HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
KW SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
FT FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 117 865 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 173 173 POTENTIAL.
FT CARBOHYD 319 319 POTENTIAL.
FT CARBOHYD 404 404 POTENTIAL.
FT CARBOHYD 471 471 POTENTIAL.
FT CARBOHYD 535 535 POTENTIAL.
FT CARBOHYD 566 566 POTENTIAL.
FT CARBOHYD 813 813 POTENTIAL.
FT VARSPPLIC 1 81 MAS10RTGKINTSRSPAPPPEASHLLGGGPEPDGAGAG
FT KPLDPRRAAAPRENGGGGAGGACGPRPYOGRSDGDED
FT -> M1AKEPSSAGSVOOQOE (IN DPX-S).
SQ SEQUENCE 865 AA; 97588 MW; 514C21E2 CRC32;
Db 128 KKVTYEDL 136
QY 1 KKVTYQEL 9
RESULT 12
ID RA32_SCHPO STANDARD: PRT: 649 AA.
AC Q09683;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DNA REPAIR PROTEIN RAD32.
GN RAD32 OR SPAC13C5.07.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIAASCOMYCETES;
OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
CN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE: 95192046.
RA TAVASSOLI M., SHAYEGHI M., NASIM A., WATTS F.Z.;
RT "Cloning and characterisation of the Schizosaccharomyces pombe rad32
RT gene: a gene required for repair of double strand breaks and
RT recombination.";
RT NUCLEIC ACIDS RES. 23:383-388(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA DEVLIN K., CHURCHER C.M., BARRELL B.G., RAUANDREAM M.A., WALSH S.V.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: REQUIRED FOR THE REPAIR OF DOUBLE STRAND BREAKS (DSB)
CC CAUSED BY GAMMA AND UV RADIATION. MAY WORK IN CONJUNCTION WITH
CC RHP51.
CC -1- SIMILARITY: BELONGS TO THE MRE11/RAD32 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

```

CC CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC DR EMBL: X82322; G908603; ALT_TERM.
DR EMBL: 250112; G908896; -.
KW DNA DAMAGE: DNA REPAIR.
SQ SEQUENCE 649 AA; 73688 MW; D1579AC4 CRC32;

Db 493 KKVTEENIE 502
  1111::1:
QY 1 KKVTAQELD 10

RESULT 13
ID RL3.MYGE STANDARD: PRT; 257 AA.
AC P47397.
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L3.
DE RPLC OR RPL3 OR MG151.
OS MYCOPLASMA GENITALIUM.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLICUTES;
OC MYCOPLASMATACEAE; MYCOPLASMA.
NC [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE: 96026346.
RA FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
RA FLEISCHMANN R.D., BOLT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J.M.,
RA FITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDSKY M., FURBRANN J.L.,
RA NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,
RA TOWB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUTCHER T.S.,
RA PETERSON S.N., SMITH H.O., HUTCHISON C.A. Iii, VENTER J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL SCIENCE 270:397-403(1995).
RN [2]
RP SEQUENCE OF 23-176 FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE: 94075230.
RA PETERSON S.N., HU P.-C., BOTT K.F., HUTCHISON C.A. Iii;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. BACTERIOL. 175:7918-7930(1993).
CC J.- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND MAY
CC PARTICIPATE IN THE FORMATION OF THE PEPTIDYLTRANSFERASE CENTER OF
CC THE RIBOSOME (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
-----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC
CC DR EMBL: U39695; G1045835; -.
DR EMBL: U02153; G406362; -.
DR TIGR: MG151; -.
DR PROSITE: PS00474; RIBOSOMAL_L3; 1.
DR PFMAM: PF00297; L3; 1.
DR RIBOSOMAL PROTEIN: RRNA-BINDING.
SQ SEQUENCE 257 AA; 28488 MW; 538C0DC6 CRC32;

Query Match 71.9%; Score 46; DB 1; Length 257;
Best Local Similarity 75.0%; Pred. No. 6.06e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

DB 94 KRITPEL 101
  11:111
QY 2 KKVTAQEL 9

RESULT 14
ID YDT3_SCHPO STANDARD: PRT: 302 AA.
AC 014208:
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 35.5 KD PROTEIN C6B12.03C IN CHROMOSOME I.
GN SPAC6B12.03C.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA: FUNGI: ASCOMYCOTA: ARCHIASCOMYCETES:
OC SCHIZOSACCHAROMYCETALES: SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972:
RA GENTILES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: 298531: E334102; -
DR HYPOTHEICAL PROTEIN.
KW SEQUENCE 302 AA; 35501 MW; 1D7F4893 CRC32;
SQ

Query Match 71.9%; Score 46; DB 1; Length 302;
Best Local Similarity 50.0%; Pred. No. 6.06e+00;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 125 KKVYIEDLN 134
  1111:::1
QY 1 KKVTAQELD 10

RESULT 15
ID YN21_CAEEL STANDARD: PRT: 489 AA.
AC P34580;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.
GN T26G10.1.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA: METAZOA: NEMATODA: SECERNENTEA: RHABDITIA: RHABDITIDA:
OC RHABDITINA: RHABDITOIDEA: RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONEFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMKEEN R.,
RA SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA SULLSTON J., THIERRY-MING J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA WOHLIDYAN P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).
```

```

CC -!- FUNCTION: PROBABLE ATP-BINDING RNA HELICASE.
CC -!- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: 229115: E1349766; -
DR PIR: S40731; S40731.
DR WORKREP: T26G10.1; CE00337.
DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
DR PFAM: PF00270; DEAD; 1.
DR PFAM: PF00271; helicase.C; 1.
KW HYPOTHEICAL PROTEIN; HELICASE; ATP-BINDING; RNA-BINDING.
FT DOMAIN 31 40
FT NP_BIND 88 95 ASP/GLU-RICH (ACIDIC).
FT SITE 194 197 ATP (BY SIMILARITY).
FT DOMAIN 471 482 DEAD BOX.
FT DOMAIN 489 AA; 54227 MW; B9EFF81A CRC32;
SQ SEQUENCE 489 AA; 54227 MW; B9EFF81A CRC32;

Query Match 71.9%; Score 46; DB 1; Length 489;
Best Local Similarity 50.0%; Pred. No. 6.06e+00;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 25 KKVYTERIE 34
  1111:::1
QY 1 KKVTAQELD 10
```

Search completed: Tue Aug 31 19:11:25 1999
Job time : 6 secs.

OC STREPTOCOCCUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS495.
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL: X61562; G47300; -
DR EMBL: X61563; G47302; -
DR EMBL: X61567; G47326; -
DR EMBL: X61561; G47298; -
DR EMBL: X61564; G47306; -
DR EMBL: X61565; G47312; -
DR EMBL: X61566; G47318; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA: 27484 MW: A5EB1ECD CRC32;

Query Match 90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 1,86e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 159 KKMVTAQELD 168
||:|||||||
QY 1 KKMVTAQELD 10

RESULT 3
ID 054779 PRELIMINARY: PRT: 236 AA.
AC 054779: 054613: 054736: 054740: 054741:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL: X61569; G47314; -
DR EMBL: X61572; G47334; -
DR EMBL: X61568; G47290; -
DR EMBL: X61570; G47316; -
DR EMBL: X61571; G47324; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA: 27468 MW: E902ED6D CRC32;

Query Match 90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 1,86e-02;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 159 KKMVTAQELD 168
||:|||||||
QY 1 KKMVTAQELD 10

RESULT 4
ID 054696 PRELIMINARY: PRT: 236 AA.
AC 054696:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156;
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL: X61573; G47304; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA: 27575 MW: A799A5F3 CRC32;

Query Match 90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 1,86e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 159 KKMVTAQELD 168
||:|||||||
QY 1 KKMVTAQELD 10

RESULT 5
ID P97163 PRELIMINARY: PRT: 236 AA.
AC P97163: P97164:
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, AND MGAS500;
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL: X61556; G47292; -
DR EMBL: X61557; G47320; -
DR EMBL: X61560; G47288; -
DR EMBL: X61550; G47310; -
DR EMBL: X61558; G47322; -
DR EMBL: X61559; G47294; -

DR EMBL: X61554; G47328; -.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 81A0C2FE CRC32;
Query Match 90.6%; Score 58; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 1,86e-02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 159 KKVTAQELD 168
QY 1 KKVTAQELD 10
RESULT 6
ID 005157; PRELIMINARY; PRT: 239 AA.
AC 005157;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE C ENTEROTOXIN (FRAGMENT).
OS STAPHYLOCOCCUS INTERMEDIUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA EDWARDS V.M., DERINGER J.R., CALLANTINE S.D., DEOBALD C.F.,
RA BECKER P.H., KAPUR V., STAUFACHER C.V., BOHACH G.A.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U91526; G1906052; -.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
FT NON_TER 1 1
SQ SEQUENCE 239 AA; 27536 MW; 390EB227 CRC32;
Query Match 87.5%; Score 56; DB 2; Length 239;
Best Local Similarity 90.0%; Pred. No. 5.91e-02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 151 KKVTAQELD 160
QY 1 KKVTAQELD 10
RESULT 7
ID 006534; PRELIMINARY; PRT: 239 AA.
AC 006534;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RL "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
INECT. IMMUN. 61:4254-4262(1993).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.

DR EMBL: L13379; G295151; -.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1 1
SQ SEQUENCE 239 AA; 27517 MW; 1293E9CA CRC32;
Query Match 87.5%; Score 56; DB 2; Length 239;
Best Local Similarity 90.0%; Pred. No. 5.91e-02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 151 KKVTAQELD 160
QY 1 KKVTAQELD 10
RESULT 8
ID 006532; PRELIMINARY; PRT: 239 AA.
AC 006532;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RL "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
INECT. IMMUN. 61:4254-4262(1993).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13375; G295143; -.
DR PROSITE: PS01123; Staph_Strep_toxin; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1 1
SQ SEQUENCE 239 AA; 27642 MW; 81CA4BC2 CRC32;
Query Match 87.5%; Score 56; DB 2; Length 239;
Best Local Similarity 90.0%; Pred. No. 5.91e-02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 151 KKVTAQELD 160
QY 1 KKVTAQELD 10
RESULT 9
ID 006535; PRELIMINARY; PRT: 239 AA.
AC 006535;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 909;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RL "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
INECT. IMMUN. 61:4254-4262(1993).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.

CC PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.

DR EMBL: L13377: G295147: -
 KM PFAM: PF01123: Staph_Strep_toxin; 1.
 FT ENTEROTOXIN; TOXIN; SUPERANTIGEN.
 SQ NON_TER 1
 SEQUENCE 239 AA; 27648 MW; 1DC80C35 CRC32;

Query Match 87.5%; Score 56; DB 2; Length 239;
 Best Local Similarity 90.0%; Pred. No. 5,91e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 151 KKSXTAQLD 160
 |||||||
 QY 1 KKSXTAQLD 10

RESULT 10
 ID 006531 PRELIMINARY; PRT: 239 AA.

AC 054739: 054737;
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.

RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 94011313.
 RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RL biological and evolutionary implications.";
 RL INFECT. IMMUN. 61:4254-4262(1993).

DR EMBL: L13376: G295145: -
 DR PROSITE: PS00277: STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278: STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123: Staph_Strep_toxin; 1.
 KM ENTEROTOXIN.
 FT NON_TER 1
 SEQUENCE 239 AA; 27618 MW; 0810B9D CRC32;

Query Match 87.5%; Score 56; DB 2; Length 239;
 Best Local Similarity 90.0%; Pred. No. 5,91e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 151 KKSXTAQLD 160
 |||||||
 QY 1 KKSXTAQLD 10

RESULT 11
 ID 006533 PRELIMINARY; PRT: 239 AA.

AC 006533:
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MCOPPELAND;
 RX MEDLINE: 94011313.
 RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RL biological and evolutionary implications.";
 RL INFECT. IMMUN. 61:4254-4262(1993).

CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
 CC PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
 DR EMBL: L13378: G295149: -

DR PFAM: PF01123: Staph_Strep_toxin; 1.
 KM ENTEROTOXIN; TOXIN; SUPERANTIGEN.
 FT NON_TER 1
 SEQUENCE 239 AA; 27651 MW; 7A5C4047 CRC32;

Query Match 87.5%; Score 56; DB 2; Length 239;
 Best Local Similarity 90.0%; Pred. No. 5,91e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 151 KKSXTAQLD 160
 |||||||
 QY 1 KKSXTAQLD 10

RESULT 12
 ID 006531 PRELIMINARY; PRT: 239 AA.

AC 006531:
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-4446;
 RX MEDLINE: 94011313.
 RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RL biological and evolutionary implications.";
 RL INFECT. IMMUN. 61:4254-4262(1993).

CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION,
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
 CC PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.

DR EMBL: L13374: G295141: -
 DR PFAM: PF01123: Staph_Strep_toxin; 1.
 DR ENTEROTOXIN; TOXIN; SUPERANTIGEN.
 FT NON_TER 1
 SEQUENCE 239 AA; 27612 MW; 52B18853 CRC32;

Query Match 87.5%; Score 56; DB 2; Length 239;
 Best Local Similarity 90.0%; Pred. No. 5,91e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 151 KKSXTAQLD 160
 |||||||
 QY 1 KKSXTAQLD 10

RESULT 13
 ID 054739 PRELIMINARY; PRT: 260 AA.

AC 054739: 054737;
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94222556.
 RA REBA R.B., KAPUR V., MOLLICK J.A., LAMPHAR J.G., MUSSER J.M.,
 RA RICH R.R.;
 RT "Molecular characterization and phylogenetic distribution of the
 RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
 RL INFECT. IMMUN. 62:1867-1874(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96178602.

```

RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL INFECT. IMMUN. 64:1161-1165(1996).
DR EMBL; U48794; G1245176; -
DR EMBL; U48792; G1245172; -
DR PFAM; PF01123; Stap_Stip_toxin; 1
SO SEQUENCE 260 AA; 29767 MW; C81448C1 CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 3.21e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKVTAQELD 183
QY 1 KKVTAQELD 10

RESULT 14
ID 054971 PRELIMINARY; PRT; 260 AA.
AC 054971;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WEILER.
RX MEDLINE; 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL INFECT. IMMUN. 62:1867-1874(1994).
DR EMBL; L29565; G476764; -
DR PFAM; PF01123; Stap_Stip_toxin; 1.
KW SUPERANTIGEN.
SQ SEQUENCE 260 AA; 29797 MW; FE391C2B CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 3.21e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKVTAQELD 183
QY 1 KKVTAQELD 10

RESULT 15
ID 054738 PRELIMINARY; PRT; 260 AA.
AC 054738;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE; 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL INFECT. IMMUN. 62:1867-1874(1994).

```

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE; 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL INFECT. IMMUN. 64:1161-1165(1996).
DR EMBL; U48793; G1245174; -
DR PFAM; PF01123; Stap_Stip_toxin; 1.
SQ SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match      82.8%; Score 53; DB 2; Length 260;
Best Local Similarity 80.0%; Pred. No. 3.21e-01;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 174 KKVTAQELD 183
QY 1 KKVTAQELD 10

```

Search completed: Tue Aug 31 19:12:21 1999
Job time : 38 secs.

THIS PAGE BLANK (USPTO)

MPEE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd.

Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:15:46 1999; Maspar time 3.61 Seconds
Tabular output not generated.

Title: >US-09-150-947-5
(1-13) from US09150947.pep
Perfect Score: 74
Sequence: 1 XTNRKKVTAQELD 13

Scoring table:
PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 16.236; Variance 48.115; scale 0.337

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 74 | 100.0 | 12 34 | W64636 | Synthetic SEB peptide | 1.06e-01 |
| 2 | 74 | 100.0 | 13 34 | W64640 | Synthetic SEB peptide | 1.06e-01 |
| 3 | 74 | 100.0 | 239 3 | R13206 | Staphylococcal entero | 1.06e-01 |
| 4 | 74 | 100.0 | 239 34 | W64647 | Synthetic SEB protein | 1.06e-01 |
| 5 | 74 | 100.0 | 239 8 | R45014 | Staphylococcal entero | 1.06e-01 |
| 6 | 74 | 100.0 | 235 20 | W06737 | Staphylococcal entero | 1.06e-01 |
| 7 | 68 | 91.9 | 221 3 | R13209 | Staphylococcal entero | 5.57e-01 |
| 8 | 68 | 91.9 | 221 8 | R45017 | Staphylococcal entero | 5.57e-01 |
| 9 | 68 | 91.9 | 250 24 | W12145 | Staphylococcal entero | 5.57e-01 |
| 10 | 68 | 91.9 | 251 24 | W12146 | Staphylococcal entero | 5.57e-01 |
| 11 | 68 | 91.9 | 251 24 | W12154 | Staphylococcal entero | 5.57e-01 |
| 12 | 68 | 91.9 | 251 24 | W12153 | Staphylococcal entero | 5.57e-01 |
| 13 | 68 | 91.9 | 251 24 | W12152 | Staphylococcal entero | 5.57e-01 |
| 14 | 68 | 91.9 | 251 24 | W12097 | Staphylococcal entero | 5.57e-01 |
| 15 | 68 | 91.9 | 251 24 | W12147 | Staphylococcal entero | 5.57e-01 |
| 16 | 68 | 91.9 | 251 24 | W12151 | Staphylococcal entero | 5.57e-01 |

| | | | | | | |
|----|----|------|--------|--------|-----------------------|----------|
| 17 | 68 | 91.9 | 251 33 | W59781 | Amino acid sequence o | 5.57e-01 |
| 18 | 68 | 91.9 | 251 33 | W59780 | Amino acid sequence o | 5.57e-01 |
| 19 | 68 | 91.9 | 251 24 | W12150 | Staphylococcus pyogen | 5.57e-01 |
| 20 | 68 | 91.9 | 251 24 | W12149 | Staphylococcus pyogen | 5.57e-01 |
| 21 | 68 | 91.9 | 251 33 | W59798 | Amino acid sequence o | 5.57e-01 |
| 22 | 68 | 91.9 | 251 24 | W12148 | Staphylococcus pyogen | 5.57e-01 |
| 23 | 64 | 86.5 | 10 34 | W64639 | Synthetic SEB peptide | 1.66e+00 |
| 24 | 64 | 86.5 | 91 27 | W24299 | Staphylococcus aureus | 1.66e+00 |
| 25 | 64 | 86.5 | 233 20 | W06738 | Staphylococcus aureus | 1.66e+00 |
| 26 | 64 | 86.5 | 233 3 | R13203 | Staphylococcal entero | 1.66e+00 |
| 27 | 64 | 86.5 | 233 27 | W5373 | Staphylococcal entero | 1.66e+00 |
| 28 | 64 | 86.5 | 233 8 | R45011 | Staphylococcal entero | 1.66e+00 |
| 29 | 64 | 86.5 | 238 3 | R13208 | Staphylococcal entero | 1.66e+00 |
| 30 | 64 | 86.5 | 238 8 | R45016 | Staphylococcal entero | 1.66e+00 |
| 31 | 64 | 86.5 | 239 3 | R13207 | Staphylococcal entero | 1.66e+00 |
| 32 | 64 | 86.5 | 239 8 | R45015 | Staphylococcal entero | 1.66e+00 |
| 33 | 62 | 83.8 | 228 3 | R13205 | Staphylococcal entero | 2.85e+00 |
| 34 | 62 | 83.8 | 228 8 | R45013 | Staphylococcal entero | 2.85e+00 |
| 35 | 59 | 79.7 | 28 19 | W04494 | Staphylococcal entero | 6.36e+00 |
| 36 | 59 | 79.7 | 36 36 | W72426 | Peptide #5 for reduci | 6.36e+00 |
| 37 | 59 | 79.7 | 38 36 | W72427 | Peptide #6 for reduci | 6.36e+00 |
| 38 | 58 | 78.4 | 12 34 | W64637 | Synthetic SEB peptide | 8.29e+00 |
| 39 | 58 | 78.4 | 13 34 | W64641 | Synthetic SEB peptide | 8.29e+00 |
| 40 | 58 | 78.4 | 13 34 | W64646 | Synthetic SEB peptide | 8.29e+00 |
| 41 | 58 | 78.4 | 14 34 | W64645 | Synthetic SEB peptide | 8.29e+00 |
| 42 | 58 | 78.4 | 24 34 | W64642 | Synthetic SEB peptide | 8.29e+00 |
| 43 | 58 | 78.4 | 35 34 | W64643 | Synthetic SEB peptide | 8.29e+00 |
| 44 | 58 | 78.4 | 230 8 | R45012 | Staphylococcal entero | 8.29e+00 |
| 45 | 58 | 78.4 | 245 27 | W35375 | Staphylococcus entero | 8.29e+00 |

ALIGNMENTS

RESULT 1
ID W64636 standard; peptide; 12 AA.
AC W64636:
DE 23-OCT-1998 (first entry)
DE Synthetic SEB peptide pSEB(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-AL.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Atad G, Kaempfer R.
DR WPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 6: Page 41; 68pp: English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced
CC PERT or by a mixture of PERTs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PERTs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PERT.
SQ Sequence 12 AA:
Query Match 100.0%; Score 74; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 tnrkkvtageid 12

OY 2 TNRKRVTAQELD 13

RESULT 2
ID W64640 standard; peptide: 13 AA.

AC W64640:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide pSEBHC(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
therapeutic; vaccine; food poisoning.
OS Synthetic.
PW Staphylococcus aureus.

FT Key Modified_site 1 Location/Qualifiers

FT /note= "N-terminal Thr modified by presence of N-lauryl-cysteine"

PN WO9829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR MPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
antagonising toxin-mediated activation of T cells and prevention or
treatment of toxic shock caused by exotoxin(s)
PS Clalm 15; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
capable of eliciting protective immunity against toxic shock induced by
PET or by a mixture of PETs. Such peptides are also capable of
antagonising toxin-mediated activation of T-cells, inhibiting expression
of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
TNF-beta genes. The peptides may be used to prepare therapeutics or
vaccines for the treatment of prophylaxis of toxin-mediated activation
of T cells and eliciting protective immunity against toxic shock induced
by PETs. They can also be used for the treatment of harmful effects
(especially food poisoning) and toxic shock caused by PET. Antiserum to
the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 tnkkvtageld 13
OY 2 TNRKRVTAQELD 13

RESULT 3
ID R13206 standard; protein: 239 AA.

AC R13206:
DT 15-OCT-1991 (first entry)
DE Staphylococcal enterotoxin B.
KW SEB; cancer treatment; pyrogen; tumouricide.
OS Staphylococcus aureus.
PW MO9110680-A.
PD 25-JUL-1991.
PE 17-JAN-1991; U00342.
PR 17-JAN-1990; US-466577.
PA (TERM/) TERMAN D S.
PI Terman DS;
DR MPI; 91-237984/32.
PT Treating cancer with enterotoxin from Staphylococcus aureus -
administered by IV injection, having same tumoricidal activity
as Staphylococcal protein A without potential toxic reactions
PS Disclosure; Fig 1; 74pp; English.
CC SEB was isolated and purified from S. aureus. It can be used for
treating cancer, activating cytokine mediators and procoagulant
systems, augmenting natural killer cell cytotoxicity, etc. The

CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEB. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of cysteine residues and
CC similar hydrophobic profiles.
CC See R13203-R13211.
SQ Sequence 239 AA;

Query Match 100.0%; Score 74; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 150 tnkkvtageld 161
OY 2 TNRKRVTAQELD 13

RESULT 4
ID W64647 standard; peptide: 239 AA.
AC W64647:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB protein fragment.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
therapeutic; vaccine; food poisoning.
OS Synthetic.
PW Staphylococcus aureus.

PN WO9829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR MPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
antagonising toxin-mediated activation of T cells and prevention or
treatment of toxic shock caused by exotoxin(s)
PS Example 8; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
capable of eliciting protective immunity against toxic shock induced by
PET or by a mixture of PETs. Such peptides are also capable of
antagonising toxin-mediated activation of T-cells, inhibiting expression
of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
TNF-beta genes. The peptides may be used to prepare therapeutics or
vaccines for the treatment of prophylaxis of toxin-mediated activation
of T cells and eliciting protective immunity against toxic shock induced
by PETs. They can also be used for the treatment of harmful effects
(especially food poisoning) and toxic shock caused by PET. Antiserum to
the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 239 AA;

Query Match 100.0%; Score 74; DB 34; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 150 tnkkvtageld 161
OY 2 TNRKRVTAQELD 13

RESULT 5
ID R45014 standard; protein: 239 AA.

AC R45014:
DT 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SEB.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
autoimmune disease; toxicity; Protein A; perfusion system.
OS Staphylococcus aureus.
PW WO9324136-A.
PD 09-DEC-1993.
PR 01-JUN-1993; U05213.

01-JUN-1992; US-891718.
PA (TERM/) STONE J L.
PI Stone JL, Terman D S.
PR WPI: 93-405418/50.
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
PS Disclosure; Fig 1; 90pp; English.
CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
SQ Sequence 239 AA;

Query Match 100.0%; Score 74; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 150 tnkkvtageld 161

Oy 2 TNKKKVTQOELD 13

RESULT 6
ID W06737 standard; Protein; 255 AA.
AC W06737;
DT 08-MAR-1997 (first entry)
DE Staphylococcus enterotoxin B.
KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
KW vaccine; adjuvant.
OS Staphylococcus sp.
FH Key location/Qualifiers
FT peptide 1..15
FN W09636366-A1.
PD 21-NOV-1996.
PE 20-MAY-1996; U07432.
PR 18-MAY-1995; US-446918.
PR 29-DEC-1995; US-580806.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
PI Dow SW, Elmslie RE, Potter TA;
DR WPI: 97-011857/01.
DR N-PSDB: 145698.
PT Recombinant molecule encoding superantigen and opt. cytokine or
PT chemokine - controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer
PS Example 1; Page 96-97; 131pp; English.
CC A cDNA clone (T45698) codes for staphylococcal enterotoxin B
CC (W06737) superantigen. Nucleic acids encoding superantigens (see
CC also W06738-39), esp. truncated forms of the superantigen lacking
CC the leader peptide, can be utilised in the gene therapy of cancer.
CC Infectious diseases and immunological disorders. The nucleic acid,
CC optionally in combination with cytokine or chemokine nucleic acids,
CC is delivered to an animal using e.g. liposomes. It acts by
CC controlling the activity of effector cells, such as T-cells,
CC macrophages, monocytes and/or natural killer cells. Localised
CC prodn. of an effective but non-toxic amount of encoded proteins
CC allows safe treatment of the animal.
SQ Sequence 255 AA;

Query Match 100.0%; Score 74; DB 20; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 tnkkvtageld 177

Oy 2 TNKKKVTQOELD 13

RESULT 7
ID R13209 standard; Protein; 221 AA.
AC R13209;
DT 15-OCT-1991 (first entry)
DE Streptococcal pyrogenic enterotoxin A.
KW SPE A: cancer treatment; pyrogen; tumouricide; scarlet fever.
OS Streptococcus NF-5 strain.
PN W0910680-A.
PD 25-JUL-1991.
PE 17-JAN-1991; U00342.
PR 17-JAN-1990; US-466577.
PA (TERM/) TERMAN D S.
PI Terman DS;
PR WPI: 91-237984/32.
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumouricidal activity
PT as staphylococcal protein A without potential toxic reactions
PS Disclosure; Fig 1; 74pp; English.
CC SPE A can be used for tumouricidal treatment, esp. with a haemolysin.
CC Synthetic polypeptides having structural homology to Streptococcal
CC pyrogenic exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles.
SQ See R13203-R13211.
Sequence 221 AA;

Query Match 91.9%; Score 68; DB 3; Length 221;
Best Local Similarity 91.7%; Pred. No. 5.57e-01;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 135 tnkkvtageld 146

Oy 2 TNKKKVTQOELD 13

RESULT 8
ID R45017 standard; Protein; 221 AA.
AC R45017;
DT 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SPE A.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
OS Staphylococcus aureus.
PN W09324136-A.
PD 09-DEC-1993.
PE 01-JUN-1993; U05213.
PR 01-JUN-1992; US-891718.
PA (TERM/) STONE J L.
PI Stone JL, Terman D S.
DR WPI: 93-405418/50.
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
PS Disclosure; Fig 1; 90pp; English.
CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
SQ Sequence 221 AA;

Query Match 91.9%; Score 68; DB 8; Length 221;
Best Local Similarity 91.7%; Pred. No. 5.57e-01;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 135 tnkkvtageld 146

Oy 2 TNKKKVTQOELD 13

CC damage. The neutralising Ab is preferably administered in
CC conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and
CC uterine cancer. It is thought that mutant SPE-A can be selectively
CC toxic to T cell lymphoma cells.
CC N.B. Sequence not given in the specification, but constructed
CC using the wild type SPE-A sequence given on pages 77-79.
SQ Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
Best Local Similarity 91.7%; Pred. No. 5.57e-01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnknwtageid 176
||||:|||||
QY 2 TNKKRYTAOELD 13

RESULT 12
ID W12153 standard; Protein: 251 AA.

DE 04-NOV-1997 (first entry)
KM Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
KM Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KM vaccine; protection; treatment; cancer; neutralising antibody;
KM streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KM fever; hypotension; group A streptococcal infection; myositis;
KM fasciitis; liver damage; T cell; lymphoma; ovarian; uterine;
OS Streptococcus pyogenes.
OS Synthetic.

FM Key Location/Qualifiers
FT peptide 1..30
FT peptide /label= sig_peptide
FT peptide 31..251
FT peptide /label= mat_peptide
FT Misc_difference 120
FT /note= "wild type Cys replaced by Ser"

PM W09640930-A1.
PD 19-DEC-1996.
PF 07-JUN-1996; U10252.
PR 07-JUN-1995; US-480261.
PA (MINU) UNIV MINNESOTA.
PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
DR WPI: 97-099936/09.
PT Mutant SPE-A toxin with at least one amino acid change is
PT substantially non-lethal - used in vaccine composition for
PT treatment of cancer and streptococcal toxic shock syndrome etc.
PS Example 4: Page -; 102pp; English.

CC The present sequence is a non-lethal Streptococcus pyogenes
CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
CC vaccines to protect animals against wild type SPE-A and to treat
CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
CC SPE-A causes neutralising antibodies (Ab) to be produced, which
CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
CC group A streptococcal infection, myositis, fasciitis and liver
CC damage. The neutralising Ab is preferably administered in
CC conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and
CC uterine cancer. It is thought that mutant SPE-A can be selectively
CC toxic to T cell lymphoma cells.
CC N.B. Sequence not given in the specification, but constructed
CC using the wild type SPE-A sequence given on pages 77-79.
SQ Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
Best Local Similarity 91.7%; Pred. No. 5.57e-01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnknwtageid 176
||||:|||||
QY 2 TNKKRYTAOELD 13

RESULT 13
ID W12152 standard; Protein: 251 AA.

DE 04-NOV-1997 (first entry)
KM Streptococcus pyogenes Streptococcal toxin A mutant Cys98Ser.
KM Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KM vaccine; protection; treatment; cancer; neutralising antibody;
KM streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KM fever; hypotension; group A streptococcal infection; myositis;
KM fasciitis; liver damage; T cell; lymphoma; ovarian; uterine;
OS Streptococcus pyogenes.
OS Synthetic.

FM Key Location/Qualifiers
FT peptide 1..30
FT peptide /label= sig_peptide
FT peptide 31..251
FT peptide /label= mat_peptide
FT Misc_difference 128
FT /note= "wild type Cys replaced by Ser"

PM W09640930-A1.
PD 19-DEC-1996.
PF 07-JUN-1996; U10252.
PR 07-JUN-1995; US-480261.
PA (MINU) UNIV MINNESOTA.
PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
DR WPI: 97-099936/09.
PT Mutant SPE-A toxin with at least one amino acid change is
PT substantially non-lethal - used in vaccine composition for
PT treatment of cancer and streptococcal toxic shock syndrome etc.
PS Example 4: Page -; 102pp; English.

CC The present sequence is a non-lethal Streptococcus pyogenes
CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
CC vaccines to protect animals against wild type SPE-A and to treat
CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
CC SPE-A causes neutralising antibodies (Ab) to be produced, which
CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
CC group A streptococcal infection, myositis, fasciitis and liver
CC damage. The neutralising Ab is preferably administered in
CC conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and
CC uterine cancer. It is thought that mutant SPE-A can be selectively
CC toxic to T cell lymphoma cells.
CC N.B. Sequence not given in the specification, but constructed
CC using the wild type SPE-A sequence given on pages 77-79.
SQ Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
Best Local Similarity 91.7%; Pred. No. 5.57e-01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnknwtageid 176
||||:|||||
QY 2 TNKKRYTAOELD 13

RESULT 14
ID W12097 standard; Protein: 251 AA.

DE 04-NOV-1997 (first entry)
KM Streptococcus pyogenes Streptococcal toxin A.
KM Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KM vaccine; protection; treatment; cancer; neutralising antibody;
KM streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KM fever; hypotension; group A streptococcal infection; myositis;
KM fasciitis; liver damage; T cell; lymphoma; ovarian; uterine;
OS Streptococcus pyogenes.
OS Synthetic.

FM Key Location/Qualifiers
FT peptide 1..30
FT peptide /label= sig_peptide
FT peptide 31..251
FT peptide /label= mat_peptide
PM W09640930-A1.
PD 19-DEC-1996.

PF 07-JUN-1996: U10252.
 PR 07-JUN-1995: US-480261.
 PA (MIND) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR N-PSDB; W12097.
 PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Disclosure, pages 77-79; 102pp; English.
 CC The present sequence is Streptococcus pyogenes Streptococcal
 CC toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising
 CC at least 1 amino acid change, can be derived. The mutant SPE-A can
 CC be used to produce vaccines to protect animals against wild type
 CC SPE-A and to treat cancer and streptococcal toxic shock syndrome
 CC (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be
 CC produced, which may be used to ameliorate STSS symptoms, e.g.
 CC fever, hypotension, group A streptococcal infection, myositis,
 CC fasciitis and liver damage. The neutralising Ab is preferably
 CC administered in conjunction with antibiotic therapy. The mutant
 CC SPE-A is especially useful for treating T cell lymphomas, and
 CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
 CC selectively toxic to T cell lymphoma cells.
 SQ Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
 Best Local Similarity 91.7%; Pred. No. 5.57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnkkmvtaqeld 176
 ||||:|||||
 QY 2 TNKKVTAQELD 13

RESULT 15
 ID W12147 standard; Protein: 251 AA.
 AC W12147;
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Asn20Asp.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine;
 OS Streptococcus pyogenes.
 OS Synthetic.
 FH Key
 FT peptide
 FT 1..30
 FT /label= sig_peptide
 FT 31..251
 FT /label= mat_peptide
 FT Misc_difference 50
 FT /note= "wild type Asn replaced by Asp"
 PN W09640930-A1.
 PD 19-DEC-1996.
 PF 07-JUN-1996: U10252.
 PR 07-JUN-1995: US-480261.
 PA (MIND) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR N-PSDB; W12097.
 PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Claim 5; Page 5; 102pp; English.
 CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is

CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 SQ Sequence 251 AA;

Query Match 91.9%; Score 68; DB 24; Length 251;
 Best Local Similarity 91.7%; Pred. No. 5.57e-01;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 165 tnkkmvtaqeld 176
 ||||:|||||
 QY 2 TNKKVTAQELD 13

Search completed: Tue Aug 31 19:16:03 1999
 Job time : 17 secs.

MUSE

(TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:15:02 1999; MasPar time 3.64 Seconds
Tabular output not generated. 143.162 Million cell updates/sec

Title: >US-09-150-947-5
Description: (1-13) from US09150947.pep
Perfect Score: 74
Sequence: 1 XTNRKRVTAQELD 13

Scoring table:
PAM 150
Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p160
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.119; Variance 28.486; scale 0.812

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|---------------------------|-----------|
| 1 | 74 | 100.0 | 266 | 1 | ENSAB6 | 1.74e-05 |
| 2 | 68 | 91.9 | 236 | 2 | enterotoxin B precurs | 5.23e-04 |
| 3 | 68 | 91.9 | 236 | 2 | enterotoxin type A precu | 5.23e-04 |
| 4 | 68 | 91.9 | 251 | 2 | exotoxin type A precu | 5.23e-04 |
| 5 | 64 | 86.5 | 233 | 2 | enterotoxin type A - Stap | 4.71e-03 |
| 6 | 64 | 86.5 | 236 | 2 | enterotoxin A - precursor | 4.71e-03 |
| 7 | 64 | 86.5 | 257 | 2 | enterotoxin A precurs | 4.71e-03 |
| 8 | 64 | 86.5 | 266 | 1 | enterotoxin C-1 precu | 4.71e-03 |
| 9 | 64 | 86.5 | 266 | 2 | enterotoxin C-2 precu | 4.71e-03 |
| 10 | 64 | 86.5 | 266 | 2 | enterotoxin C3 - Stap | 4.71e-03 |
| 11 | 62 | 83.8 | 258 | 2 | enterotoxin D precurs | 1.38e-02 |
| 12 | 58 | 78.4 | 257 | 2 | enterotoxin E precurs | 1.12e-01 |
| 13 | 52 | 70.3 | 807 | 2 | VirB4 homolog - Helic | 2.24e+00 |
| 14 | 51 | 68.9 | 803 | 2 | dipeptidyl aminopepti | 3.62e+00 |
| 15 | 51 | 68.9 | 803 | 2 | dipeptidyl aminopepti | 3.62e+00 |
| 16 | 51 | 68.9 | 865 | 2 | hypothetical protein | 5.82e+00 |
| 17 | 50 | 67.6 | 1252 | 2 | hypothetical protein | 9.47e+01 |
| 18 | 49 | 66.2 | 153 | 2 | cell-division protein | 1.47e+01 |
| 19 | 48 | 64.9 | 637 | 2 | leukotoxin A - Actino | 1.47e+01 |
| 20 | 48 | 64.9 | 1055 | 1 | vitellogenin precurs | 1.47e+01 |
| 21 | 48 | 64.9 | 1782 | 2 | dynin heavy chain, c | 2.31e+01 |
| 22 | 48 | 64.9 | 4644 | 1 | conserved hypothetical | 2.31e+01 |
| 23 | 47 | 63.5 | 148 | 2 | H69116 | 2.31e+01 |

| 24 | 47 | 63.5 | 538 | 2 | S12570 | homeotic protein blco | 2.31e+01 |
|----|----|------|--|---|--------|-----------------------|----------|
| 25 | 47 | 63.5 | 649 <th>2</th> <th>S58097</th> <th>probable phosphoester</th> <th>2.31e+01</th> | 2 | S58097 | probable phosphoester | 2.31e+01 |
| 26 | 46 | 62.2 | 200 <th>2</th> <th>S23524</th> <th>GTP-binding protein N</th> <th>3.61e+01</th> | 2 | S23524 | GTP-binding protein N | 3.61e+01 |
| 27 | 46 | 62.2 | 200 <th>2</th> <th>S49225</th> <th>guanine nucleotide re</th> <th>3.61e+01</th> | 2 | S49225 | guanine nucleotide re | 3.61e+01 |
| 28 | 46 | 62.2 | 257 <th>2</th> <th>G64216</th> <th>ribosomal protein L3</th> <th>3.61e+01</th> | 2 | G64216 | ribosomal protein L3 | 3.61e+01 |
| 29 | 46 | 62.2 | 264 <th>2</th> <th>A47737</th> <th>osteopontin precursor</th> <th>3.61e+01</th> | 2 | A47737 | osteopontin precursor | 3.61e+01 |
| 30 | 46 | 62.2 | 417 <th>2</th> <th>C32185</th> <th>Frr CD protein - Myxo</th> <th>3.61e+01</th> | 2 | C32185 | Frr CD protein - Myxo | 3.61e+01 |
| 31 | 46 | 62.2 | 489 <th>2</th> <th>S40731</th> <th>ATP-dependent RNA hel</th> <th>3.61e+01</th> | 2 | S40731 | ATP-dependent RNA hel | 3.61e+01 |
| 32 | 46 | 62.2 | 489 <th>2</th> <th>T01959</th> <th>hypothetical protein</th> <th>3.61e+01</th> | 2 | T01959 | hypothetical protein | 3.61e+01 |
| 33 | 46 | 62.2 | 589 <th>2</th> <th>T01163</th> <th>hypothetical protein</th> <th>3.61e+01</th> | 2 | T01163 | hypothetical protein | 3.61e+01 |
| 34 | 46 | 62.2 | 727 <th>2</th> <th>S27043</th> <th>neurotransmitter tran</th> <th>3.61e+01</th> | 2 | S27043 | neurotransmitter tran | 3.61e+01 |
| 35 | 46 | 62.2 | 727 <th>2</th> <th>S56506</th> <th>Na+/Cl(-)-dependent n</th> <th>3.61e+01</th> | 2 | S56506 | Na+/Cl(-)-dependent n | 3.61e+01 |
| 36 | 46 | 62.2 | 818 <th>2</th> <th>S57078</th> <th>probable protein kina</th> <th>3.61e+01</th> | 2 | S57078 | probable protein kina | 3.61e+01 |
| 37 | 46 | 62.2 | 1084 <th>2</th> <th>A28555</th> <th>middle wall protein p</th> <th>3.61e+01</th> | 2 | A28555 | middle wall protein p | 3.61e+01 |
| 38 | 46 | 62.2 | 1179 <th>2</th> <th>C36792</th> <th>hypothetical protein</th> <th>3.61e+01</th> | 2 | C36792 | hypothetical protein | 3.61e+01 |
| 39 | 45 | 60.8 | 212 <th>2</th> <th>C71623</th> <th>hypothetical protein</th> <th>5.60e+01</th> | 2 | C71623 | hypothetical protein | 5.60e+01 |
| 40 | 45 | 60.8 | 230 <th>2</th> <th>S09648</th> <th>nucleoprotein NS1 - 1</th> <th>5.60e+01</th> | 2 | S09648 | nucleoprotein NS1 - 1 | 5.60e+01 |
| 41 | 45 | 60.8 | 230 <th>1</th> <th>MNTV1</th> <th>nonstructural protein</th> <th>5.60e+01</th> | 1 | MNTV1 | nonstructural protein | 5.60e+01 |
| 42 | 45 | 60.8 | 351 <th>2</th> <th>S49887</th> <th>hypothetical protein</th> <th>5.60e+01</th> | 2 | S49887 | hypothetical protein | 5.60e+01 |
| 43 | 45 | 60.8 | 466 <th>2</th> <th>JC6525</th> <th>processing peptidase</th> <th>5.60e+01</th> | 2 | JC6525 | processing peptidase | 5.60e+01 |
| 44 | 45 | 60.8 | 572 <th>2</th> <th>S73730</th> <th>MG307 homolog H08_orf</th> <th>5.60e+01</th> | 2 | S73730 | MG307 homolog H08_orf | 5.60e+01 |
| 45 | 45 | 60.8 | 793 <th>1</th> <th>JC6161</th> <th>kinesin-associated pr</th> <th>5.60e+01</th> | 1 | JC6161 | kinesin-associated pr | 5.60e+01 |

ALIGNMENTS

| RESULT | 1 | ALIGNMENTS |
|----------------------|--|-------------------------|
| ENTRY | ENSAB6 | #type complete |
| TITLE | enterotoxin B precursor - Staphylococcus aureus | |
| ORGANISM | 24-Apr-1988 #sequence_revision 15-Oct-1996 #text_change | |
| DATE | 11-Sep-1998 | |
| ACCESSIONS | S27360; A92065; S27240; A01815 | |
| REFERENCE | S27360 | Jones, C.L.; Khan, S.A. |
| #authors | J. Bacteriol. (1986) 166:29-33 | |
| #journal | Nucleotide sequence of the enterotoxin B gene from | |
| #title | Staphylococcus aureus. | |
| #cross-references | MUID:86168029 | |
| #accession | S27360 | |
| #molecule_type | DNA | |
| #residues | 1-266 ##label JON | |
| #cross-references | EMBL:MI1118; NID:g152999; PID:g153000 | |
| #experimental_source | strain S6 | |
| REFERENCE | A92065 | |
| #authors | Huang, I.Y.; Bergdoll, M.S. | |
| #journal | J. Biol. Chem. (1970) 245:3511-3515 | |
| #title | The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence. | |
| #cross-references | MUID:71007902 | |
| #accession | A92065 | |
| #molecule_type | protein | |
| #residues | 28-55,'NND',59-68,'NE',71,'FDLIY',78-117,'119-127','N',129,'D',131-132,'ENT',136-148,'GN',151-156,'Y',157-184,'EQ',187-232,'N',234-245,'ND',248-266 ##label HUA | |
| #experimental_source | strain S-6 | |
| REFERENCE | A92064 | |
| #authors | Huang, I.Y.; Bergdoll, M.S. | |
| #journal | J. Biol. Chem. (1970) 245:3511-3517 | |
| #title | The primary structure of staphylococcal enterotoxin B. II. Isolation, composition, and sequence of chymotryptic peptides. | |
| #cross-references | MUID:71007901 | |
| #contents | annotation; chymotryptic peptides | |
| REFERENCE | A92063 | |
| #authors | Huang, I.Y.; Bergdoll, M.S. | |
| #journal | J. Biol. Chem. (1970) 245:3493-3510 | |
| #title | The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, and sequence of tryptic peptides from oxidized entero-toxin B. | |
| #cross-references | MUID:71007900 | |

##contents annotation: tryptic peptides
REFERENCE A90548
#authors Schanz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
#journal Dunery, D.A.; Bergdoll, M.S.
#title Biochemistry (1965) 4:1011-1016
#cross-references EMBL:X61569; NID:q47315; PID:q47316
#contents Purification of staphylococcal enterotoxin B.
#cross-references MUID:66035792
#contents annotation: biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.;
Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
Shenichukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of
staphylococcal enterotoxin B.
#accession S27240
#molecule_type protein
#residues 28-42;128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin; extracellular protein; toxin
FEATURE
1-27 #domain signal sequence #status predicted #label SIG\
28-266 #product enterotoxin B #status experimental #label MAT\
120-140 #disulfide_bonds #status experimental
SUMMARY #length 266 #molecular_weight 31436 #checksum 4249
Query Match 100.0%; Score 74; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 177 TRKKRYTAQELD 188
|||
Qy 2 TRKKRYTAQELD 13
RESULT 2
ENTRY 518783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes
phage (strain MGAS158 isolate Nebraska and others)
(fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS158 isolate Nebraska; strain MGAS485 isolate
Yugoslavia; strain MGAS491 isolate United Kingdom; strain
MGAS624 isolate Germany; strain MGAS495 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
ACCESSIONS 518783; 518793; 518794; 518801; 518798
REFERENCE 518782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession 518783
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61568; NID:q47289; PID:q47290
#experimental_source strain MGAS158 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518793
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEA
#cross-references EMBL:X61569; NID:q47313; PID:q47314
#experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518794
#status nucleic acid sequence not shown; translation not shown

##molecule_type DNA
#residues 1-236 #label NEZ
#cross-references EMBL:X61570; NID:q47315; PID:q47316
#experimental_source strain MGAS491 isolate United Kingdom unassigned
phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518801
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEX
#cross-references EMBL:X61572; NID:q47333; PID:q47334
#experimental_source strain MGAS624 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518798
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEO
#cross-references EMBL:X61571; NID:q47323; PID:q47324
#experimental_source strain MGAS495 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
1-22 #domain signal sequence (fragment) #status predicted
#label SIG\
23-236 #product exotoxin type A (fragment) #status predicted
#label MAT
SUMMARY #length 236 #checksum 612
Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 5.23e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 157 TRKKRYTAQELD 168
|||
Qy 2 TRKKRYTAQELD 13
RESULT 3
ENTRY 518786 #type fragment
TITLE exotoxin type A precursor (allele 2) - Streptococcus pyogenes
phage (strain MGAS250 isolate California and others)
(fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS250 isolate California; strain MGAS251 isolate
California; strain MGAS256 isolate California; strain
MGAS285 isolate Colorado; strain MGAS480 isolate
Yugoslavia; strain MGAS492 isolate United Kingdom; strain
MGAS496 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
ACCESSIONS 518786; 518787; 518788; 518790; 518792; 518795; 518799
REFERENCE 518782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession 518786
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEL
#cross-references EMBL:X61561; NID:q47297; PID:q47298
#experimental_source strain MGAS250 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991


```
#accession S18787
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61562; NID:947299; PID:947300
##experimental_source strain MGAS251 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18788
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEZ
##cross-references EMBL:X61563; NID:947301; PID:947302
##experimental_source strain MGAS256 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18790
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61564; NID:947305; PID:947306
##experimental_source strain MGAS285 isolate Colorado unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18792
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61565; NID:947311; PID:947312
##experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18795
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61566; NID:947317; PID:947318
##experimental_source strain MGAS492 isolate United Kingdom unassigned
phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18799
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NES
##cross-references EMBL:X61567; NID:947325; PID:947326
##experimental_source strain MGAS496 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

GENETICS
#gene speA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
1-22
#domain signal sequence (fragment) #status predicted
#label SIG\
#product exotoxin type A (fragment) #status predicted
#label MAT
23-236
#length 236 #checksum 1685

SUMMARY
Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 5.23e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKKMTAQLD 168
|||||
QY 2 TNKKKVTAGELD 13

RESULT 4
ENTRY S29659 #type complete
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes
phase T12
```

```
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change
25-Mar-1998
ACCESSIONS S29659; S18782; S18784; S18785; S18791; S18796; S18797;
S18800
REFERENCE
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin
(erythrogenic toxin) gene from Streptococcus pyogenes
bacteriophage T12.
#cross-references MUID:86166804
#accession S29659
##molecule-type DNA
##residues 1-251 ##label WEZ
##cross-references GB:U040453; EMBL:M19350; NID:91877426; PID:91877430
REFERENCE
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18782
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 9-244 ##label NEL
##cross-references EMBL:X61560; NID:947287; PID:947288
##experimental_source Streptococcus pyogenes strain MGAS156 isolate
Nebraska unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18784
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 9-244 ##label NEA
##cross-references EMBL:X61556; NID:947291; PID:947292
##experimental_source Streptococcus pyogenes strain MGAS165 isolate
Minnesota unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18785
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 9-244 ##label NEZ
##cross-references EMBL:X61559; NID:947293; PID:947294
##experimental_source Streptococcus pyogenes strain MGAS167 isolate
Texas unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18791
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 9-244 ##label NEY
##cross-references EMBL:X61555; NID:947309; PID:947310
##experimental_source Streptococcus pyogenes strain MGAS327 isolate
Arizona unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18796
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 9-244 ##label NEO
##cross-references EMBL:X61557; NID:947319; PID:947320
##experimental_source Streptococcus pyogenes strain MGAS493 isolate
France unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18797
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 9-244 ##label NEH
```

```
##cross-references EMBL:X61558; NID:q47321; PID:q47322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18800
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-228 #label NES
##cross-references EMBL:X61554; NID:q47327; PID:q47328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
Zealand unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
1-30 #domain signal sequence #status predicted #label SIG\
31-251 #product exotoxin type A #status predicted #label MAT
SUMMARY #length 251 #molecular-weight 29246 #checksum 1475
Query Match 91.9%; Score 68; DB 2; Length 251;
Best Local Similarity 91.7%; Pred. No. 5.23e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 165 TNKKKVTAGLELD 176
|:|:|:|:|:|:|
Oy 2 TNKKKVTAGLELD 13

RESULT 5
ENTRY A29566 #type complete
TITLE enterotoxin A - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change
18-Jun-1993
ACCESSIONS A29566
REFERENCE
#authors Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
#journal J. Biol. Chem. (1987) 262:7006-7013
#title Complete amino acid sequence of staphylococcal enterotoxin A.
#cross-references MUID:87222293
#accession A29566
##molecule_type protein
##residues 1-233 #label HVA
GENETICS
#gene entA
#map_position 6
SUMMARY #length 233 #molecular-weight 27079 #checksum 9580
Query Match 86.5%; Score 64; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 4.71e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 145 TNKKKVTAGLELD 156
|:|:|:|:|:|:|
Oy 2 TNKKKVTAGLELD 13

RESULT 6
ENTRY S18789 #type fragment
TITLE exotoxin A precursor (allele 4) - Streptococcus pyogenes
(strain MGAS262 isolate California) (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes
#strain MGAS262 isolate California
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
25-Mar-1998
ACCESSIONS S18789
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
```

```
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18789
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 #label NEL
##cross-references EMBL:X61573; NID:q47303; PID:q47304
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE
1-22 #domain signal sequence (fragment) #status predicted
23-236 #label SIG\
#product exotoxin A (fragment) #status predicted #label
MAT
SUMMARY #length 236 #checksum 3493
Query Match 86.5%; Score 64; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 4.71e-03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 157 TSKKKVTAGLELD 168
|:|:|:|:|:|:|
Oy 2 TNKKKVTAGLELD 13

RESULT 7
ENTRY A28664 #type complete
TITLE enterotoxin A precursor - Staphylococcus aureus (strain
FRI337)
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
ACCESSIONS A28664
REFERENCE
#authors Betley, M.J.; Mekalanos, J.J.
#journal J. Bacteriol. (1988) 170:34-41
#title Nucleotide sequence of the type A staphylococcal enterotoxin
gene.
#cross-references MUID:88086892
#accession A28664
##molecule_type DNA
##residues 1-257 #label BET
##cross-references GB:M18970; NID:g153120; PID:g153121
##experimental_source strain FRI337
SUMMARY #length 257 #molecular-weight 29659 #checksum 2543
Query Match 86.5%; Score 64; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.71e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 169 TNKKKVTAGLELD 180
|:|:|:|:|:|:|
Oy 2 TNKKKVTAGLELD 13

RESULT 8
ENTRY ENSG1 #type complete
TITLE enterotoxin C-1 precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change
05-Sep-1997
ACCESSIONS S06356; A01816
REFERENCE S06356
#authors Bobach, G.A.; Schlievert, P.M.
#journal Mol. Gen. Genet. (1987) 209:15-20
#title Nucleotide sequence of the staphylococcal enterotoxin C1 gene
```

and relatedness to other pyrogenic toxins.
#cross-references MUID:88038352
#accession S06356
##molecule_type DNA
##residues 1-266 ##label BOH
#cross-references EMBL:X05815; NID:g46566; PID:g46567
REFERENCE A01816
#authors Schmidt, J.J.; Spero, L.
#journal J. Biol. Chem. (1983) 258:6300-6306
#title The complete amino acid sequence of Staphylococcal enterotoxin C-1.
#cross-references MUID:83213327
#accession A01816
##molecule_type protein
##residues 28-75, 'IL', 78-176, 'N', 178-266 ##label SCH
SUMMARY 120-137
#length 266 #molecular_weight 30546 #checksum 4489
#disulfide_bonds #status experimental
#product enterotoxin C-1 #status experimental #label MAT
1-27 #domain signal sequence #status predicted #label SIG
28-266 #product enterotoxin C-1 #status experimental #label MAT
SUMMARY 120-137
#length 266 #molecular_weight 30546 #checksum 4489
Query Match 86.5%; Score 64; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 4,71e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 176 TDKKSVTAQELD 187
1:1111111111
Qy 2 TNKKRVTAQELD 13
RESULT 9
ENTRY A60114 #type complete
TITLE enterotoxin C-2 precursor - Staphylococcus aureus
ALTERNATE_NAMES
ORGANISM #formal_name Staphylococcus aureus
DATE 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 08-Sep-1997
ACCESSIONS A60114; B60114; A33866
REFERENCE A60114
#authors Bohach, G.A.; Schlievert, P.M.
#journal Infect. Immun. (1989) 57:2249-2252
#title Conservation of the biologically active portions of staphylococcal enterotoxins CI and C2.
#cross-references MUID:89277549
#accession A60114
##status not compared with conceptual translation
##molecule_type DNA
##residues 1-266 ##label BOH
#accession B60114
##molecule_type protein
##residues 28-66 ##label BOH2
REFERENCE A33866
#authors Couch, J.L.; Betley, M.J.
#journal J. Bacteriol. (1989) 171:4507-4510
#title Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests that intergenic recombination causes antigenic variation.
#cross-references MUID:89327174
#accession A33866
##molecule_type DNA
##status preliminary
#cross-references MUID:89327174
GENETICS 1-266 #label COU
#cross-references GB:M28364; NID:g153003; PID:g153004
CLASSIFICATION entc2
#gene enterotoxin B
FEATURE 1-27 #domain signal sequence #status predicted #label SIG

28-266 #product enterotoxin C-2 #status predicted #label MAT
SUMMARY 120-137
#length 266 #molecular_weight 30604 #checksum 5494
Query Match 86.5%; Score 64; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 4,71e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 176 TDKKSVTAQELD 187
1:1111111111
Qy 2 TNKKRVTAQELD 13
RESULT 10
ENTRY S11885 #type complete
TITLE enterotoxin C3 - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Mar-1998
ACCESSIONS S11885
REFERENCE S11885
#authors Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
#journal Mol. Gen. Genet. (1990) 220:329-333
#title Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three Type C staphylococcal enterotoxins.
#cross-references MUID:90220508
#accession S11885
##status preliminary
##residues 1-266 ##label HOV
#cross-references GB:X51661; NID:g46570; PID:g46571
CLASSIFICATION #superfamily enterotoxin B
SUMMARY 120-137
#length 266 #molecular_weight 30671 #checksum 6135
Query Match 86.5%; Score 64; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 4,71e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 176 TDKKSVTAQELD 187
1:1111111111
Qy 2 TNKKRVTAQELD 13
RESULT 11
ENTRY A33953 #type complete
TITLE enterotoxin D precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 08-Sep-1997
ACCESSIONS A33953
REFERENCE A33953
#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.
#cross-references MUID:89359112
#accession A33953
##status preliminary
##molecule_type DNA
##residues 1-258 ##label BAY
#cross-references GB:M28521; NID:g1492109; PID:g758691
SUMMARY 120-137
#length 258 #molecular_weight 29746 #checksum 39
Query Match 83.8%; Score 62; DB 2; Length 258;
Best Local Similarity 75.0%; Pred. No. 1,38e-02;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 170 TDKKRVTAQELD 181
1:1111111111
Qy 2 TNKKRVTAQELD 13
RESULT 12

[6]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RP MEDLINE: 98181012.
RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARIA R.R.;
RT Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. MOL. BIOL. 277:61-79(1998).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M1118; G153000; -.
DR PIR: A01815; ENSAB6.
DR PIR: S27360; S27360.
DR PDB: 1SEB: 20-JUN-96.
DR PDB: 3SEB: 28-JAN-98.
DR PDB: 3SEB: 27-MAY-98.
DR PDB: 1SE3: 16-JUN-97.
DR PDB: 1SE4: 15-OCT-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERNANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 266
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
SQ SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
Query Match 100.0%; Score 74; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 8.34e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 177 TNKKKVTAEILD 188
Qy 2 TNKKKVTAEILD 13
RESULT 2
ID SPEA_STRPY STANDARD; PRT; 251 AA.
AC P08095;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE (SPE A).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 8616804.
RN WEEKS C.R., FERRETTI J.J.;

"Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12.";
RL INFECT. IMMUN. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 8628413.
RA JOHNSON U.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B.";
RL MOL. GEN. GENET. 203:354-356(1986).
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC FEVER.
CC -1- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U40453; G1877430; -.
DR EMBL: X03929; G47442; -.
DR PIR: A26152; A26152.
DR PIR: S29659; S29659.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
DR HSSP: P01552; 1SEB.
KW TOXIN; SIGNAL.
FT SIGNAL 1 30
FT CHAIN 31 251
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
FT CONFLICT 40 40
FT CONFLICT 43 43
FT CONFLICT 47 59
FT CONFLICT 129 129
FT CONFLICT 165 178
SQ SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;
Query Match 91.9%; Score 68; DB 1; Length 251;
Best Local Similarity 91.7%; Pred. No. 4.14e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 165 TNKKKVTAEILD 176
Qy 2 TNKKKVTAEILD 13
RESULT 3
ID ETXA_STAUA STANDARD; PRT; 257 AA.
AC P13163;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE A PRECURSOR (SFA).
DE ENTA.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN [1]
RP SEQUENCE FROM N.A.


```

RESULT 5
ID ETC3_STAUB STANDARD: PRT: 266 AA.
AC P23313;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ENT3.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90220508.
RA HOYE C.J., HACKETT S.P., BOHACH G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RL MOL. GEN. GENET. 220:329-333(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECP.
RX MEDLINE: 97064178.
RA FIELDS B.A., MALCHIOTI E.L., LI H., YSEHN X., STAUFACHER C.V.,
RA SCHLIEVERT P.M., KARJALAINEN K., MARIUZZA R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RL NATURE 384:188-192(1996).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X51661; G46571; .
DR PIR: S11885; S11885.
DR PDB: 1JCK; 12-NOV-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph-Strep-toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-3.
FT DISULFID 120 137 BY SIMILARITY.
SQ SEQUENCE 266 AA; 30671 MW; 27B4DD0A CRC32;

Query Match 86.5%; Score 64; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 5.12e-04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 176 TDKSVTAOEID 187
QY 2 TNKKRVTAEID 13

```

```

RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-66.
RX MEDLINE: 89277549.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RL INFECT. IMMUN. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE: 96027099.
RA PAPAGEORGIOU A.C., ACHARYA K.R., SHAPIRO R., PASSALACQUA E.F.,
RA BREHM R.D., TRANTER H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT staphylococcus aureus reveals a zinc-binding site."
RL STRUCTURE 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE: 96022987.
RA SWAMINATHAN S., FUREY W.F. JR., FLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL NAT. STRUCT. BIOL. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC3.
RX MEDLINE: 97334373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. MOL. BIOL. 269:270-280(1997).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
DR PIR: A60114; A60114.
DR PDB: 1STE; 23-DEC-96.
DR PDB: 1SE2; 08-MAR-96.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph-Strep-toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; A115FD37 CRC32;

Query Match 86.5%; Score 64; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 5.12e-04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 176 TDKSVTAOEID 187
QY 2 TNKKRVTAEID 13

```

```

RESULT 6
ID ETC2_STAUB STANDARD: PRT: 266 AA.
AC P34071;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ENT2.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89359112.

```


RA BAYLES K.W., IANDOLO J.J.:
RT "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D.";
RL J. BACTERIOL. 171:4799-4806(1989).
[2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE: 97157473
RA SUNDBLOM M., ABRAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,
DOHLSTER M.:
RT "The crystal structure of staphylococcal enterotoxin type D reveals
RT Zn²⁺-mediated homodimerization.";
RL EMBO J. 15:6832-6840(1996)
CC -1- SUBUNIT: HOMODIMER, ZINC-DEPENDENT.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: M28521; G758691; .
DR PIR: A33953; A33953.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
DR HSSP: P13163; ISXT.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
FT SIGNAL 1 25
FT CHAIN 1 25
FT METAL 26 258 ENTEROTOXIN D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 2D1AA120 CRC32;

Query Match 83.88; Score 62; DB 1; Length 258;
Best Local Similarity 75.08; Pred. No. 1,75e-03;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 170 TDKKNTVOELD 181
1:1111111111
2 TDKKNTVOELD 13

RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.:
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL NAT. STRUCT. BIOL. 2:680-686(1995).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: M21319; G153002; .
DR PIR: A28179; A28179.
DR PDB: 1SBE; 1S-OCT-95.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 1 27
FT CHAIN 28 257 ENTEROTOXIN E.
SQ SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;

Query Match 78.48; Score 58; DB 1; Length 257;
Best Local Similarity 75.08; Pred. No. 1.92e-02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 169 TSKREYVOELD 180
1:1111111111
2 TDKKNTVOELD 13

RESULT 9
ID DPP6_RAT STANDARD; PRT: 859 AA.
AC P46101;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
GN DPP6.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATIUS.
NC [1]
RP SEQUENCE FROM N.A.
RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.:
RT "Differential expression of two distinct forms of mRNA encoding
RT members of a dipeptidyl aminopeptidase family.";
RL PROC. NATL. ACAD. SCI. U.S.A. 89:197-201(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
CC FUNCTION. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: DPPX-S IS EXPRESSED IN BRAIN AND SOME
CC PERIPHERAL TISSUES INCLUDING KIDNEY, OVARY, AND TESTIS; IN
CC CONTRAST DPPX-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN.
CC -1- ALTERNATIVE PRODUCTS: TWO DISTINCT FORMS (DPPX-L AND -S) SHARE AN
CC IDENTICAL TRANSMEMBRANE DOMAIN AND A LONG C-TERMINAL EXTRACELLULAR
CC DOMAIN, BUT HAVE LONG AND SHORT N-TERMINAL CYTOPLASMIC DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: M76426; G408714; -
 DR EMBL: M76427; G408716; -
 DR PFAM: PF00326; Prolyl_oligopep; 1.
 DR PFAM: PF00930; Dppiv_N-term; 1.
 KM HYDROLASE: DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
 KM SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
 FT DOMAIN 1 89 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 90 110 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 111 859 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 167 167 POTENTIAL.
 FT CARBOHYD 168 168 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 398 398 POTENTIAL.
 FT CARBOHYD 465 465 POTENTIAL.
 FT CARBOHYD 529 529 POTENTIAL.
 FT CARBOHYD 560 560 POTENTIAL.
 FT CARBOHYD 807 807 POTENTIAL.
 FT VARSPPLIC 1 75 MASLYORFTGKINTSRSPAPPEASRLGCGPEEDAGSKP
 FT LGPOAOVAPRRGAGGRPRFOYQARSDDDED -> MTT
 FT AKPSASGKSVQOQDQ (IN DPPX-S).
 SQ SEQUENCE 859 AA; 97301 MW; B43COE82 CRC32;

Query Match 68.9%; Score 51; DB 1; Length 859;
 Best Local Similarity 54.5%; Pred. No. 9,938-01;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 120 SOKKKVTEDL 130
 QY : ||||| : : :
 2 TNKKKVTAEEL 12

RESULT 10
 ID DPP6_BOVIN STANDARD; PRT; 863 AA.
 AC P42659;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
 DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
 GN DPP6.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC TISSUE-BRAIN;
 RX MEDLINE: 92108018.
 RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;
 RT "differential expression of two distinct forms of mRNA encoding
 RT members of a dipeptidyl aminopeptidase family.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 89:197-201(1992).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
 CC FUNCTION. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
 CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
 CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN. DPPX-L
 CC IS EXPRESSED EXCLUSIVELY IN THE BRAIN WHEREAS DPPX-S IS FOUND IN
 CC BRAIN, KIDNEY, OVARY AND TESTIS.
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM
 CC (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE
 CC SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 59B; ALSO KNOWN AS THE
 CC PROLYL OLIGOPEPTIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: M76428; G408718; -
 DR EMBL: M76429; G408720; -
 DR PFAM: PF00326; Prolyl_oligopep; 1.
 DR PFAM: PF00930; Dppiv_N-term; 1.
 KM HYDROLASE: DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
 KM SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
 FT DOMAIN 1 93 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 94 114 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 115 863 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 171 171 POTENTIAL.
 FT CARBOHYD 402 402 POTENTIAL.
 FT CARBOHYD 469 469 POTENTIAL.
 FT CARBOHYD 533 533 POTENTIAL.
 FT CARBOHYD 564 564 POTENTIAL.
 FT CARBOHYD 811 811 POTENTIAL.
 FT VARSPPLIC 1 79 MASLYORFTGKINTSRSPAPPEASRLGCGPEEDAGSKP
 FT LGPOAOVAPRRGAGGRPRFOYQARSDDDED -> MTT
 FT AKPSASGKSVQOQDQ (IN DPPX-S).
 SQ SEQUENCE 863 AA; 96556 MW; 8DA40472 CRC32;

Query Match 68.9%; Score 51; DB 1; Length 863;
 Best Local Similarity 54.5%; Pred. No. 9,938-01;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 124 SOKKKVTEDL 134
 QY : ||||| : : :
 2 TNKKKVTAEEL 12

RESULT 11
 ID DPP6_HUMAN STANDARD; PRT; 865 AA.
 AC P42658;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
 DE RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
 GN DPP6.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CARNIVORINIA; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HIPOCAMPUS;
 RX MEDLINE: 93372805.
 RA YOKOTANI N., DOI K., WENTHOLD R.J., WADA K.;
 RT "non-conservation of a catalytic residue in a dipeptidyl
 RT aminopeptidase. iv-related protein encoded by a gene on human
 RT chromosome 7.";
 RL HUM. MOL. GENET. 2:1037-1039(1993).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
 CC FUNCTION. HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
 CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
 CC FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM
 CC (DPPX-L) ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE
 CC SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 59B; ALSO KNOWN AS THE
 CC PROLYL OLIGOPEPTIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its


```

RT subtlis chromosome containing the replication origin."
RL DNA RES. 1:1-14(1994).
CC -1- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
CC (BY SIMILARITY).
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
CC METALLOPROTEASE).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D26185; G467458; -
CC EMBL: Z99104; E1182002; -
CC SUBTILIS: BG10132; FTSH.
CC PROSITE: PS00674; AAA: 1.
CC PRAM: PF00004; AAA: 1.
CC CELL DIVISION; ATP-BINDING; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE;
CC ZINC.
CC FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 8 28 POTENTIAL.
CC FT DOMAIN 29 109 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 110 130 POTENTIAL.
CC FT DOMAIN 131 637 CYTOPLASMIC (POTENTIAL).
CC FT NP_BIND 139 146 ATP (POTENTIAL).
CC FT METAL 423 423 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT ACT_SITE 424 424 BY SIMILARITY.
CC FT METAL 427 427 ZINC (CATALYTIC) (BY SIMILARITY).
CC SQ SEQUENCE 637 AA; 70937 MW; 08C92C38 CRC32;

Query Match 64.9%; Score 48; DB 1; Length 637;
Best Local Similarity 54.5%; Pred. No. 4.84e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 385 NKKRIDARDID 395
QY 3 NKKKVTQAQELD 13

RESULT 15
ID VIT_BOMO STANDARD; PRT; 1782 AA.
AC Q27309;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE VITELLOGENIN PRECURSOR [CONTAINS: VITELLIN LIGHT CHAIN (VL); VITELLIN
DE HEAVY CHAIN (VH)].
GN VG.
OS BOMBYX MORI (SILK MOTH).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; LEPIDOPTERA; BOMBYCOIDEA; BOMBYCIDAE; BOMBYX.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-25 AND 367-380.
RC STRAIN-KINSHU X SHOMA; TISSUE-FAT BODY;
RX MEDLINE: 94250682.
RA YANO K.-I., SAKURAI M.T., WATABE S., IZUMI S., TOMINO S.;
RT "Structure and expression of mRNA for vitellogenin in Bombyx mori.";
RL BIOCHIM. BIOPHYS. ACTA 1218:1-10(1994).
CC -1- FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF
CC NUTRIENTS DURING EMBRYONIC DEVELOPMENT.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE FEMALE FAT BODY ON DAY-
CC 2 OF SPINNING STAGE, REACHING MAXIMAL LEVELS AT LARVAL-PUPAL.
CC ECDYSIS AND DECLINING THEREAFTER. NOT FOUND IN THE MALE TISSUES.
CC -1- INDUCTION: BY ECDYSTEROID AND JUVENILE HORMONE.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO HEAVY AND TWO LIGHT CHAINS.
CC -1- TISSUE SPECIFICITY: PRODUCED BY THE FAT BODY, WHERE IT IS CLEAVED
CC BEFORE BEING SECRETED INTO HEMOLYMPH. SEQUESTERED THEN BY A SINGLE

```

```

CC CLASS OF RECEPTOR MEDIATED ENDOCYTOSIS IN THE OVARY.
CC -1- PTM: GLYCOSYLATED AND PHOSPHORYLATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13160; G217296; -
CC EMBL: D30733; G871834; -
CC EMBL: D30732; G871834; JOINED.
CC GLYCOPROTEIN; PHOSPHORYLATION; STORAGE PROTEIN; SIGNAL.
CC FT SIGNAL 1 15
CC FT CHAIN 16 1782 VITELLOGENIN.
CC FT CHAIN 16 370 VITELLIN LIGHT CHAIN.
CC FT CHAIN 16 366 VITELLIN LIGHT CHAIN (RARE).
CC FT CHAIN 371 1782 VITELLIN HEAVY CHAIN.
CC FT CHAIN 367 1782 VITELLIN HEAVY CHAIN (RARE).
CC FT DOMAIN 336 345 POLY-SER.
CC FT DOMAIN 385 395 POTENTIAL.
CC FT CARBOHYD 569 569 POTENTIAL.
CC FT CARBOHYD 587 587 POTENTIAL.
CC FT CARBOHYD 1357 1357 POTENTIAL.
CC FT CARBOHYD 1463 1463 POTENTIAL.
CC FT CARBOHYD 1596 1596 POTENTIAL.
CC SQ SEQUENCE 1782 AA; 203053 MW; 6AEFCB1 CRC32;

Query Match 64.9%; Score 48; DB 1; Length 1782;
Best Local Similarity 54.5%; Pred. No. 4.84e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1536 TNRKRINDDL 1546
QY 2 TNRKKVTAQEL 12

```

Search completed: Tue Aug 31 19:13:45 1999
Job time : 5 secs.

(TM)

Distribution rights by Oxford Molecular Ltd

Distribution rights by Oxford Molecular Ltd

Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on: Tue Aug 31 19:14:03 1999; MasPar time 5.30 Seconds
```

Tabular output not generated.

Title: >US-09-150-947-5

Perfect score: 74

SECURITY + SUPPLY DIV TEC

Gap 15

Searched: 179066 seqs, 54579741 residues

| Post-processing: | Minimum Match | 04 |
|------------------|---------------|----|
|------------------|---------------|----|

Database:

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 22.886; Variance 25.997; scale 0.880

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB | ID | Description | pred. No. |
|------------|-------|-------------|--------|----|--------|-------------------------|-----------|
| 1 | 69 | 93.2 | 268 | 2 | 085217 | ENTEROTOXIN J. | 8.06e-05 |
| 2 | 68 | 91.9 | 236 | 2 | P97163 | TYPE A EXOTOXIN PRECUR | 1.48e-04 |
| 3 | 68 | 91.9 | 236 | 2 | 054779 | TYPE A EXOTOXIN PRECUR | 1.48e-04 |
| 4 | 68 | 91.9 | 236 | 2 | 057453 | TYPE A EXOTOXIN PRECUR | 1.48e-04 |
| 5 | 64 | 86.5 | 236 | 2 | 054696 | TYPE A EXOTOXIN PRECUR | 1.61e-03 |
| 6 | 64 | 86.5 | 239 | 2 | 006531 | ENTEROTOXIN TYPE C-4 (| 1.61e-03 |
| 7 | 64 | 86.5 | 239 | 2 | 005157 | TYPE C ENTEROTOXIN (FR | 1.61e-03 |
| 8 | 64 | 86.5 | 239 | 2 | 053678 | ENTEROTOXIN (FRAGMENT) | 1.61e-03 |
| 9 | 64 | 86.5 | 239 | 2 | 006535 | ENTEROTOXIN TYPE C-3 (| 1.61e-03 |
| 10 | 64 | 86.5 | 239 | 2 | 006532 | ENTEROTOXIN TYPE C-7 (| 1.61e-03 |
| 11 | 64 | 86.5 | 239 | 2 | 006534 | ENTEROTOXIN TYPE C (SE | 1.61e-03 |
| 12 | 63 | 85.1 | 260 | 2 | 006533 | ENTEROTOXIN TYPE C (SE | 1.61e-03 |
| 13 | 63 | 85.1 | 260 | 2 | 054739 | SUPERANTIGEN TYPE C (SE | 2.90e-03 |
| 14 | 63 | 85.1 | 260 | 2 | 054971 | SUPERANTIGEN SSA. | 2.90e-03 |
| 15 | 63 | 85.1 | 260 | 2 | 054738 | SUPERANTIGEN SSA. | 2.90e-03 |
| 16 | 61 | 82.4 | 241 | 2 | 053585 | ENTEROTOXIN H PRECURSO | 9.23e-03 |
| 17 | 57 | 77.0 | 258 | 2 | 085382 | EXTRACELLULAR ENTEROTO | 8.84e-02 |
| 18 | 56 | 75.7 | 242 | 2 | 054476 | ENTEROTOXIN. | 1.35e-01 |
| 19 | 56 | 75.7 | 242 | 2 | 085383 | ENTEROTOXIN. | 1.35e-01 |
| 20 | 52 | 70.3 | 807 | 2 | 025189 | VIRAL HOMOLOG. | 1.31e+00 |

| | | | | | | | | | | | | | | |
|-----------------------|--|---|--------------|-------|------------|-------------------------|------------------|--|--|--|--|--|--|--|
| 21 | 52 | 70.3 | 850 | 5 | Q21350 | K08F4.1 PROTEIN. | 1.31e+00 | | | | | | | |
| 22 | 51 | 68.9 | 526 | 5 | P91037 | SIMILAR TO UDP GLUCURO | 2.21e+00 | | | | | | | |
| 23 | 50 | 67.6 | 1252 | 4 | Q75068 | KIAA0480 PROTEIN. | 3.70e+00 | | | | | | | |
| 24 | 48 | 64.9 | 204 | 14 | Q66075 | TRANSCRIPTIONAL ACTIVA | 1.01e+01 | | | | | | | |
| 25 | 48 | 64.9 | 914 | 5 | Q22715 | T24B8.4 PROTEIN. | 1.01e+01 | | | | | | | |
| 26 | 48 | 64.9 | 946 | 5 | Q19370 | F12F6.5. | 1.01e+01 | | | | | | | |
| 27 | 48 | 64.9 | 1055 | 2 | Q43892 | LEUKOTOXIN. | 1.01e+01 | | | | | | | |
| 28 | 48 | 64.9 | 1761 | 10 | Q48867 | MODIFICATION METHYLASE | 1.01e+01 | | | | | | | |
| 29 | 47 | 63.5 | 148 | 1 | Q27886 | CONSERVED PROTEIN. | 1.66e+01 | | | | | | | |
| 30 | 47 | 63.5 | 334 | 2 | Q52631 | GLYCERALDEHYDE-3-PHOS | 1.66e+01 | | | | | | | |
| 31 | 47 | 63.5 | 518 | 8 | Q47869 | CYCLOCHROME C OXIDASE S | 1.66e+01 | | | | | | | |
| 32 | 47 | 63.5 | 538 | 5 | Q24615 | BCD | 1.66e+01 | | | | | | | |
| 33 | 47 | 63.5 | 1215 | 5 | Q77202 | MOSIN-1A. | 1.66e+01 | | | | | | | |
| 34 | 46 | 62.2 | 200 | 10 | Q41668 | GUANINE NUCLEOTIDE REG | 2.70e+01 | | | | | | | |
| 35 | 46 | 62.2 | 464 | 13 | Q91693 | MOTHERS AGAINST DPP. | 2.70e+01 | | | | | | | |
| 36 | 46 | 62.2 | 489 | 10 | Q82610 | T5H22.3 PROTEIN. | 2.70e+01 | | | | | | | |
| 37 | 46 | 62.2 | 589 | 10 | Q65226 | F7H22.15 PROTEIN. | 2.70e+01 | | | | | | | |
| 38 | 46 | 62.2 | 589 | 10 | Q04973 | 2-ISOPROPYLMALATE SYNT | 2.70e+01 | | | | | | | |
| 39 | 46 | 62.2 | 612 | 10 | Q004974 | 2-ISOPROPYLMALATE SYNT | 2.70e+01 | | | | | | | |
| 40 | 46 | 62.2 | 1189 | 4 | Q43604 | TATA BINDING PROTEIN A | 2.70e+01 | | | | | | | |
| 41 | 46 | 62.2 | 1199 | 4 | Q34387 | COFACTOR OF INITIATOR | 2.70e+01 | | | | | | | |
| 42 | 46 | 62.2 | 1199 | 4 | Q60668 | TBP-ASSOCIATED FACTOR | 2.70e+01 | | | | | | | |
| 43 | 46 | 60.8 | 1354 | 6 | Q77819 | CORNEL EPITHELIAL RHO | 4.34e+01 | | | | | | | |
| 44 | 45 | 62.2 | 230 | 2 | Q56040 | EPSC. | 4.34e+01 | | | | | | | |
| 45 | 45 | 60.8 | 793 | 11 | P70188 | KINESIN-ASSOCIATED PRO | 4.34e+01 | | | | | | | |
| ALIGNMENTS | | | | | | | | | | | | | | |
| RESULT | 1 | ALIGNMENTS | | | | | | | | | | | | |
| ID | 085217 | PRELIMINARY; | PRT; | 268 | AA. | | | | | | | | | |
| AC | 085217 | | | | | | | | | | | | | |
| DT | 01-NOV-1998 | (TREMBLREL. 08, CREATED) | | | | | | | | | | | | |
| DT | 01-NOV-1998 | (TREMBLREL. 08, LAST SEQUENCE UPDATE) | | | | | | | | | | | | |
| DT | 01-NOV-1998 | (TREMBLREL. 08, LAST ANNOTATION UPDATE) | | | | | | | | | | | | |
| DE | ENTEROTOXIN J. | | | | | | | | | | | | | |
| GN | SEI. | | | | | | | | | | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | | | | | | | | | | |
| OG | PLASMID PIB485. | | | | | | | | | | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | | | | | | | | | | |
| CC | STAPHYLOCOCCUS. | | | | | | | | | | | | | |
| RN | [1] | | | | | | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | | | | | | |
| RC | STRAIN-KS11410; | | | | | | | | | | | | | |
| RA | ZHANG S., IANDOLO J.J., STEWART G.C.; | | | | | | | | | | | | | |
| RT | "The enterotoxin D plasmid of Staphylococcus aureus encodes a second | | | | | | | | | | | | | |
| RT | enterotoxin determinant (sef)." | | | | | | | | | | | | | |
| RL | SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS. | | | | | | | | | | | | | |
| DR | EMBL; AF053140; G3372532; - | | | | | | | | | | | | | |
| DR | PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1. | | | | | | | | | | | | | |
| DR | PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. | | | | | | | | | | | | | |
| KW | PLASMID. | | | | | | | | | | | | | |
| SO | SEQUENCE | 268 | AA; | 31230 | MM; | 52EBIB06 | CRC32; | | | | | | | |
| Query Match | | | | | | | | | | | | | | |
| Best Local Similarity | | 93.2%; | Score | 69; | DB | 2; | Length 268; | | | | | | | |
| Matches | | 11; | Conservative | 0; | Mismatches | 1; | Indels 0; Gaps 0 | | | | | | | |
| Db | 169 | TNKKKVTIOELD | 180 | | | | | | | | | | | |
| Oy | 2 | TNKKKVTIOELD | 13 | | | | | | | | | | | |
| RESULT 2 | | | | | | | | | | | | | | |
| ID | P97163 | PRELIMINARY; | PRT; | 236 | AA. | | | | | | | | | |
| AC | P97163; P97164; | | | | | | | | | | | | | |
| DT | 01-MAY-1997 | (TREMBLREL. 03, CREATED) | | | | | | | | | | | | |
| DT | 01-MAY-1997 | (TREMBLREL. 03, LAST SEQUENCE UPDATE) | | | | | | | | | | | | |
| DT | 01-NOV-1998 | (TREMBLREL. 08, LAST ANNOTATION UPDATE) | | | | | | | | | | | | |
| DE | TYPE A EXOTOXIN PRECURSOR (FRAGMENT). | | | | | | | | | | | | | |
| GN | SEPA. | | | | | | | | | | | | | |
| OS | STREPTOCOCCUS PYOGENES. | | | | | | | | | | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; | | | | | | | | | | | | | |

```

OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, AND MGAS500;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the spea
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61556; G47292; -.
DR EMBL; X61557; G47320; -.
DR EMBL; X61560; G47288; -.
DR EMBL; X61555; G47310; -.
DR EMBL; X61558; G47322; -.
DR EMBL; X61559; G47294; -.
DR EMBL; X61554; G47328; -.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph-Strep-toxin; 1.
KM SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 81A0C2FE CRC32;

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 1.48e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKRVTAQELD 168
Oy 2 TNKRVTAQELD 13

RESULT 3
ID 054779 PRELIMINARY; PRT; 236 AA.
AC 054779; 054613; 054736; 054740; 054741;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the spea
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61569; G47314; -.
DR EMBL; X61572; G47334; -.
DR EMBL; X61568; G47290; -.
DR EMBL; X61570; G47316; -.
DR EMBL; X61571; G47324; -.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph-Strep-toxin; 1.
KM SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; E902ED6D CRC32;

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 1.48e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKRVTAQELD 168
Oy 2 TNKRVTAQELD 13

```

```

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKRVTAQELD 168
Oy 2 TNKRVTAQELD 13

RESULT 4
ID 057453 PRELIMINARY; PRT; 236 AA.
AC 057453;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS496;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the spea
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61562; G47300; -.
DR EMBL; X61563; G47302; -.
DR EMBL; X61567; G47326; -.
DR EMBL; X61561; G47288; -.
DR EMBL; X61564; G47306; -.
DR EMBL; X61565; G47312; -.
DR EMBL; X61566; G47318; -.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph-Strep-toxin; 1.
KM SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; A5EB1ECD CRC32;

Query Match 91.9%; Score 68; DB 2; Length 236;
Best Local Similarity 91.7%; Pred. No. 1.48e-04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 157 TNKRVTAQELD 168
Oy 2 TNKRVTAQELD 13

RESULT 5
ID 054696 PRELIMINARY; PRT; 236 AA.
AC 054696;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the spea
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. EXP. MED. 174:1271-1274(1991).

```

DR EMBL: X61573; G47304; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW SIGNAL.

FT NON_TER 1
FT SIGNAL <1 22
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27575 MW; A799A5F3 CRC32;

Query Match 86.5%; Score 64; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 1,61e-03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 157 TSKKMTA0E1D 168
Y 2 TNKKVTA0E1D 13

RESULT 6 PRELIMINARY; PRT; 239 AA.
ID 006531
AC 006531;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-4 (SEC446) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FRMICTURES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-4446;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
CC PYROGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13374; G295141; -
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; 52B18853 CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1,61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKVTAE1D 160
Y 2 TNKKVTA0E1D 13

RESULT 7 PRELIMINARY; PRT; 239 AA.
ID 005157
AC 005157;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE C ENTEROTOXIN (FRAGMENT).
OS STAPHYLOCOCCUS INTERMEDIUS.
OC BACTERIA; FRMICTURES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95-011195;
RA EDWARDS V.M., DERINGER J.R., CALLANTINE S.D., DEOBALD C.F.,
RA BERGER P.H., KAPUR V., STAUFACHER C.V., BOHACH G.A.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U91526; G1906052; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27536 MW; 390EB227 CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1,61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKVTAE1D 160
Y 2 TNKKVTA0E1D 13

RESULT 8 PRELIMINARY; PRT; 239 AA.
ID 053678
AC 053678;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FRMICTURES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
DR EMBL: L13376; G295145; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; 0810BB9D CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1,61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKVTAE1D 160
Y 2 TNKKVTA0E1D 13

RESULT 9 PRELIMINARY; PRT; 239 AA.
ID 006535
AC 006535;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FRMICTURES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRI 909;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
CC PYROGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13377; G295147; -

DR PFAM: PF01123; Strep-Strep.toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27648 MW; 1DC80C35 CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKSVTAQELD 160
1:1111111111
QY 2 TNKKKVTAAQELD 13

RESULT 10
ID 006532 PRELIMINARY; PRT; 239 AA.
AC 006532;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-740N;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
CC PYGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13375; G295143; -
DR PFAM: PF01123; Strep-Strep.toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; 81CA4BC2 CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKSVTAQELD 160
1:1111111111
QY 2 TNKKKVTAAQELD 13

RESULT 11
ID 006534 PRELIMINARY; PRT; 239 AA.
AC 006534;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
CC PYGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13379; G295151; -

DR PFAM: PF01123; Strep-Strep.toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27517 MW; 1293E9CA CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKSVTAQELD 160
1:1111111111
QY 2 TNKKKVTAAQELD 13

RESULT 12
ID 006533 PRELIMINARY; PRT; 239 AA.
AC 006533;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MNCOPELAND;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
CC PYGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13378; G295149; -
DR PFAM: PF01123; Strep-Strep.toxin; 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; 7A5C4047 CRC32;

Query Match 86.5%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.61e-03;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 149 TDKKSVTAQELD 160
1:1111111111
QY 2 TNKKKVTAAQELD 13

RESULT 13
ID 054739 PRELIMINARY; PRT; 260 AA.
AC 054739; 054737;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94222556.
RA REBA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INFECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96178602.

RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
 RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
 RT variants provides evidence for horizontal transfer of ssa within
 RT Streptococcus pyogenes.";
 DR EMBL: U48794; G1245176; -;
 DR EMBL: U48792; G1245172; -;
 DR PFAM: PF01123; Stap_Stip_toxin; 1.
 SO SEQUENCE 260 AA; 29767 MW; C81448C1 CRC32;

Query Match 85.1%; Score 63; DB 2; Length 260;
 Best Local Similarity 83.3%; Pred. No. 2.90e-03;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 172 TNKKVTAOELD 183
 QY 2 TNKKVTAOELD 13

RESULT 14
 ID 054971; PRELIMINARY; PRT; 260 AA.
 AC 054971;
 RT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 RT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SUPERANTIGEN.
 GN SSA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RX 1;
 RP SEQUENCE FROM N.A.
 PC STRAIN-WELTER;
 RX MEDLINE: 94222556.
 RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
 RA RICH R.R.;
 RT "Molecular characterization and phylogenetic distribution of the
 RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
 RL INFECT. IMMUN. 62:1867-1874(1994).
 DR EMBL: L29565; G476764; -;
 DR PFAM: PF01123; Stap_Stip_toxin; 1.
 KW SUPERANTIGEN.
 SQ SEQUENCE 260 AA; 29797 MW; FE391C2B CRC32;

Query Match 85.1%; Score 63; DB 2; Length 260;
 Best Local Similarity 83.3%; Pred. No. 2.90e-03;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 172 TNKKVTAOELD 183
 QY 2 TNKKVTAOELD 13

RESULT 15
 ID 054738; PRELIMINARY; PRT; 260 AA.
 AC 054738;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SUPERANTIGEN SSA.
 GN SSA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RX 1;
 RP SEQUENCE FROM N.A.
 PC STRAIN-MGAS 1842;
 RX MEDLINE: 94222556.
 RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
 RA RICH R.R.;
 RT "Molecular characterization and phylogenetic distribution of the
 RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
 RL INFECT. IMMUN. 62:1867-1874(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MGAS 1842;
 RX MEDLINE: 96178602.
 RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
 RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
 RT variants provides evidence for horizontal transfer of ssa within
 RT Streptococcus pyogenes.";
 RL INFECT. IMMUN. 64:1161-1165(1996).
 DR EMBL: U48793; G1245174; -;
 DR PFAM: PF01123; Stap_Stip_toxin; 1.
 SO SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match 85.1%; Score 63; DB 2; Length 260;
 Best Local Similarity 83.3%; Pred. No. 2.90e-03;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 172 TNKKVTAOELD 183
 QY 2 TNKKVTAOELD 13

Search completed: Tue Aug 31 19:14:46 1999
 Job time : 43 secs.

THIS PAGE BLANK (USPTO)

M P E R E H
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MSPrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:18:17 1999; Maspar time 4.12 Seconds

Tabular output not generated. 67.029 Million cell updates/sec

Title: >US-09-150-947-6
Description: (1-13) from US09150947.pep
Perfect Score: 81
Sequence: 1 YNKKATVQELD 13
Scoring table: PAM150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.360; Variance 49.153; scale 0.353

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 81 | 100.0 | 12 34 | W64637 | Synthetic SEB peptide | 1.54e-02 |
| 2 | 81 | 100.0 | 13 34 | W64641 | Synthetic SEB peptide | 1.54e-02 |
| 3 | 81 | 100.0 | 13 34 | W64646 | Synthetic SEB peptide | 1.54e-02 |
| 4 | 81 | 100.0 | 14 34 | W64644 | Synthetic SEB peptide | 1.54e-02 |
| 5 | 81 | 100.0 | 14 34 | W64645 | Synthetic SEB peptide | 1.54e-02 |
| 6 | 81 | 100.0 | 24 34 | W64642 | Synthetic SEB peptide | 1.54e-02 |
| 7 | 81 | 100.0 | 35 34 | W64643 | Synthetic SEB peptide | 1.54e-02 |
| 8 | 64 | 79.0 | 10 34 | W64638 | Synthetic SEB peptide | 1.96e+00 |
| 9 | 59 | 72.8 | 28 19 | W04494 | Staphylococcal entero | 7.72e+00 |
| 10 | 59 | 72.8 | 36 36 | W72426 | Peptide #5 for reduci | 7.72e+00 |
| 11 | 59 | 72.8 | 36 36 | W72427 | Peptide #6 for reduci | 7.72e+00 |
| 12 | 59 | 72.8 | 91 27 | W24299 | Staphylococcal aureus | 7.72e+00 |
| 13 | 59 | 72.8 | 233 3 | R13203 | Staphylococcal entero | 7.72e+00 |
| 14 | 59 | 72.8 | 233 8 | R45011 | Staphylococcal entero | 7.72e+00 |
| 15 | 59 | 72.8 | 233 27 | W35373 | Staphylococcal entero | 7.72e+00 |
| 16 | 59 | 72.8 | 233 20 | W06738 | Staphylococcal entero | 7.72e+00 |

| | | | | | | |
|----|----|------|--------|--------|------------------------|----------|
| 17 | 58 | 71.6 | 12 34 | W64636 | Synthetic SEB peptide | 1.01e+01 |
| 18 | 58 | 71.6 | 13 34 | W64640 | Synthetic SEB peptide | 1.01e+01 |
| 19 | 58 | 71.6 | 239 34 | W64647 | Synthetic SEB protein | 1.01e+01 |
| 20 | 58 | 71.6 | 239 8 | R45014 | Staphylococcal entero | 1.01e+01 |
| 21 | 58 | 71.6 | 239 3 | R13206 | Staphylococcal entero | 1.01e+01 |
| 22 | 58 | 71.6 | 255 20 | W06737 | Staphylococcal entero | 1.01e+01 |
| 23 | 57 | 70.4 | 228 8 | R13205 | Staphylococcal entero | 1.32e+01 |
| 24 | 57 | 70.4 | 228 8 | R45013 | Staphylococcal entero | 1.32e+01 |
| 25 | 54 | 66.7 | 24 36 | W72423 | Peptide #2 for reduci | 2.94e+01 |
| 26 | 54 | 66.7 | 28 36 | W72425 | Peptide #4 for reduci | 2.94e+01 |
| 27 | 53 | 65.4 | 10 34 | W64639 | Synthetic SEB peptide | 3.83e+01 |
| 28 | 53 | 65.4 | 230 3 | R13204 | Staphylococcal entero | 3.83e+01 |
| 29 | 53 | 65.4 | 230 8 | R45012 | Staphylococcal entero | 3.83e+01 |
| 30 | 53 | 65.4 | 245 27 | W35374 | Staphylococcal entero | 3.83e+01 |
| 31 | 53 | 65.4 | 245 27 | W35375 | Staphylococcal entero | 3.83e+01 |
| 32 | 52 | 64.2 | 221 3 | R13209 | Staphylococcal pyrogen | 4.97e+01 |
| 33 | 52 | 64.2 | 221 8 | R45017 | Staphylococcal entero | 4.97e+01 |
| 34 | 52 | 64.2 | 250 24 | W12145 | Staphylococcal pyrogen | 4.97e+01 |
| 35 | 52 | 64.2 | 251 24 | W12147 | Streptococcus pyogene | 4.97e+01 |
| 36 | 52 | 64.2 | 251 24 | W12153 | Streptococcus pyogene | 4.97e+01 |
| 37 | 52 | 64.2 | 251 24 | W12097 | Streptococcus pyogene | 4.97e+01 |
| 38 | 52 | 64.2 | 251 33 | W59781 | Amino acid sequence o | 4.97e+01 |
| 39 | 52 | 64.2 | 251 33 | W59780 | Streptococcus pyogene | 4.97e+01 |
| 40 | 52 | 64.2 | 251 24 | W12151 | Streptococcus pyogene | 4.97e+01 |
| 41 | 52 | 64.2 | 251 24 | W12150 | Streptococcus pyogene | 4.97e+01 |
| 42 | 52 | 64.2 | 251 24 | W12152 | Streptococcus pyogene | 4.97e+01 |
| 43 | 52 | 64.2 | 251 24 | W12146 | Streptococcus pyogene | 4.97e+01 |
| 44 | 52 | 64.2 | 251 24 | W12149 | Streptococcus pyogene | 4.97e+01 |
| 45 | 52 | 64.2 | 401 36 | W22779 | Human septin-2 protei | 4.97e+01 |

ALIGNMENTS

RESULT 1
ID W64637 standard; peptide: 12 AA.
AC W64637:
DE 23-Oct-1998 (first entry)
KW Synthetic SEB peptide p12(151-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-AL.
PD 09-JUL-1998.
PR 30-DEC-1997; IL0438.
PF 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Atad G, Kaempfer R.
DR WPI: 98-38042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 8, Page 41, 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced
CC by PERT or by a mixture of PERTs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PERTs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PERT.
SQ Sequence 12 AA:
Query Match 100.0%; Score 81; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YNKKKATVQELD 13

RESULT 2
ID W64641 standard; peptide: 13 AA.

DE 23-OCT-1998 (first entry)
AC W64641.
DE Synthetic SEB peptide p12LC(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.

FH Key
FT Modified_site 1 location/Qualifiers
/note= "N-terminal Tyr modified by presence of N-lauryl-cysteyl"

PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 16; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA;

Query Match 100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvqeld 13
OY 2 YNKKKATVQELD 13

RESULT 3
ID W64646 standard; peptide: 13 AA.
AC W64646.
DE 23-OCT-1998 (first entry)
DE Synthetic SEB peptide AC p12(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.

FH Key
FT Modified_site 1 location/Qualifiers
/note= "N-terminal Tyr modified by N-acetyl group"
FT MISC.difference 14 /note= "D-form residue"

PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;

DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 24; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA;

Query Match 100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkktatvqeld 12
OY 2 YNKKKATVQELD 13

RESULT 4
ID W64644 standard; peptide: 14 AA.

DE 23-OCT-1998 (first entry)
AC W64644.
DE Synthetic SEB peptide Cys-p12(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.

PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI: 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 21; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvqeld 13
OY 2 YNKKKATVQELD 13

RESULT 5

ID W64645 standard: peptide; 14 AA.
 AC W64645;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide D'Ala.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 FH Staphylococcus aureus.
 FT Key
 FT Misc_difference 1 Location/Qualifiers
 FT Misc_difference 14 /note- "D-form residue"
 FT Misc_difference 14 /note- "D-form residue"
 PN MO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 23: Page 41: 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 ynkktatvgeld 13
 QY 2 YNKKKATVQELD 13
 RESULT 6
 ID W64642 standard: peptide; 24 AA.
 AC W64642;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide dimer.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 FH Staphylococcus aureus.
 FT Key
 FT Misc_difference 1 Location/Qualifiers
 FT Misc_difference 14 /note- "D-form residue"
 FT Misc_difference 14 /note- "D-form residue"
 PN MO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 18: Page 41: 68pp; English.
 CC W64656-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 81; DB 34; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ynkktatvgeld 12
 QY 2 YNKKKATVQELD 13
 RESULT 7
 ID W64643 standard: peptide; 35 AA.
 AC W64643;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide trimer.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 FH Staphylococcus aureus.
 FT Key
 FT Misc_difference 1 Location/Qualifiers
 FT Misc_difference 14 /note- "D-form residue"
 FT Misc_difference 14 /note- "D-form residue"
 PN MO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 19: Page 41: 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 81; DB 34; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ynkktatvgeld 12
 QY 2 YNKKKATVQELD 13
 RESULT 8
 ID W64638 standard: peptide; 10 AA.
 AC W64638;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide pSEB(152-161).
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 FH Staphylococcus aureus.

PN W09829444-A1.
 PD 09-JUL-1998.
 PE 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention of
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 10; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophyllaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 10 AA.

Query Match 79.0%; Score 64; DB 34; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.96e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 kkatvqeld 10
 |||||
 QY 4 KKKATVOELD 13

RESULT 9
 ID W04494 standard; peptide; 28 AA.
 AC W04494.
 DT 10-DEC-1996 (first entry)
 DE Staphylococcal enterotoxin A residues 146-173, T-cell agonist.
 KW Staphylococcal enterotoxin A; agonist; T-cell proliferation;
 KW treatment; immunodeficiency; autoimmune disease; TNF-alpha;
 KW tumour necrosis factor alpha.
 OS Staphylococcus spp.
 PN US5545716-A.
 PD 13-AUG-1996.
 PF 08-SEP-1992; 941497.
 PR 08-SEP-1992; US-941497.
 PR 29-MAR-1994; US-220378.
 PA (UYFL) UNIV FLORIDA.
 PI Griegs ND, Johnson HM, Pontzer CH;
 DR WPI: 96-383718/38.
 PT Peptide fragments of Staphylococcal enterotoxin A (SEA) - useful as
 PT SEA agonists for stimulating T-cell proliferation, e.g. in treatment
 PT of immunodeficiency and autoimmune diseases
 PS Example 1; Columns 15-16; 17pp; English.
 CC The present peptide, comprising residues 146-173 of Staphylococcal
 CC enterotoxin A (SEA), is useful as an SEA agonist for stimulating
 CC T-cell proliferation, e.g. in the treatment of immunodeficiency and
 CC autoimmune diseases. Supernatant from PBMC stimulated with
 CC 100 microm of the peptide for 18 hrs., was collected and assayed
 CC for TNF-alpha activity by cytotoxicity on L-929 cells. The result
 CC given as units/ml of TNF-alpha activity was 1.85, compared to 24.1
 CC for the most effective agonist, comprising SEA residues 121-149.
 SQ Sequence 28 AA.

Query Match 72.8%; Score 59; DB 19; Length 28;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 nkknvqveld 11
 |||||
 QY 3 NKKKATVOELD 13

RESULT 10
 ID W72426 standard; peptide; 36 AA.
 AC W72426;
 DT 22-DEC-1998 (first entry)
 DE Peptide #5 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PF 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 KD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1TX23X4X5N #1,
 CC KX6X78X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE) Ab
 CC are used: (i) for diagnostic detection of SPE or SEB, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 SQ Sequence 36 AA.

Query Match 72.8%; Score 59; DB 36; Length 36;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvqveld 22
 |||||
 QY 3 NKKKATVOELD 13

RESULT 11
 ID W72427 standard; peptide; 38 AA.
 AC W72427;
 DT 22-DEC-1998 (first entry)
 DE Peptide #6 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PF 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGX1TX23X45N #1,
CC KX6X7X8X9X10X11X12X13X14X15X16X17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC Staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
CC are used: (1) for diagnostic detection of SPEA or SEB, SEB and SED, in
CC usual immunoassays; (11) to inhibit blastogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (111) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
SQ Sequence 38 AA;

Query Match 72.8%; Score 59; DB 36; Length 38;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvteyeld 22
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 12
ID W24299 standard; Protein: 91 AA.
AC W24299;
DT 14-APR-1998 (first entry)
DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
KW Staphylococcus aureus WCW 29; antagonist; antibacterial; immunogen;
OS Staphylococcus aureus.
FH Key Location/Qualifiers
FT MISC-difference 29 /note= "Unspecified amino acid"
PN W09731114-A2.
PD 28-AUG-1997.
PF 25-FEB-1997; G00524.
PR 26-FEB-1996; GB-004045.
PA (SMK) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Hodgson JE;
DR WPI: 97-435166/40.
DR N-PSD; V01865.
PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for
PT isolating antagonist of the polypeptide(s) useful as anti-bacterials
PS Claim 11; Page 33; 117pp: English.
CC The present sequence represents a novel polypeptide, which is optionally
CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
CC it, are derived from Staphylococcus aureus. Cells expressing ligands
CC binding the polypeptide can be used to isolated candidate compounds
CC that bind and inhibit the activity of the polypeptide. Such compounds
CC can be used as anti-bacterial compounds. The polypeptide may also be
CC used as an immunogen to vaccinate an animal for protection against
CC Staphylococcus aureus caused disease.
SQ Sequence 91 AA;

Query Match 72.8%; Score 59; DB 27; Length 91;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 40 nkknvteyeld 50
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 13
ID R13203 standard; protein: 233 AA.
AC R13203;
DT 15-OCT-1991 (first entry)
DE Staphylococcal enterotoxin A.
KW SEA; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.
PN W09110680-A.
PD 25-JUL-1991.
PF 17-JUN-1991; U00342.
PR 17-JAN-1990; US-466577.
PA (TERM/) TERMAN D S.
PI Terman DS;
DR WPI: 91-237984/32.
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
PS Disclosure: Fig 1: 74pp: English.
CC SEA was isolated and purified from S. aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEA. Synthetic
CC polypeptides having structural homology to SEA. Synthetic
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of cysteine residues and
CC see also R13204-R13211.
SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 3; Length 233;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvteyeld 156
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 14
ID R45011 standard; protein: 233 AA.
AC R45011;
DT 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SEA.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
OS Staphylococcus aureus.
FH Key Location/Qualifiers
FT MISC-difference 49 /note= "given in the specification as O, no further
FT details given"
PN W09324136-A.
PD 09-DEC-1993.
PF 01-JUN-1993; U05213.
PR 01-JUN-1992; US-891718.
PA (STON/) STONE J L.
PA (TERM/) TERMAN D S.
PI Stone JL, Terman DS;
DR WPI: 93-405418/50.
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases
PS Disclosure: Fig 1: 90pp: English.
CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 8; Length 233;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvteyeld 156
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 15
 ID W35373 standard; peptide: 233 AA.
 AC W35373;
 DT 20-APR-1998 (first entry)
 DE Staphylococcus enterotoxin SEA wild-type superantigen.
 KW SEA: Staphylococcus enterotoxin; superantigen; conjugate;
 treatment; cancer; infection; autoimmune disease; antibody.
 OS Staphylococcus sp.
 PN W09736932-A1.
 PD 09-OCT-1997.
 PE 26-MAR-1997; SE0537.
 PR 12-AUG-1996; US-695692.
 PR 29-MAR-1996; SE-001245.
 RA (PHRA) PHARMACIA & UPJOHN AB.
 PI Abrahmsen L, Antonsson P, Björck P, Dohlssten M,
 PI Forsberg G, Hansson J, Kalland T;
 DR WPI; 97-503052/46.
 PT Conjugate of target seeking moiety and modified superantigen -
 PT useful for activating the immune system to treat cancer, viral
 PT infections, parasitic infestations and autoimmune diseases
 PS Claim 8; pages 36-37; 58pp; English.
 CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
 CC SEA superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to
 CC T cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 27; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 146 nkknvtyvgeld 156
 |||: |||||
 QY 3 NKKKATVOELD 13

Search completed: Tue Aug 31 19:18:57 1999
 Job time : 40 secs.

MUSE (TM)

Release 3.1A John F. Collins, BioComputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msrch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:17:39 1999; MasPar time 3.78 Seconds
Tabular output not generated. 137.823 Million cell updates/sec

Title: >US-09-150-947-6
Description: (1-13) from US09150947.pep
Perfect Score: 81
Sequence: 1 XNNKKATVQELD 13

Scoring table: PAM 150
Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pif60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 24.268; Variance 31.113; scale 0.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------------------------------|-----------|
| 1 | 59 | 72.8 | 233 | 2 | A29566 enterotoxin A - Staph | 2.55e+01 |
| 2 | 59 | 72.8 | 257 | 2 | A28664 enterotoxin A precursor | 2.55e+01 |
| 3 | 58 | 72.8 | 362 | 2 | S27530 sporulation protein - | 2.55e+01 |
| 4 | 58 | 71.6 | 266 | 1 | ENSAB6 enterotoxin B precursor | 4.14e+01 |
| 5 | 57 | 70.4 | 258 | 2 | A33953 enterotoxin D precursor | 6.68e+01 |
| 6 | 53 | 65.4 | 257 | 2 | A28179 enterotoxin E precursor | 4.30e+00 |
| 7 | 53 | 65.4 | 671 | 2 | A40692 signal recognition pa | 4.30e+00 |
| 8 | 53 | 65.4 | 880 | 2 | S51473 probable membrane pro | 4.30e+00 |
| 9 | 53 | 65.4 | 1233 | 2 | I54383 gene SBI.8/DXS423E pr | 4.30e+00 |
| 10 | 52 | 64.2 | 127 | 2 | B69767 conserved hypotetica | 6.76e+00 |
| 11 | 52 | 64.2 | 146 | 2 | S49746 probable membrane pro | 6.76e+00 |
| 12 | 52 | 64.2 | 236 | 2 | S18786 exotoxin type A precu | 6.76e+00 |
| 13 | 52 | 64.2 | 236 | 2 | S18783 exotoxin type A precu | 6.76e+00 |
| 14 | 52 | 64.2 | 251 | 2 | S29659 exotoxin type A precu | 6.76e+00 |
| 15 | 51 | 63.0 | 224 | 2 | S58590 ribosomal protein S3 | 1.05e+01 |
| 16 | 51 | 63.0 | 239 | 1 | R3R23 ribosomal protein S3 | 1.05e+01 |
| 17 | 51 | 63.0 | 262 | 2 | C70372 flagellar hook basal | 1.05e+01 |
| 18 | 51 | 63.0 | 412 | 2 | S48881 rRNA (guanine-2'-O- | 1.05e+01 |
| 19 | 51 | 63.0 | 3418 | 1 | G02334 breast cancer tumor s | 1.05e+01 |
| 20 | 50 | 61.7 | 274 | 2 | B64087 outer membrane protei | 1.64e+01 |
| 21 | 50 | 61.7 | 391 | 2 | S18666 KIN17 protein - mouse | 1.64e+01 |
| 22 | 50 | 61.7 | 1075 | 1 | OYRTHX heat-stable enterotox | 1.64e+01 |
| 23 | 50 | 61.7 | 1223 | 2 | I38111 phosphorylase kinase | 1.64e+01 |

| 24 | 50 | 61.7 | 3685 | 1 | A27605 | dystrophin, muscle - | 1.64e+01 |
|----|----|------|------|---|--------|-----------------------|----------|
| 25 | 49 | 60.5 | 290 | 2 | S66072 | hypothetical protein | 2.52e+01 |
| 26 | 49 | 60.5 | 384 | 2 | S46523 | transcription factor | 2.52e+01 |
| 27 | 49 | 60.5 | 452 | 2 | T01694 | calcium-dependent pro | 2.52e+01 |
| 28 | 49 | 60.5 | 455 | 2 | S55019 | MAD polypeptide - fru | 2.52e+01 |
| 29 | 49 | 60.5 | 465 | 2 | S68987 | transcription activat | 2.52e+01 |
| 30 | 49 | 60.5 | 599 | 2 | T02984 | CDPK-related protein | 2.52e+01 |
| 31 | 49 | 60.5 | 607 | 2 | T03023 | calcium-dependent pro | 2.52e+01 |
| 32 | 49 | 60.5 | 625 | 2 | T02033 | calcium/calmodulin-de | 2.52e+01 |
| 33 | 49 | 60.5 | 803 | 2 | I68600 | dipeptidyl aminopepti | 2.52e+01 |
| 34 | 49 | 60.5 | 803 | 2 | A41793 | dipeptidyl aminopepti | 2.52e+01 |
| 35 | 49 | 60.5 | 831 | 2 | B64528 | conserved hypotetica | 2.52e+01 |
| 36 | 49 | 60.5 | 865 | 2 | I54331 | dipeptidyl aminopepti | 2.52e+01 |
| 37 | 49 | 60.5 | 1134 | 2 | A60234 | IgA Fc receptor precu | 2.52e+01 |
| 38 | 49 | 60.5 | 1164 | 1 | FCSCOG | IgA Fc receptor precu | 2.52e+01 |
| 39 | 49 | 60.5 | 1369 | 2 | JC4860 | protein-tyrosine kina | 2.52e+01 |
| 40 | 49 | 60.5 | 3678 | 2 | S28916 | dystrophin - mouse | 2.52e+01 |
| 41 | 48 | 59.3 | 303 | 2 | E69164 | conserved hypotetica | 3.86e+01 |
| 42 | 48 | 59.3 | 324 | 2 | S48122 | transcription factor | 3.86e+01 |
| 43 | 48 | 59.3 | 332 | 2 | S15347 | transcription factor | 3.86e+01 |
| 44 | 48 | 59.3 | 844 | 2 | T00529 | bZIP-like protein - A | 3.86e+01 |
| 45 | 48 | 59.3 | 1381 | 2 | S60004 | hypothetical protein | 3.86e+01 |

ALIGNMENTS

| RESULT | 1 | ALIGNMENTS |
|--|---|----------------|
| ENTRY | A29566 | #type complete |
| TITLE | enterotoxin A - Staphylococcus aureus | |
| ORGANISM | #formal_name Staphylococcus aureus | |
| DATE | 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 18-Jun-1993 | |
| ACCESSIONS | A29566 | |
| REFERENCE | A29566 | |
| #authors | Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J. | |
| #journal | J. Biol. Chem. (1987) 262:7006-7013 | |
| #title | Complete amino acid sequence of staphylococcal enterotoxin A. | |
| #cross-references MIMD:87222293 | | |
| #accession | A29566 | |
| #molecule_type | protein | |
| #residues | 1-233 #label HUA | |
| GENETICS | | |
| #gene | entra | |
| #map_position | 6 | |
| SUMMARY | #length 233 #molecular_weight 27079 #checksum 9580 | |
| Query Match | 72.8% Score 59; DB 2; Length 233; | |
| Best Local Similarity | 81.8% Pred. NO. 2.55e+01; | |
| Matches | 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |
| Db | 146 NKKKATVQELD 156 | |
| Qy | | |
| Qy | 3 NKKKATVQELD 13 | |
| RESULT | 2 | |
| ENTRY | A28664 | #type complete |
| TITLE | enterotoxin A precursor - Staphylococcus aureus (strain FRI337) | |
| ORGANISM | #formal_name Staphylococcus aureus | |
| DATE | 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Mar-1998 | |
| ACCESSIONS | A28664 | |
| REFERENCE | A28664 | |
| #authors | Betley, M.J.; Mekalanos, J.J. | |
| #journal | J. Bacteriol. (1988) 170:34-41 | |
| #title | Nucleotide sequence of the type A staphylococcal enterotoxin gene. | |
| #cross-references MIMD:88086892 | | |
| #accession | A28664 | |
| #molecule_type | DNA | |
| #residues | 1-257 #label BET | |
| #cross-references GB:M1870; NID:g153120; PID:g153121 | | |

```
##experimental_source strain FR137
SUMMARY      #length 257 #molecular-weight 29669 #checksum 2543
Query Match  72.8%; Score 59; DB 2; Length 257;
Best Local Similarity 81.8%; Pred. No. 2.55e-01;
Matches      9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 170 NKKNTVOELD 180
      |||:|||||
Qy 3  NKKKATVOELD 13

RESULT 3
ENTRY   S27530      #type complete
TITLE   sporulation protein Clostridium acetobutylicum
ORGANISM
#formal_name Clostridium acetobutylicum
DATE    06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
09-Sep-1997
ACCESSIONS
REFERENCE S27530
#authors Reid, S.J.; Hancock, K.; Santangelo, J.D.; Woods, D.R.
#submission Submitted to the EMBL Data Library, March 1992
#description Cloning and sequencing of a spoIID gene from Clostridium
acetobutylicum.
#accession S27530
#status preliminary
#molecule_type DNA
##residues 1362 #label REI
##cross-references EMBL:M67835; NID:g144914; PID:g144915
SUMMARY   #length 362 #molecular-weight 40998 #checksum 3634

Query Match  72.8%; Score 59; DB 2; Length 362;
Best Local Similarity 58.3%; Pred. No. 2.55e-01;
Matches      7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKDNVVEELD 78
      |||:|||||
Qy 2  YNKKKATVOELD 13

RESULT 4
ENTRY   ENSAB6      #type complete
TITLE   enterotoxin B precursor - Staphylococcus aureus
ORGANISM
#formal_name Staphylococcus aureus
DATE    24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change
11-Sep-1998
ACCESSIONS
REFERENCE S27360; A92065; S27240; A01815
#authors Jones, C.L.; Khan, S.A.
#journal J. Bacteriol. (1986) 166:29-33
#title Nucleotide sequence of the enterotoxin B gene from
Staphylococcus aureus.
#cross-references MUID:86168029
#accession S27360
#molecule_type DNA
##residues 1-266 #label JON
##cross-references EMBL:M1118; NID:g152999; PID:g153000
REFERENCE
#experimental_source strain S6
A92065
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3518-3525
#title The primary structure of staphylococcal enterotoxin B. III.
The cyanogen bromide peptides of reduced and aminoethylated
enterotoxin B, and the complete amino acid sequence.
#cross-references MUID:71007902
#accession A92065
#molecule_type protein
#residues 28-55; 'NND', 59-68; 'NE', 71; 'FDIIV', 78-117; 119-127; 'N',
129; 'D', 131-132; 'ENT', 136-148; 'GN', 151-156; 'Y',
157-184; 'ED', 187-232; 'N', 234-245; 'ND', 248-266 #label
HDA
##experimental_source strain S-6
A92064
```

```
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3511-3517
#title The primary structure of staphylococcal enterotoxin B. II.
Isolation, composition, and sequence of chymotryptic
peptides.
#cross-references MUID:71007901
#contents annotation: chymotryptic peptides
REFERENCE A92063
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3493-3510
#title The primary structure of staphylococcal enterotoxin B. I.
Isolation, composition, and sequence of tryptic peptides
from oxidized entero-toxin B.
#cross-references MUID:71007900
#contents annotation: tryptic peptides
REFERENCE A90548
#authors Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
Dunnery, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin B.
#cross-references MUID:66035792
#contents annotation: biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinsky, E.Y.; Kolesov, M.I.; Maurer-Fogy, I.;
Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of
staphylococcal enterotoxin B.
#accession S27240
#molecule_type protein
##residues 28-42;128-148 #label ALA
#superfamily enterotoxin B
#domain signal sequence #status predicted #label SIG\
#product enterotoxin B #status experimental #label MAT\
#disulfide_bonds #status experimental
SUMMARY   #length 266 #molecular-weight 31436 #checksum 4249

Query Match  71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 4.14e-01;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 178 NKKKATVOELD 188
      |||||:|||||
Qy 3  NKKKATVOELD 13

RESULT 5
ENTRY   A33953      #type complete
TITLE   enterotoxin D precursor - Staphylococcus aureus
ORGANISM
#formal_name staphylococcus aureus
DATE    09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
09-Sep-1997
ACCESSIONS
REFERENCE A33953
#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of the gene encoding
staphylococcal enterotoxin D.
#cross-references MUID:89359112
#accession A33953
#status preliminary
#molecule_type DNA
##residues 1-258 #label BAY
##cross-references GB:M8521; NID:g1492109; PID:g758691
SUMMARY   #length 258 #molecular-weight 29746 #checksum 39

Query Match  70.4%; Score 57; DB 2; Length 258;
Best Local Similarity 72.7%; Pred. No. 6.68e-01;
Matches      8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

Db 171 DKKATVOELD 181
:|:|:|
QY 3 NKKKATVOELD 13

RESULT 6
ENTRY A28179 #type complete
TITLE enterotoxin E precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Sep-1997

ACCESSIONS
REFERENCE A28179
#authors Couch, J.L.; Solitis, M.T.; Betley, M.J.
#journal J. Bacteriol. (1988) 170:2954-2960
#title Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
#cross-references MVID:88257005
#accession A28179
#molecule_type DNA
##residues 1-257 #label COU
#cross-references GB:M21319; NID:g153001; PID:g153002
SUMMARY #length 257 #molecular_weight 29358 #checksum 2562

Query Match 65.4%: Score 53; DB 2; Length 257;
Best Local Similarity 72.7%: Pred. No. 4.30e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 170 SKKEVTVOELD 180
:|:|:|
QY 3 NKKKATVOELD 13

RESULT 7
ENTRY A40692 #type complete
TITLE signal recognition particle 72k chain - dog
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997

ACCESSIONS
REFERENCE A40692
#authors Lutcke, H.; Prehn, S.; Ashford, A.J.; Remus, M.; Frank, R.; Dobberstein, B.
#journal J. Cell Biol. (1993) 121:977-985
#title Assembly of the 68- and 72-kD proteins of signal recognition particle with 7S RNA.
#cross-references MVID:93273803
#accession A40692
##status preliminary
#molecule_type mRNA; protein
##residues 1-671 #label LUT
#cross-references EMBL:X67813; NID:g297767; PID:g297768
#note Sequence extracted from NCBI backbone (NCBIP:132901)
SUMMARY #length 671 #molecular_weight 74493 #checksum 6822

Query Match 65.4%: Score 53; DB 2; Length 671;
Best Local Similarity 33.3%: Pred. No. 4.30e+00;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 460 YGRKKAISDLE 471
:|:|:|
QY 2 YNKKATVOELD 13

RESULT 8
ENTRY S51473 #type complete
TITLE probable membrane protein YLR386w - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Nov-1997
ACCESSIONS S51473

REFERENCE S51466
#authors Du, Z.
#submission submitted to the EMBL Data Library, December 1994
#description The sequence of S. cerevisiae cosmid L3502.
#accession S51473
#molecule_type DNA
##residues 1-880 #label DUZ
#cross-references EMBL:U19104; NID:g609423; PID:g609424; MIPS:YLR386w

GENETICS
#map_position 12R
KEYWORDS transmembrane protein
FEATURES
FEATURE 426-442 #domain transmembrane #status predicted #label TMM
SUMMARY #length 880 #molecular_weight 99771 #checksum 5546

Query Match 65.4%: Score 53; DB 2; Length 880;
Best Local Similarity 50.0%: Pred. No. 4.30e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 14 YEKRAALELE 25
:|:|:|
QY 2 YNKKATVOELD 13

RESULT 9
ENTRY I54383 #type complete
TITLE gene SBI.8/DXS423E protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 28-Feb-1997

ACCESSIONS
REFERENCE I54383
#authors Rocques, P.J.; Clark, J.; Ball, S.; Crew, J.; Gill, S.; Christodoulou, Z.; Borts, R.H.; Louis, E.J.; Davies, K.E.; Cooper, C.S.
#journal Hum. Mol. Genet. (1995) 4:243-249
#title The human SBI.8 gene (DXS423E) encodes a putative chromosome segregation protein conserved in lower eukaryotes and prokaryotes.
#cross-references MVID:952676737
#accession I54383
##status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues 1-1233 #label RES
#cross-references GB:S78271; NID:g999379; PID:g999380

GENETICS
SUMMARY SBI.8/DXS423E
#gene #length 1233 #molecular_weight 143204 #checksum 7067

Query Match 65.4%: Score 53; DB 2; Length 1233;
Best Local Similarity 41.7%: Pred. No. 4.30e+00;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKRRKGMDELE 337
:|:|:|
QY 2 YNKKATVOELD 13

RESULT 10
ENTRY B69767 #type complete
TITLE conserved hypothetical protein yzcC - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998

ACCESSIONS
REFERENCE B69767
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertello, M.G.; Bessières, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brigandt, S.C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denzot, F.; Devine, K.M.; Duesterhoeft, A.;

Enllich, S.D.; Emerson, P.T.; Entian, K.D.; Erlington, J.;
Fabre, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Funo, S.; Galizzi, A.; Gallenon, N.; Gilm,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Giseppl, G.; Guy, B.J.; Haga, K.; Halseh, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinis, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Mauel, C.; Medigue, C.; Medina, M.; Mellado, R.P.; Mizuno,
M.; Moesli, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Prescan, E.; Puig, P.; Purnelle, B.; Rapoport, G.;
Ray, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanton, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Seliguchi, J.;
Sekowska, A.; Seror, S.J.; Serrito, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Tepstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.;
Wambutt, R.; Wedler, E.; Wedler, H.; Weitzengger, T.;
Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.;
Yoshikawa, H.; Danchin, A.
Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
#journal 12
#title Nature (1997) 390:249-256
#cross-references MUID:98044033
#accession B69767
#status preliminary: nucleic acid sequence not shown:
translation not shown
##molecule_type DNA
##residues 1-127 ##label KUN
##cross-references GB:299105; GB:AL009126; NID:q2632457; PID:e1182223;
##experimental_source strain 168
GENETICS
#gene yzc
SUMMARY #length 127 #molecular-weight 13950 #checksum 9937
Query Match 64.2%; Score 52; DB 2; Length 127;
Best Local Similarity 45.3%; Pred. No. 6.76e+00;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 107 FTKKQTVHDM 117
: ||| |||:
QY 2 YNKKATVOEL 12
RESULT 11
ENTRY 549746 #type complete
TITLE probable mbtype protein YML033w - yeast (Saccharomyces
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change
21-Nov-1997
ACCESSIONS 549746
REFERENCE 549741
#author Baddock, K.; Churcher, C.
#submission submitted to the EMBL Data Library, November 1994
#accession 549746
##molecule_type DNA
##residues 1-146 ##label BAD
##cross-references EMBL:246659; NID:g575680; PID:g575686; MIPS:YML033w
GENETICS
#feature position 13L
KEYWORDS transmembrane protein
FEATURE
19-35 #domain transmembrane #status predicted #label TMM

SUMMARY #length 146 #molecular-weight 17729 #checksum 5607
Query Match 64.2%; Score 52; DB 2; Length 146;
Best Local Similarity 54.5%; Pred. No. 6.76e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 40 YNKKATVOEL 50
: ||| |||:
QY 2 YNKKATVOEL 12
RESULT 12
ENTRY 518786 #type fragment
TITLE exotoxin type A precursor (allele 2) - Streptococcus pyogenes
#fragment
#formal_name Streptococcus pyogenes phage
strain MGA5250 isolate California; strain MGA5251 isolate
California; strain MGA5256 isolate California; strain
MGA5285 isolate Colorado; strain MGA5480 isolate
Yugoslavia; strain MGA5492 isolate United Kingdom; strain
MGA5496 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
ACCESSIONS 518786; 518787; 518788; 518790; 518792; 518795; 518799
REFERENCE 518782
#author Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the spe gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession 518786
#status nucleic acid sequence not shown: translation not shown
##molecule_type DNA
##residues 1-236 ##label NE1
##cross-references EMBL:X61561; NID:q47297; PID:q47298
##experimental_source strain MGA5250 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518787
#status nucleic acid sequence not shown: translation not shown
##molecule_type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61562; NID:q47299; PID:q47300
##experimental_source strain MGA5251 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518788
#status nucleic acid sequence not shown: translation not shown
##molecule_type DNA
##residues 1-236 ##label NEZ
##cross-references EMBL:X61563; NID:q47301; PID:q47302
##experimental_source strain MGA5256 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518790
#status nucleic acid sequence not shown: translation not shown
##molecule_type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61564; NID:q47305; PID:q47306
##experimental_source strain MGA5285 isolate Colorado unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession 518792
#status nucleic acid sequence not shown: translation not shown
##molecule_type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61565; NID:q47311; PID:q47312
##experimental_source strain MGA5480 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18795
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61566; NID:947317; PID:947318
##experimental_source strain MGAS492 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18799
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NES
##cross-references EMBL:X61567; NID:947325; PID:947326
##experimental_source strain MGAS496 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene SPEA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22 #domain signal sequence (fragment) #status predicted
#label SIG
#product exotoxin type A (fragment) #status predicted
#label MAT

SUMMARY
#length 236 #checksum 1685

Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATVOELD 168
111:11111
QY 3 NKKKATVOELD 13

RESULT 13
ENTRY S18783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS624 isolate Germany; strain MGAS495 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998
S18783; S18793; S18794; S18801; S18798
S18782
Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. (1991) 174:1271-1274
#journal Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M01D:92044323
#accession S18783
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEL
##cross-references EMBL:X61568; NID:947289; PID:947290
##experimental_source strain MGAS158 isolate Nebraska unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18793
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61569; NID:947313; PID:947314
##experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18794
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NE2
##cross-references EMBL:X61570; NID:947315; PID:947316
##experimental_source strain MGAS491 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18801
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEV
##cross-references EMBL:X61571; NID:947323; PID:947324
##experimental_source strain MGAS624 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene SPEA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22 #domain signal sequence (fragment) #status predicted
#label SIG
#product exotoxin type A (fragment) #status predicted
#label MAT

SUMMARY
#length 236 #checksum 512

Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATVOELD 168
111:11111
QY 3 NKKKATVOELD 13

RESULT 14
ENTRY S29659 #type complete
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes (fragment)
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change 25-Mar-1998
S29659; S18782; S18784; S18785; S18791; S18796; S18797;
S18800
S29659
#accession S29659
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references M01D:86166804
#accession S29659
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-251 ##label WEE
##cross-references GB:040453; EMBL:M19350; NID:91877426; PID:91877430
S18782
Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. (1991) 174:1271-1274
#journal Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M01D:92044323

```

#accession S18782
#status .
#molecule_type DNA
#residues 9-244 ##label NEF
##cross-references EMBL:X61560; NID:947287; PID:947288
##experimental_source Streptococcus pyogenes strain MGAS156 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18784
#status
#molecule_type DNA
#residues 9-244 ##label NEA
##cross-references EMBL:X61556; NID:947291; PID:947292
##experimental_source Streptococcus pyogenes strain MGAS165 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18785
#status
#molecule_type DNA
#residues 9-244 ##label NEZ
##cross-references EMBL:X61559; NID:947293; PID:947294
##experimental_source Streptococcus pyogenes strain MGAS167 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18791
#status
#molecule_type DNA
#residues 9-244 ##label NEY
##cross-references EMBL:X61555; NID:947309; PID:947310
##experimental_source Streptococcus pyogenes strain MGAS327 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18796
#status
#molecule_type DNA
#residues 9-244 ##label NFO
##cross-references EMBL:X61557; NID:947319; PID:947320
##experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18797
#status
#molecule_type DNA
#residues 9-244 ##label NEH
##cross-references EMBL:X61558; NID:947321; PID:947322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18800
#status
#molecule_type DNA
#residues 9-228 ##label NFS
##cross-references EMBL:X61554; NID:947327; PID:947328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
Zealand unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

GENETICS
#gene speA
#classification #superfamily enterotoxin B
#keywords exotoxin
#feature
1-30 #domain signal sequence #status predicted #label SIG\
31-251 #product exotoxin type A #status predicted #label MAT
SUMMARY #length 251 #molecular-weight 29246 #checksum 1475

Query Match 64.2%; Score 52; DB 2; Length 251;

```

```

Best Local Similarity 72.7%; Pred. No. 6.76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 166 NKKKATVOELD 176
Qy 3 NKKKATVOELD 13

RESULT 15
ENTRY S58590 #type complete
TITLE ribosomal protein S3 - maize chloroplast
ORGANISM #formal_name chloroplast Zea mays #common_name maize
DATE 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change
17-Mar-1999
ACCESSIONS S58590
REFERENCE S58531
#authors Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
#journal J. Mol. Biol. (1995) 251:614-628
#title Complete sequence of the maize chloroplast genome: gene
content, hotspots of divergence and fine tuning of genetic
information by transcript editing.

#cross-references M01D:95395841
#accession S58590
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-224 ##label MAI
##cross-references EMBL:X86563; NID:9902200; PID:9902260
#note the nucleotide sequence was submitted to the EMBL Data
Library, April 1995

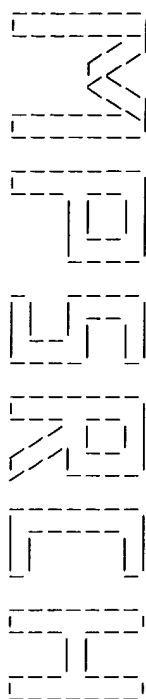
GENETICS
#gene rps3
#classification #superfamily Escherichia coli ribosomal protein S3
#keywords chloroplast; protein biosynthesis; ribosome
SUMMARY #length 224 #molecular-weight 25916 #checksum 3426

Query Match 63.0%; Score 51; DB 2; Length 224;
Best Local Similarity 50.0%; Pred. No. 1.05e+01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKKGAIEELE 102
Qy 4 KKKATVOELD 13

Search completed: Tue Aug 31 19:17:59 1999
Job time : 20 secs.

```


 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

 Msearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Aug 31 19:16:21 1999: Maspar time 2.54 Seconds
 144.646 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-150-947-6
 Description: (1-13) from US09150947.pep
 Perfect Score: 81
 Sequence: 1 XYNNKKATVQELD 13

Scoring table:
 PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 24.929; Variance 27.412; scale 0.909

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|------------|------------------------|-----------|
| 1 | 59 | 72.8 | 257 | 1 | ETXA_STAAU | ENTEROTOXIN TYPE A PRE | 4.80e+02 |
| 2 | 58 | 71.6 | 266 | 1 | ETXB_STAAU | ENTEROTOXIN TYPE B PRE | 8.32e+02 |
| 3 | 57 | 70.4 | 258 | 1 | ETXD_STAAU | ENTEROTOXIN TYPE D PRE | 1.43e+01 |
| 4 | 53 | 65.4 | 257 | 1 | ETXE_STAAU | ENTEROTOXIN TYPE E PRE | 1.18e+00 |
| 5 | 53 | 65.4 | 670 | 1 | SR72_CANFA | SIGNAL RECOGNITION PAR | 1.18e+00 |
| 6 | 52 | 64.2 | 146 | 1 | YMD3_YEAST | HYPOTHETICAL 17.7 KD P | 1.97e+00 |
| 7 | 52 | 64.2 | 251 | 1 | SPEA_STAPY | EXOTOXIN TYPE A PRECUR | 1.97e+00 |
| 8 | 51 | 63.0 | 187 | 1 | YCFL_CYAPA | HYPOTHETICAL 21.2 KD P | 3.26e+00 |
| 9 | 51 | 63.0 | 224 | 1 | RR3_MAIZE | CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 10 | 51 | 63.0 | 239 | 1 | RR3_ORYSA | CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 11 | 51 | 63.0 | 412 | 1 | PT56_YEAST | RIBOSE METHYLTRANSFERA | 3.26e+00 |
| 12 | 51 | 63.0 | 566 | 1 | LIGA_MOUSE | LIGATIN (FRAGMENT). | 3.26e+00 |
| 13 | 51 | 63.0 | 3418 | 1 | BRC2_HUMAN | BREAST CANCER TYPE 2 S | 3.26e+00 |
| 14 | 50 | 61.7 | 268 | 1 | NO20_MEDTR | EARLY NODULIN 20 PRECU | 5.36e+00 |
| 15 | 50 | 61.7 | 274 | 1 | HEL_HAETN | LIPOPROTEIN E PRECURSO | 5.36e+00 |
| 16 | 50 | 61.7 | 386 | 1 | YAMH_SCHPO | HYPOTHETICAL 44.5 KD P | 5.36e+00 |
| 17 | 50 | 61.7 | 1072 | 1 | HSEB_RAT | HEAT-STABLE ENTEROTOXI | 5.36e+00 |
| 18 | 50 | 61.7 | 1223 | 1 | KPB1_HUMAN | PHOSPHORYLASE B KINASE | 5.36e+00 |
| 19 | 50 | 61.7 | 3683 | 1 | DMD_HUMAN | DYSTROPHIN. | 5.36e+00 |
| 20 | 49 | 60.5 | 290 | 1 | YABG_BACSU | HYPOTHETICAL 33.3 KD P | 8.72e+00 |
| 21 | 49 | 60.5 | 455 | 1 | MAD_DROME | MOTHERS AGAINST DPP PR | 8.72e+00 |
| 22 | 49 | 60.5 | 559 | 1 | KIE2_XENLA | KINESIN-LIKE PROTEIN K | 8.72e+00 |
| 23 | 49 | 60.5 | 670 | 1 | SR72_HUMAN | SIGNAL RECOGNITION PAR | 8.72e+00 |

| RESULT | ID | ETXA_STAAU | STANDARD | PRT | 257 AA. | ALIGNMENTS |
|--------|--|-----------------------------------|----------|-----|---------|------------|
| AC | P13163 | | | | | |
| DT | 01-JAN-1990 | (REL. 13, CREATED) | | | | |
| DT | 01-JAN-1990 | (REL. 13, LAST SEQUENCE UPDATE) | | | | |
| DT | 15-JUL-1998 | (REL. 36, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN TYPE A PRECURSOR (SEA). | | | | | |
| GN | ENTA. | | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE. | | | | | |
| OC | STAPHYLOCOCCUS. | | | | | |
| RN | [1] | | | | | |
| RC | SEQUENCE FROM N.A. | | | | | |
| RC | STRAIN-FRI337. | | | | | |
| RX | MEDLINE: 88086892. | | | | | |
| RA | BETLEY M.J., MEKALANOS J.J. | | | | | |
| RT | "Nucleotide sequence of the type A staphylococcal enterotoxin gene." | | | | | |
| RL | J. BACTERIOL. 170:34-41(1988). | | | | | |
| RN | [2] | | | | | |
| RP | SEQUENCE OF 25-257. | | | | | |
| RX | MEDLINE: 87222293. | | | | | |
| RA | HUANG T.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J. | | | | | |
| RT | Complete amino acid sequence of staphylococcal enterotoxin A." | | | | | |
| RL | J. BIOL. CHEM. 262:7006-7013(1987). | | | | | |
| RN | [3] | | | | | |
| RC | X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). | | | | | |
| RX | MEDLINE: 95354648. | | | | | |
| RA | SCHAD E.M., ZAITSEVA I., ZAITSEV V.N., DOHLSTEN M., KALLAND T., SCHLIEVERT P.M., OHLENDORF D.H., SVENSSON L.A. | | | | | |
| RT | "Crystal structure of the superantigen staphylococcal enterotoxin type A." | | | | | |
| RL | EMBO J. 14:3292-3301(1995). | | | | | |
| RN | [4] | | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). | | | | | |
| RX | MEDLINE: 97113025. | | | | | |
| RA | SUNDSTROM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEN M., ABRAMSEN L. | | | | | |
| RT | "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding." | | | | | |
| RL | J. BIOL. CHEM. 271:32212-32216(1996). | | | | | |
| RN | [5] | | | | | |
| RP | 3D-STRUCTURE MODELLING. | | | | | |
| RX | MEDLINE: 96022987. | | | | | |
| RA | SWAMINATHAN S., FUREY W.F., JR., PLETCHER J., SAX M. | | | | | |
| RT | "Residues defining V beta specificity in staphylococcal enterotoxins." | | | | | |

```

RL NAT. STRUCT. BIOL. 2:680-686(1995).
RL [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE: 9734373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. MOL. BIOL. 269:270-280(1997).
CC -1- SUBUNIT: MONOMER.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18970; G153121; -
DR PIR: A28664; A28664.
DR PIR: A29566; A29566.
DR PDB: 1SEF: 11-JUL-96.
DR PDB: 1SEA: 15-OCT-95.
DR PDB: 1SXT: 19-NOV-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph-Strep-toxin; 1.
DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
KW SIGNAL
FT CHAIN 1 24
FT DISULFID 25 257 ENTEROTOXIN A.
FT METAL 120 130 ZINC.
FT METAL 25 25 ZINC.
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 2).
SO SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;

Query Match 72.8%; Score 59; DB 1; Length 257;
Best Local Similarity 81.8%; Pred. No. 4,806-02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 170 NKKMTVOELD 180
OY 3 NKKMTVOELD 13

RESULT 2
ID ETRB STAU STANDARD: PRT: 266 AA.
AC P01552;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN ENTB.
OS STAPHYLOCOCCUS AUREUS.
CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
CC [1]
CC SEQUENCE FROM N.A.
RX MEDLINE: 86168029.
RA JONES C.L., KHAN S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus."
RL J. BACTERIOL. 166:29-33(1986).
RN [2]
RN SEQUENCE OF 40-91 FROM N.A.

RX MEDLINE: 85298255.
RA RANELLI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and staphylococcus aureus."
RL PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985).
RN [3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE: 71007902.
RA HUANG I.-Y., BERGDOLL M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence."
RL J. BIOL. CHEM. 245:3518-3525(1970).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP MEDLINE: 93063291.
RA SHAMIRAVATHAN S., FUREY M.F., JR., PLETCHER J., SAX M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen."
RL NATURE 359:801-806(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE: 94203282.
RA JARDERZKY T.S., BROWN J.H., GORCA J.C., STERN L.J., URBAN R.G.,
RA CHI Y.I., STAUFACHER C., STROMINGER J.L., WILEY D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen."
RL NATURE 368:711-718(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE: 98181012.
RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors."
RL J. MOL. BIOL. 277:61-79(1998).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M1118; G153000; -
DR PIR: A01815; ENSAB6.
DR PIR: S27360; S27360.
DR PDB: 1SEB: 20-JUN-96.
DR PDB: 2SEB: 28-JAN-98.
DR PDB: 3SEB: 27-MAY-98.
DR PDB: 1SE3: 16-JUN-97.
DR PDB: 1SE4: 15-OCT-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph-Strep-toxin; 1.
DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
KW SIGNAL
FT CHAIN 1 27
FT DISULFID 28 266 ENTEROTOXIN B.
FT METAL 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77 DOFLYDLI -> NEFFDYLI (IN REF. 3).
FT CONFLICT 118 118 MISSING (IN REF. 3).
FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
FT CONFLICT 133 135 OTD -> ENT (IN REF. 3).
FT CONFLICT 149 150 NG -> GN (IN REF. 3).
FT CONFLICT 156 156 Y -> YY (IN REF. 3).
FT CONFLICT 185 186 OE -> EQ (IN REF. 3).
FT CONFLICT 233 233 D -> N (IN REF. 3).
FT CONFLICT 246 247 DN -> ND (IN REF. 3).

```


SQ SEQUENCE 266 AA: 31436 MW: E2C09D63 CRC32:

Query Match 71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 8.32e-02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 178 NKKKATVOEID 188
|||||
QY 3 NKKKATVOEID 13

RESULT 3

ID ETXD_STAAU STANDARD: PRT: 258 AA.
AC P20723:
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE D PRECURSOR (SED).
GN ENTD.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN STAPHYLOCOCCUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 89359112.
RA BAYLES K.W., IANDOLO J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D."
RL J. BACTERIOL. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235.
RX MEDLINE: 97157473.
RA DUNSTON M., ABRAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn²⁺-mediated homodimerization."
RL EMBO J. 15:6837-6840(1996).
CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M28521; G758691; -
DR PIR: A33953; A33953.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
DR HSSP: P13163; ISXT.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
FT CHAIN 1 25
FT SIGNAL 1 25
FT CHAIN 26 258
FT METAL 212 212
FT METAL 250 250
FT METAL 252 252
FT VARIANT 114 114
SQ SEQUENCE 258 AA: 29746 MW: 2D1AA120 CRC32:

Query Match 70.4%; Score 57; DB 1; Length 258;

Best Local Similarity 72.7%; Pred. No. 1.43e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 171 DKKNTVOEID 181
|||||

QY 3 NKKKATVOEID 13

RESULT 4

ID ETXE_STAAU STANDARD: PRT: 257 AA.
AC P12993:
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN ENTE.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN STAPHYLOCOCCUS.
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC STRAIN-MJ265;
RX MEDLINE: 88257005.
RA COUCH J.L., SOLTIS M.T., BETLEY M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene."
RL J. BACTERIOL. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELLING.
RX MEDLINE: 96022887.
RA SWAMINATHAN S., FUREY W.F., PLETCHER J., SAX M.;
RT "Residues defining v beta specificity in staphylococcal enterotoxins."
RL NAT. STRUCT. BIOL. 2:680-686(1995).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21319; G153002; -
DR PIR: A28179; A28179.
DR PDB: 1SEE; 15-OCT-95.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT SIGNAL 28 257
FT CHAIN 28 257
SQ SEQUENCE 257 AA: 29358 MW: 88BA67C3 CRC32:

Query Match 65.4%; Score 53; DB 1; Length 257;

Best Local Similarity 72.7%; Pred. No. 1.18e+00;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 170 SKKEVVOEID 180
|||||
QY 3 NKKKATVOEID 13

RESULT 5

ID SR72_CANFA STANDARD: PRT: 670 AA.
AC P33731:
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).
GN SRP72.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.

FT CONFLICT 40 40 H -> Q (IN REF. 2).
 FT CONFLICT 43 43 S -> N (IN REF. 2).
 FT CONFLICT 47 59 NLONTYFEXGDP -> TKITIFFMKAVTL (IN
 REF. 2).
 FT CONFLICT 129 129 I -> L (IN REF. 2).
 FT CONFLICT 165 178 TNKKMTAQLDYK -> QIKNGSGRISYT (IN
 REF. 2).
 FT SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;

Query Match
 Best Local Similarity 72.7%; Score 52; DB 1; Length 251;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 166 NKKMTAQLD 176
 |||:||||
 QY 3 NKKMTAQLD 13

RESULT 8
 ID YCFA.CYAPA STANDARD: PRT; 187 AA.
 AC P48192;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 21.2 KD PROTEIN YCFA.
 GN YCFA.
 OS CYANOPHORA PARADOXA.
 OG CYANELLE.
 OC EUKARYOTA; GLAUCOCYSTOPHYCEAE; CYANOPHORACEAE; CYANOPHORA.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-LB555 / PRINGSHEIM;
 RA STREWALT V.L., MICHALOWSKI C.B., LUFELHARDT W., BOHNERT H.J.,
 BRYANT D.A.;
 RA SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL -1- SIMILARITY: BELONGS TO THE YCFA FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE YCFA FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC
 CC EMBL: U30821; GI016091; -;
 DR MENDEL; 7950; CYAPA:ycfa.1.
 KW CYANELLE; HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 187 AA; 21207 MW; B5D7E756 CRC32;

Query Match
 Best Local Similarity 87.5%; Score 51; DB 1; Length 187;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 97 YNKKKCTV 104
 |||||:||
 QY 2 YNKKKCTV 9

RESULT 9
 ID RR3.MAIZE STANDARD: PRT; 224 AA.
 AC P0586;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
 GN RPS3.
 OS ZEA MAYS (MAIZE).
 OG CHLOROPLAST.
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
 CC POACEAE; ZEA.
 CC [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 87231045.
 RA MCLAUGHIN W.E., LARRINUA I.M.;
 RT "The sequence of the maize plastid encoded rps3 locus."
 RL NUCLEIC ACIDS RES. 15:4689-4689(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95395841.
 RA MAIER R.M., NECKERMANN K., IGLOI G.L., KOESSEL H.;
 RT "Complete sequence of the maize chloroplast genome: gene content,
 hotspots of divergence and fine tuning of genetic information by
 transcript editing."
 RL J. MOL. BIOL. 251:614-628(1995).
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X00340; G12469; -;
 DR EMBL: M31336; G552741; -;
 DR EMBL: X86563; G902260; -;
 DR MAIZEDB: 66303; -;
 DR PROSITE: P500548; RIBOSOMAL_S3; 1.
 DR PFAM: PF00417; S3.C; 1.
 DR PFAM: PF00417; S3.N; 1.
 DR MENDEL; 13473; ZEMA:rps3.1.
 KW RIBOSOMAL PROTEIN; CHLOROPLAST.
 SQ SEQUENCE 224 AA; 25916 MW; 3ED95CFF CRC32;

Query Match
 Best Local Similarity 50.0%; Score 51; DB 1; Length 224;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKKGAIELE 102
 |||||:||
 QY 4 KKKGAIELE 13

RESULT 10
 ID RR3-ORYZA STANDARD: PRT; 239 AA.
 AC P12146;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
 GN RPS3.
 OS ORYZA SATIVA (RICE).
 OG CHLOROPLAST.
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
 CC POACEAE; ORYZA.
 CC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA SUGIURA M.;
 RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP COMPLETE GENOME.
 RX MEDLINE: 89364698.
 RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,
 MORI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-Q.,
 KANO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;
 RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
 intermolecular recombination between distinct trna genes accounts for
 a major plastid DNA inversion during the evolution of the cereals."
 RL MOL. GEN. GENET. 217:185-194(1989).
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X15901; G12025; -
 CC PIR: J0265; R3823; -
 CC PROSITE: P500548; RIBOSOMAL_S3; 1.
 CC PFM: PF00189; S3_C; 1.
 CC PFM: PF00417; S3_N; 1.
 CC MENDEL: 13258; ORFS:RPS3; 1.
 CC RIBOSOMAL PROTEIN; CHLOROPLAST
 CC SEQUENCE 239 AA; 27518 MW; 38E916EE CRC32;

Query Match 63.0%; Score 51; DB 1; Length 239;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 108 KKAIEELE 117
 Y 4 KKAIVQELD 13

RESULT 11
 ID PT56-YEAST STANDARD; PRT; 412 AA.
 AC P25270;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE RIBOSE METHYLTRANSFERASE PET56 (PG 2.1.1.-) (MITOCHONDRIAL LARGE
 DE RIBOSOMAL RNA RIBOSE METHYLASE) (21S RNA [Gm2251] 2'-O-
 DE METHYLTRANSFERASE).
 GN PET56 OR YOR201C.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCCHAROMYCETALES;
 CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94090319.
 RA SIRUM-CONNOLLY K., MASON T.L.;
 RT "Functional requirement of a site-specific ribose methylation in
 RT ribosomal RNA.";
 RL SCIENCE 262:1886-1889(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA HUGHES B., POHL T.M.;
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE OF 1-95 FROM N.A.
 RX MEDLINE; 86093663.
 RA STRUHL K.;
 RT "Nucleotide sequence and transcriptional mapping of the yeast
 RT pet56-his3-decl gene region.";
 RL NUCLEIC ACIDS RES. 13:8587-8601(1985).
 CC -1- FUNCTION: ENCODES AN ESSENTIAL RIBOSE METHYLTRANSFERASE THAT
 CC SPECIFICALLY MODIFIES TO 2'-O-METHYLGUANOSINE A UNIVERSALLY
 CC CONSERVED NUCLEOTIDE, G-2270, IN THE PEPTIDYL TRANSFERASE CENTER
 CC OF THE MITOCHONDRIAL LARGE RIBOSOMAL RNA (21S). THIS MODIFICATION
 CC SEEMS TO BE IMPORTANT FOR THE NORMAL ACCUMULATION OF THIS LATTER
 CC 21S SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: L19947; G431760; -
 DR EMBL: X03245; G37780; -
 DR EMBL: Z75107; E252073; -
 DR PIR: S07682; S07682.
 DR SGD: L0001392; PET156.
 DR PFM: PF00588; SpoU methylase; 1.
 CC MITOCHONDRION; TRANSFERASE; METHYLTRANSFERASE.
 CC SEQUENCE 412 AA; 46387 MW; B3436655 CRC32;

Query Match 63.0%; Score 51; DB 1; Length 412;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 79 YGKKAHVEK 89
 Y 2 YNKKRATVQELD 12

RESULT 12
 ID LIGA-MOUSE STANDARD; PRT; 566 AA.
 AC Q61211;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE LIGATIN (FRAGMENT).
 GN LGTN.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97224508.
 RA MALNAR-DRAGOJEVIC D., TRACHTULEC Z., VINCEK V.;
 RT "Assignment of the mouse ligatin gene (Lgtn) to chromosome 1f by in
 RT situ hybridization.";
 RL GENOMICS 40:192-193(1997).
 CC -1- FUNCTION: TRAFFICKING RECEPTOR FOR PHOSPHOLIPOPROTEINS. LOCALIZES
 CC PROPHOSPHOLIPOPROTEINS WITHIN ENDOSOMES AND AT THE CELL PERIPHERY
 CC WHERE THEY PARTICIPATE IN SPECIFIC METABOLIC PROCESSES AS WELL AS
 CC INTERCELLULAR ADHESION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: U58337; G1377880; -
 CC MGD; MGI:109342; LGTN.
 CC MEMBRANE.
 CC NON_TER 1 1
 FT NON_TER 1 1
 FT SEQUENCE 566 AA; 62239 MW; AAB58F4B CRC32;

Query Match 63.0%; Score 51; DB 1; Length 566;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 503 YNKKVTVRNLDE 514
 Y 2 YNKKRATVQELD 13

RESULT 13
 ID BRG2_HUMAN STANDARD; PRT; 3418 AA.
 AC P51587;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN.


```

FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 268 EARLY NODULIN 20.
FT DOMAIN 23 ? PLASTOCYANIN-LIKE.
FT DOMAIN 136 145 POLY-PRO.
SQ SEQUENCE 268 AA; 28668 MW; 29EAF8F CRC32;

Query Match
Best Local Similarity 41.7%; Score 50; DB 1; Length 268;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 65 YNKTESYHEVE 76
||| :||:
QY 2 YNKKATVQELD 13

```

```

Query Match
Best Local Similarity 70.0%; Score 50; DB 1; Length 274;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 77 KKAADVADLD 86
||||| :||
QY 4 KKAATVQELD 13

```

Search completed: Tue Aug 31 19:16:26 1999
Job time : 5 secs.

```

RESULT 15
ID HEL_HAEIN STANDARD: PRT; 274 AA.
AC P26093;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE LIPOPROTEIN E PRECURSOR (OUTER MEMBRANE PROTEIN P4) (OMP P4).
CN HEL OR OMP P4 OR H10693.
OS HAEMOPHILUS INFLUENZAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURILLACEAE;
OC HAEMOPHILUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 263-274.
KC STRAIN-RD / KW20B;
KA MEDLINE; 91348867.
RA GREEN B.A., FARLEY J.E., QUINN-DEY T., DEICH R.A., ZLOTNICK G.W.;
RT "The e (P4) outer membrane protein of Haemophilus influenzae:
RT biologic activity of anti-e serum and cloning and sequencing of the
RT structural gene";
RL INFECT. IMMUN. 59:3191-3198(1991).
RN [2]
RP SEQUENCE FROM N.A.
KC STRAIN-RD / KW20;
RX MEDLINE; 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
RA UTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEORGESEN N.S.M.,
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL SCIENCE 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
CC ANCHOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M68502; G148896; -
DR EMBL: U32752; G1573696; -
DR PIR: A43604; A43604.
DR TIGR: H10693; -
DR PROSITE: PS00013; PROKAR.LIPOPROTEIN. 1.
KW OUTER MEMBRANE; LIPOPROTEIN; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 274 LIPOPROTEIN E.
FT LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
FT CONFLICT 30 30 G -> E (IN REF. 1).
SQ SEQUENCE 274 AA; 30431 MW; 55289338 CRC32;

```



```

OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
CN SCHIZOSACCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.;
SL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AL022305; E1285407; -.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 460 AA; 52670 MW; 835D7303 CRC32;

Query Match
Best Local Similarity 74.1%; Score 60; DB 3; Length 460;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 105 YKKKKGKIEELN 116
OY 2 YNKKKATVOELD 13

RESULT 3
ID 045833 PRELIMINARY; PRT; 362 AA.
AC 045833;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
GN SPOUTID
OS CLOSTRIDIUM ACETOBUTYLICUM.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
CN CLOSTRIDIUM.
RN [1]
RP SEQUENCE FROM N.A.
RA REDD S.J., HANCOCK K., SANTANGELO J.D., WOODS D.R.;
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M87835; G144915; -.
KW SPOULATION.
SQ SEQUENCE 362 AA; 40998 MW; 75E3556E CRC32;

Query Match
Best Local Similarity 72.8%; Score 59; DB 2; Length 362;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKKDVSVEELD 78
OY 2 YNKKKATVOELD 13

RESULT 4
ID 054971 PRELIMINARY; PRT; 260 AA.
AC 054971;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GN DE SUPERANTIGEN.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CN STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WELLER;
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INECT. IMMUN. 62:1867-1874(1994).
DR EMBL: L29655; G476764; -.
PFAM: PF01123; Strep_Toxin: 1.
KW SUPERANTIGEN.
SQ SEQUENCE 260 AA; 29797 MW; FE391C2B CRC32;

```

```

Query Match
Best Local Similarity 71.6%; Score 58; DB 2; Length 260;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKQVTVQELD 183
OY 3 NKKKATVOELD 13

RESULT 5
ID 054738 PRELIMINARY; PRT; 260 AA.
AC 054738;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GN DE SUPERANTIGEN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CN STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE: 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen ssa allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL INECT. IMMUN. 64:1161-1165(1996).
DR EMBL: U48793; G1245174; -.
PFAM: PF01123; Strep_Toxin: 1.
KW SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match
Best Local Similarity 71.6%; Score 58; DB 2; Length 260;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKQVTVQELD 183
OY 3 NKKKATVOELD 13

RESULT 6
ID 054739 PRELIMINARY; PRT; 260 AA.
AC 054739; 054737;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GN DE SUPERANTIGEN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CN STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE: 96178602.

```


Query Match . 69.1%; Score 56; DB 13; Length 1232;
Best Local Similarity 50.0%; Pred. No. 6.64e-01;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRADMDELE 337
1:1:1:1:1:1:
QY 2 YNKKKATVQELD 13

RESULT 11
ID P87145 PRELIMINARY; PRT; 811 AA.
AC P87145;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE HYPOTHEICAL 92.5 KD PROTEIN C25H2.03 IN CHROMOSOME II.
GN SPSC25H2.03.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9712;
RA DURSO G., LYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,
RA RAJANIREM M.A., CONNOR R.E.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: TO YEAST YLR386W.
DR EMBL: 295397; E316120; -;
KX: HYPOTHEICAL PROTEIN: TRANSMEMBRANE.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT TRANSMEM 362 382 POTENTIAL.
FT TRANSMEM 602 622 POTENTIAL.
FT TRANSMEM 630 650 POTENTIAL.
SQ SEQUENCE 811 AA; 92452 MW; E1E2FB77 CRC32;

Query Match . 67.9%; Score 55; DB 3; Length 811;
Best Local Similarity 58.3%; Pred. No. 1.10e+00;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 14 YDKRKATVELE 25
1:1:1:1:1:1:
QY 2 YNKKKATVQELD 13

RESULT 12
ID 007382 PRELIMINARY; PRT; 490 AA.
AC 007382;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE HISTIDINE KINASE LTKINA.
GN LTKINA.
OS LACTOCOCCUS LACTIS CREMORIS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC LACTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RX MEDLINE; 97316457.
RA O'CONNELL-MOTHERWAY M., FITZGERALD G.F., VAN SINDEREN D.;
RT "Cloning and sequence analysis of putative histidine protein kinases
isolated from Lactococcus lactis MG1363."
RL APPL. ENVIRON. MICROBIOL. 63:2454-2459(1997).
DR EMBL: U81166; G2182835; -;
DR PFAM: PF00512; signal; 1.
SQ SEQUENCE 490 AA; 55884 MW; 05197910 CRC32;

Query Match . 66.7%; Score 54; DB 2; Length 490;
Best Local Similarity 70.0%; Pred. No. 1.80e+00;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 7 FNKKRETVEE 16
1:1:1:1:1:1:
QY 2 YNKKKATVQELD 11

RESULT 13
ID 073696 PRELIMINARY; PRT; 1233 AA.
AC 073696;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE MITOSIS-SPECIFIC CHROMOSOME SEGREGATION PROTEIN SMC1 HOMOLOG.
GN SMC1.
OS FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
OC TETRAODONTIFORMES; TETRAODONTIOIDEI; TETRAODONTIDAE; FUGU.
RN [1]
RP SEQUENCE FROM N.A.
RA RIBOLDI TUNNICLIFFE G.R., PLATZER M., NYAKATURA G., ELGAR G.S.,
RA BRENNER S., ROSENTHAL A.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF026198; G3098266; -;
SQ SEQUENCE 1233 AA; 143100 MW; FBD2F859 CRC32;

Query Match . 66.7%; Score 54; DB 13; Length 1233;
Best Local Similarity 50.0%; Pred. No. 1.80e+00;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRADMDELD 337
1:1:1:1:1:1:
QY 2 YNKKKATVQELD 13

RESULT 14
ID 053585 PRELIMINARY; PRT; 241 AA.
AC 053585;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE ENTEROTOXIN H PRECURSOR.
GN SER.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D4508;
RA REN K., BANNAN J.D., PANCHOLI V., CHEUNG A.L., ROBBINS J.C.,
RA FISCHETTI V.A., ZABRISKIE J.B.;
RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U11702; G510692; -;
DR PFAM: PF01123; Staph_toxin; 1.
KW SIGNAL.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 241 ENTEROTOXIN H.
SQ SEQUENCE 241 AA; 27858 MW; AEA5A04A CRC32;

Query Match . 65.4%; Score 53; DB 2; Length 241;
Best Local Similarity 72.7%; Pred. No. 2.94e+00;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 153 NKKNVLOELD 163
1:1:1:1:1:1:
QY 3 NKKKATVQELD 13

RESULT 15
ID 065075 PRELIMINARY; PRT; 271 AA.
AC 065075;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 30.9 KD PROTEIN (FRAGMENT).
GN SB50.
OS PICEA MARIANA.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC PICEA.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.,
RL GENERICS 0:0-0(1998).
DR EMBL; AF051236; G2982303; -.
KM HYPOTHETICAL PROTEIN.
FT NON_TER 1
SQ SEQUENCE 271 AA; 30897 MW; 1DEA85B1 CRC32;

Query Match 65.4%; Score 53; DB 10; Length 271;
Best Local Similarity 54.5%; Pred. No. 2.94e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 115 YSKTKAVEDL 125
QY 2 YNKKKATVQEL 12

Search completed: Tue Aug 31 19:17:22 1999
Job time : 38 secs.

THIS PAGE BLANK (USPTO)


```

Oy      1 YNKKKATVQELDYNNKKKATVQELD 24
      |||||||
RESULT  2
ID      W64643 standard; peptide; 35 AA.
AC      W64643:
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide trimer.
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW      toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW      therapeutic; vaccine; food poisoning.
OS      Synthetic.
OS      staphylococcus aureus.
PN      WO9829444-A1.
PD      09-JUL-1998.
PF      30-DEC-1997; IL0438.
PR      30-DEC-1996; IL-119938.
PS      (YISS ) YISSUM RES & DEV CO.
PT      WPI: 98-388042/33.
DR      WPI: 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT      antagonising toxin-mediated activation of T cells and prevention or
PS      treatment of toxic shock caused by exotoxin(s)
PR      Claim 19: Page 41: 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
CC      fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC      capable of eliciting protective immunity against toxic shock induced by
CC      PET or by a mixture of PETs. Such peptides are also capable of
CC      antagonising toxin-mediated activation of T-cells, inhibiting expression
CC      of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC      TNF-beta genes. The peptides may be used to prepare therapeutics or
CC      vaccines for the treatment of prophylaxis of toxin-mediated activation
CC      of T cells and eliciting protective immunity against toxic shock induced
CC      by PETs. They can also be used for the treatment of harmful effects
CC      (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC      the peptides can also be used for alleviating toxic shock induced by PET.
SQ      Sequence 35 AA.

Query Match      100.0%; Score 162; DB 34; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.70e-08;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 ynkktatvgeldynkkktatvgeld 24
Oy      1 YNKKKATVQELDYNNKKKATVQELD 24
      |||||||
RESULT  3
ID      W64637 standard; peptide; 12 AA.
AC      W64637:
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide p12(151-161).
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW      toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW      therapeutic; vaccine; food poisoning.
OS      Synthetic.
OS      staphylococcus aureus.
PN      WO9829444-A1.
PD      09-JUL-1998.
PF      30-DEC-1997; IL0438.
PR      30-DEC-1996; IL-119938.
PS      (YISS ) YISSUM RES & DEV CO.
PT      WPI: 98-388042/33.
DR      WPI: 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT      antagonising toxin-mediated activation of T cells and prevention or
PS      treatment of toxic shock caused by exotoxin(s)
PR      Claim 8; Page 41: 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
CC      fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC      capable of eliciting protective immunity against toxic shock induced by
CC      PET or by a mixture of PETs. Such peptides are also capable of
```

```

CC      antagonising toxin-mediated activation of T-cells, inhibiting expression
CC      of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC      TNF-beta genes. The peptides may be used to prepare therapeutics or
CC      vaccines for the treatment of prophylaxis of toxin-mediated activation
CC      of T cells and eliciting protective immunity against toxic shock induced
CC      by PETs. They can also be used for the treatment of harmful effects
CC      (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC      the peptides can also be used for alleviating toxic shock induced by PET.
SQ      Sequence 12 AA;

Query Match      50.0%; Score 81; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.34e+00;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 ynkktatvgeld 12
Oy      1 YNKKKATVQELD 12
      |||||||
RESULT  4
ID      W64641 standard; peptide; 13 AA.
AC      W64641:
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide p12C(150-161).
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW      toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW      therapeutic; vaccine; food poisoning.
OS      Synthetic.
OS      staphylococcus aureus.
FH      Key
FT      Modified_site 1 Location/Qualifiers
FT      /note="N-terminal Tyr modified by presence of
FT      N-lauryl-cysteyl"
PN      WO9829444-A1.
PD      09-JUL-1998.
PF      30-DEC-1997; IL0438.
PR      30-DEC-1996; IL-119938.
PS      (YISS ) YISSUM RES & DEV CO.
PT      WPI: 98-388042/33.
DR      WPI: 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT      antagonising toxin-mediated activation of T cells and prevention or
PS      treatment of toxic shock caused by exotoxin(s)
PR      Claim 16; Page 41: 68pp; English.
CC      W64636-W64657 are peptides homologous to the amino acid sequence of a
CC      fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC      capable of eliciting protective immunity against toxic shock induced by
CC      PET or by a mixture of PETs. Such peptides are also capable of
CC      antagonising toxin-mediated activation of T-cells, inhibiting expression
CC      of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC      TNF-beta genes. The peptides may be used to prepare therapeutics or
CC      vaccines for the treatment of prophylaxis of toxin-mediated activation
CC      of T cells and eliciting protective immunity against toxic shock induced
CC      by PETs. They can also be used for the treatment of harmful effects
CC      (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC      the peptides can also be used for alleviating toxic shock induced by PET.
SQ      Sequence 13 AA;

Query Match      50.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.34e+00;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 ynkktatvgeld 13
Oy      1 YNKKKATVQELD 12
      |||||||
RESULT  5
ID      W64646 standard; peptide; 13 AA.
AC      W64646:
DT      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide Ac-p12(150-161).
KW      Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
```

KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 OS Staphylococcus aureus.
 FH Modified_site 1 Location/Qualifiers
 FT Key
 FT MISC_difference 14 /note= "N-terminal Tyr modified by N-acetyl group"
 FT /note= "D-form residue"
 PN WO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R.
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 24; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced
 CC by PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 13 AA;
 Query Match 50.0%; Score 81; DB 34; Length 13;
 Best Local Similarity 100.0%; Pred. NO. 1.34e+00;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ynkktatvgeld 12
 1 YNKKKATVQELD 12
 QY
 RESULT 6
 ID W64645 standard; peptide: 14 AA.
 AC W64645;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide D-Ala.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 OS Staphylococcus aureus.
 FH Key
 FH MISC_difference 1 Location/Qualifiers
 FT MISC_difference 14 /note= "D-form residue"
 FT /note= "D-form residue"
 FT MISC_difference 14 /note= "D-form residue"
 PN WO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R.
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 23; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced
 CC by PERT or by a mixture of PERTs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 14 AA;
 Query Match 50.0%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. NO. 1.34e+00;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 ynkktatvgeld 13
 1 YNKKKATVQELD 12
 QY
 RESULT 7
 ID W64644 standard; peptide: 14 AA.
 AC W64644;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide Cys-p12(150-161).
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 OS Staphylococcus aureus.
 FH Key
 FH MISC_difference 14 /note= "D-form residue"
 FT MISC_difference 14 /note= "D-form residue"
 FT /note= "D-form residue"
 PN WO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R.
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 21; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced
 CC by PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 14 AA;
 Query Match 50.0%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. NO. 1.34e+00;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 ynkktatvgeld 13
 1 YNKKKATVQELD 12
 QY
 RESULT 8
 ID W72426 standard; peptide: 36 AA.
 AC W72426;
 DT 22-DEC-1998 (first entry)
 DE Peptide #5 for reducing symptoms of toxic shock syndrome.
 KM Toxic shock syndrome; immunogenic response; bacterial infection;
 KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 OS Synthetic.
 OS Staphylococcus sp.

US Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and streptococcal toxins - used to diagnose, treat or prevent toxic shock and autoimmune diseases
PS Claim 4: Page 54: 69pp; English.
CC The present invention describes peptides having consensus sequences #1 or #2, optionally as part of a larger molecule of size at least 6-8 kd.
CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X4X5N #1, X6X7X8X9X10X11X12X13DX14X15X16RX17X18X21X20X21X22X23X24Y #2, where X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa) or are absent; X27 = L or Y; all other X may be any aa. The peptides can be used to generate serum antibodies (Ab) that bind at least one staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab are used: (i) for diagnostic detection of SPSA or SEA, SEB and SED, in usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear cells in presence of these toxins (i.e. to protect against or alleviate toxic shock or autoimmune disease associated with bacterial infections); and (iii) for passive immunisation against effects of the toxins. The peptides generate Ab that are cross-reactive with toxins from a variety of bacteria. The present sequence represents a specifically claimed example of a peptide of the present invention.
SQ Sequence 36 AA;

Query Match 50.0%; Score 81; DB 36; Length 36;
Best Local Similarity 57.1%; Pred. No. 1.34e+00;

Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 12 nkknvtvgelgykirkylvdn 32
|||:|||||:|:|:|:
QY 2 NKKKATVOELDYNKKKATVOE 22

RESULT 9
ID W72427 standard; peptide: 38 AA.

AC W72427:
DT 22-DEC-1998 (first entry)
DE Peptide #6 for reducing symptoms of toxic shock syndrome.
KW Toxic shock syndrome; immunogenic response; bacterial infection;
KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KW autoimmune disease.
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and streptococcal toxins - used to diagnose, treat or prevent toxic shock and autoimmune diseases
PS Claim 4: Page 54: 69pp; English.
CC The present invention describes peptides having consensus sequences #1 or #2, optionally as part of a larger molecule of size at least 6-8 kd.
CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X4X5N #1, X6X7X8X9X10X11X12X13DX14X15X16RX17X18X21X20X21X22X23X24Y #2, where X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa) or are absent; X27 = L or Y; all other X may be any aa. The peptides can be used to generate serum antibodies (Ab) that bind at least one staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab are used: (i) for diagnostic detection of SPSA or SEA, SEB and SED, in usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear cells in presence of these toxins (i.e. to protect against or alleviate toxic shock or autoimmune disease associated with bacterial infections);

CC and (iii) for passive immunisation against effects of the toxins. The peptides generate Ab that are cross-reactive with toxins from a variety of bacteria. The present sequence represents a specifically claimed example of a peptide of the present invention.
SQ Sequence 38 AA;

Query Match 50.0%; Score 81; DB 36; Length 38;
Best Local Similarity 57.1%; Pred. No. 1.34e+00;
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 12 nkknvtvgelgykirkylvdn 32
|||:|||||:|:|:|:
QY 2 NKKKATVOELDYNKKKATVOE 22

RESULT 10
ID W72423 standard; peptide: 24 AA.

AC W72423:
DT 22-DEC-1998 (first entry)
DE Peptide #2 for reducing symptoms of toxic shock syndrome.
KW Toxic shock syndrome; immunogenic response; bacterial infection;
KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KW autoimmune disease.
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and streptococcal toxins - used to diagnose, treat or prevent toxic shock and autoimmune diseases
PS Claim 4: Page 54: 69pp; English.
CC The present invention describes peptides having consensus sequences #1 or #2, optionally as part of a larger molecule of size at least 6-8 kd.
CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X4X5N #1, X6X7X8X9X10X11X12X13DX14X15X16RX17X18X21X20X21X22X23X24Y #2, where X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa) or are absent; X27 = L or Y; all other X may be any aa. The peptides can be used to generate serum antibodies (Ab) that bind at least one staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab are used: (i) for diagnostic detection of SPSA or SEA, SEB and SED, in usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear cells in presence of these toxins (i.e. to protect against or alleviate toxic shock or autoimmune disease associated with bacterial infections); and (iii) for passive immunisation against effects of the toxins. The peptides generate Ab that are cross-reactive with toxins from a variety of bacteria. The present sequence represents a specifically claimed example of a peptide of the present invention.
SQ Sequence 24 AA;

Query Match 46.9%; Score 76; DB 36; Length 24;
Best Local Similarity 55.0%; Pred. No. 3.82e+00;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 knkvvtvgelgykirkylvdn 20
||:|||||:|:|:|:
QY 3 KKKATVOELDYNKKKATVOE 22

RESULT 11
ID W72425 standard; peptide: 28 AA.

AC W72425:
DT 22-DEC-1998 (first entry)
DE Peptide #4 for reducing symptoms of toxic shock syndrome.
KW Toxic shock syndrome; immunogenic response; bacterial infection;
KM staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KW autoimmune disease.
OS Synthetic.

OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09645325-A1.
 PD 15-OCT-1998.
 PR 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UNIRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriekie JB;
 DR WPI: 96-568335/48.
 PT New peptides that generate antibodies against staphylococcal and streptococcal toxins - used to diagnose, treat or prevent toxic shock and autoimmune diseases
 PS Claim 4: Page 54: 69pp: English.
 CC The present invention describes peptides having consensus sequences #1 or #2, optionally as part of a larger molecule of size at least 6-8 kD. Where consensus sequence #1 and #2 are: X25X26VGXITX3X4X5N #1, CC KX6X78X9X10X11X12X13DX14X15X16RX17X18X20X21X22X23X24Y #2, where X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa) or are absent; X27 = L or Y; all other X may be any aa. The peptides can be used to generate serum antibodies (Ab) that bind at least one staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear cells in presence of these toxins (i.e. to protect against or alleviate toxic shock or autoimmune disease associated with bacterial infections); and (iii) for passive immunisation against effects of the toxins. The peptides generate Ab that are cross-reactive with toxins from a variety of bacteria. The present sequence represents a specifically claimed example of a peptide of the present invention.
 SQ Sequence 28 AA:

Query Match 46.9%; Score 76; DB 36; Length 28;
 Best Local Similarity 55.0%; Pred. No. 3.82e+00;
 Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 3 kknvtgelykirkylvgn 22
 11: |||||: :|||:
 QY 3 NKKATVQELDYNNKKTVOE 22

RESULT 12
 ID R45017 standard; protein: 221 AA.
 AC R45017:
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SPE A.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; perfusion system.
 OS Staphylococcus aureus.
 PN W09324136-A.
 PD 09-DEC-1993.
 PR 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/30.
 PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune diseases
 PS Disclosure: Fig 1: 90pp: English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs) which may be used in the methods of the invention for treating cancer in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administered by i.v. injection.
 CC Sequence 221 AA:

Query Match 44.4%; Score 72; DB 8; Length 221;
 Best Local Similarity 62.5%; Pred. No. 8.74e+00;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 136 nkkmwtageidykvrk 151
 11: | |||||: :|
 QY 2 NKKATVQELDYNNKRR 17

RESULT 13
 ID R13209 standard; protein: 221 AA.
 AC R13209:
 DT 15-OCT-1991 (first entry)
 DE Streptococcal pyrogenic enterotoxin A.
 KW SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 OS Streptococcus Nr-5 strain.
 PN W09110680-A.
 PD 23-JUL-1991.
 PR 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus - administered by IV injection, having same tumouricidal activity as staphylococcal protein A without potential toxic reactions
 PS Disclosure: Fig 1: 74pp: English.
 CC SPE A can be used for tumouricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to Streptococcal pyrogenic exotoxins are claimed, provided the homology includes CC residues and similar hydropathy profiles.
 CC See R13203-R13211.
 SQ Sequence 221 AA:

Query Match 44.4%; Score 72; DB 3; Length 221;
 Best Local Similarity 62.5%; Pred. No. 8.74e+00;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 136 nkkmwtageidykvrk 151
 11: | |||||: :|
 QY 2 NKKATVQELDYNNKRR 17

RESULT 14
 ID W12145 standard; protein: 250 AA.
 AC W12145:
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes streptococcal toxin A mutant delta98.
 KW Streptococcal toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 FH Key
 FT peptide 1..30 location/Qualifiers
 FT peptide /label= sig_peptide
 FT peptide 31..250 /label= mat_peptide
 PN W09640930-A1.
 PD 19-DEC-1996.
 PR 07-JUN-1996; U10252.
 PR 07-JUN-1995; US-480261.
 PA (MINU) UNIV MINNESOTA.
 PA Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR WPI: 97-099936/09.
 PT Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Claim 5: Page -: 102pp: English.
 CC The present sequence is a non-lethal Streptococcus pyogenes streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which

CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 SQ Sequence 250 AA;

Query Match

Best Local Similarity 62.5%; Score 72; DB 24; Length 250;
 Pred. No. 8.74e+00;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 165 nkkmvtageidykvrk 180

QY 2 NKKKATVOELDYNNKK 17

RESULT 15

ID W12150 standard; Protein: 251 AA.

AC W12150;
 DT 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 OS Streptococcus pyogenes.
 OS Synthetic.

EH Key Location/Qualifiers

FT peptide 1..30

FT peptide /label= sig_peptide

FT peptide 31..251

FT peptide /label= mat_peptide

FT peptide /note= "wild type Lys replaced by Asn"

FT peptide /misc_difference 46

PN MO9640930-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; U10252.

PR 07-JUN-1995; US-480261.

PA (MIND) UNIV MINNESOTA.

PI Chlendorf D, Roggiani M, Schlievert PM, Stoehr J;

PI MPI: 97-09936/09.

PT Mutant SPE-A toxin with at least one amino acid change is

PT substantially non-lethal - used in vaccine composition for

PT treatment of cancer and streptococcal toxic shock syndrome etc.

PS Example 4; Page 7; 102pp; English.

CC The present sequence is a non-lethal Streptococcus pyogenes

CC vaccine to protect animals against wild type SPE-A and to treat

CC cancer and streptococcal toxic shock syndrome (STSS). The mutant

CC SPE-A causes neutralising antibodies (Ab) to be produced, which

CC can be used to ameliorate STSS symptoms, e.g. fever, hypotension,

CC group A streptococcal infection, myositis, fasciitis and liver

CC damage. The neutralising Ab is preferably administered in

CC conjunction with antibiotic therapy. The mutant SPE-A is

CC especially useful for treating T cell lymphomas, and ovarian and

CC uterine cancer. It is thought that mutant SPE-A can be selectively

CC toxic to T cell lymphoma cells.

CC N.B. Sequence not given in the specification, but constructed

CC using the wild type SPE-A sequence given on pages 77-79.

SQ Sequence 251 AA;

Query Match

Best Local Similarity 62.5%; Score 72; DB 24; Length 251;
 Pred. No. 8.74e+00;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 166 nkkmvtageidykvrk 181

QY 2 NKKKATVOELDYNNKK 17

MUSEUM
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:20:35 1999; MasPar time 4.14 Seconds
Tabular output not generated. 232.052 Million cell updates/sec

Title: >US-09-150-947-7
Description: (1-24) from US09150947.pep
Perfect Score: 162
Sequence: 1 YNKKATVQELDYNKKATVQELD 24

Scoring table:
PAM 150
Gap 15

Searched: 122810 segs, 4006593 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p160
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 28.079; Variance 51.999; scale 0.540

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|-------------|-----------|
| 1 | 72 | 44.4 | 236 | 2 | S18783 | 5.98e-01 |
| 2 | 72 | 44.4 | 236 | 2 | S18786 | 5.98e-01 |
| 3 | 72 | 44.4 | 251 | 2 | S29659 | 5.98e-01 |
| 4 | 71 | 43.8 | 85 | 2 | S24453 | 8.48e-01 |
| 5 | 71 | 43.8 | 289 | 2 | S73935 | 8.48e-01 |
| 6 | 70 | 43.2 | 266 | 1 | ENSAC1 | 1.20e+00 |
| 7 | 70 | 43.2 | 266 | 2 | A60114 | 1.20e+00 |
| 8 | 70 | 43.2 | 266 | 2 | S11885 | 1.20e+00 |
| 9 | 70 | 43.2 | 266 | 1 | ENSAB6 | 1.20e+00 |
| 10 | 69 | 42.6 | 561 | 2 | S52319 | 1.68e+00 |
| 11 | 68 | 42.0 | 236 | 2 | S18789 | 2.38e+00 |
| 12 | 68 | 42.0 | 566 | 2 | S54091 | 2.38e+00 |
| 13 | 68 | 42.0 | 945 | 2 | A64714 | 2.38e+00 |
| 14 | 68 | 42.0 | 946 | 2 | A71805 | 2.38e+00 |
| 15 | 67 | 41.4 | 422 | 2 | H70914 | 3.34e+00 |
| 16 | 66 | 40.7 | 159 | 2 | C65113 | 4.67e+00 |
| 17 | 65 | 40.1 | 1252 | 2 | T00263 | 6.51e+00 |
| 18 | 64 | 39.5 | 206 | 2 | S25937 | 9.06e+00 |
| 19 | 64 | 39.5 | 227 | 2 | C64355 | 9.06e+00 |
| 20 | 64 | 39.5 | 258 | 2 | A33953 | 9.06e+00 |
| 21 | 64 | 39.5 | 1284 | 1 | MMVZAI | 9.06e+00 |
| 22 | 63 | 38.9 | 205 | 1 | B44963 | 1.26e+01 |
| 23 | 63 | 38.9 | 262 | 2 | C70372 | 1.26e+01 |

| | | | | | | | |
|----|----|------|------|---|--------|------------------------|----------|
| 24 | 63 | 38.9 | 452 | 1 | WHHUF | phenylalanine 4-mono | 1.26e+01 |
| 25 | 62 | 38.3 | 204 | 2 | S24985 | nef protein - human i | 1.73e+01 |
| 26 | 62 | 38.3 | 501 | 2 | S44258 | sucrose-6-phosphate h | 1.73e+01 |
| 27 | 62 | 38.3 | 561 | 2 | S41808 | glucose-6-phosphate i | 1.73e+01 |
| 28 | 62 | 38.3 | 1436 | 2 | D71618 | hypothetical protein i | 1.73e+01 |
| 29 | 61 | 37.7 | 65 | 2 | I36850 | A26L protein - variol | 2.39e+01 |
| 30 | 61 | 37.7 | 139 | 2 | T00120 | hypothetical protein | 2.39e+01 |
| 31 | 61 | 37.7 | 233 | 2 | A29566 | hypothetical protein | 2.39e+01 |
| 32 | 61 | 37.7 | 257 | 2 | A28664 | enterotoxin A - Staph | 2.39e+01 |
| 33 | 61 | 37.7 | 290 | 2 | C64209 | hypothetical protein | 2.39e+01 |
| 34 | 61 | 37.7 | 469 | 2 | F69403 | hypothetical protein | 2.39e+01 |
| 35 | 61 | 37.7 | 872 | 1 | S53319 | acetaldehyde dehydrog | 2.39e+01 |
| 36 | 61 | 37.7 | 1193 | 2 | C71605 | hypothetical protein | 2.39e+01 |
| 37 | 61 | 37.7 | 2380 | 2 | E71604 | hypothetical protein | 2.39e+01 |
| 38 | 60 | 37.0 | 177 | 2 | S39859 | transcription antiter | 3.28e+01 |
| 39 | 60 | 37.0 | 302 | 2 | B70746 | probable cma2 protei | 3.28e+01 |
| 40 | 60 | 37.0 | 342 | 2 | E70109 | hypothetical protein | 3.28e+01 |
| 41 | 60 | 37.0 | 569 | 2 | S74053 | probable acylaminoacy | 3.28e+01 |
| 42 | 60 | 37.0 | 654 | 2 | S70905 | transferrin-binding p | 3.28e+01 |
| 43 | 60 | 37.0 | 663 | 2 | S51865 | K6P1 protein - yeast | 3.28e+01 |
| 44 | 60 | 37.0 | 671 | 2 | A40692 | signal recognition pa | 3.28e+01 |
| 45 | 60 | 37.0 | 1553 | 2 | S67483 | adenosinetriphosphata | 3.28e+01 |

ALIGNMENTS

| RESULT ENTRY TITLE | 1 | ALIGNMENTS |
|---|---|------------|
| S18783 exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isolate Nebraska and others) (fragment) | #type fragment #formal_name Streptococcus pyogenes phage strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS624 isolate Germany; strain MGAS495 isolate Germany 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998 | |
| DATE | 02-Jul-1998 | |
| ACCESSIONS | S18783; S18793; S18794; S18801; S18798 | |
| REFERENCE | S18782 | |
| ALTERNATE_NAMES | Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. | |
| ORGANISM | J. Exp. Med. (1991) 174:1271-1274 | |
| #variety | Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes. | |
| #title | Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes. | |
| #cross-references MUID:92044323 | | |
| #accession S18783 | nucleic acid sequence not shown; translation not shown | |
| #status | nucleic acid sequence not shown; translation not shown | |
| #molecule_type DNA | | |
| #residues | 1-236 #label NEF | |
| #cross-references EMBL:X61568; NID:947289; PID:947290 | | |
| #experimental_source strain MGAS158 isolate Nebraska unassigned phage | | |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | |
| #accession S18793 | nucleic acid sequence not shown; translation not shown | |
| #status | nucleic acid sequence not shown; translation not shown | |
| #molecule_type DNA | | |
| #residues | 1-236 #label NEA | |
| #cross-references EMBL:X61569; NID:947313; PID:947314 | | |
| #experimental_source strain MGAS485 isolate Yugoslavia unassigned phage | | |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | |
| #accession S18794 | nucleic acid sequence not shown; translation not shown | |
| #status | nucleic acid sequence not shown; translation not shown | |
| #molecule_type DNA | | |
| #residues | 1-236 #label NEZ | |
| #cross-references EMBL:X61570; NID:947315; PID:947316 | | |
| #experimental_source strain MGAS491 isolate United Kingdom unassigned phage | | |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | |
| #accession S18801 | nucleic acid sequence not shown; translation not shown | |
| #status | nucleic acid sequence not shown; translation not shown | |

```

##residues      1-236 ##label NEV
##crosstalk-references EMBL:X61572; NID:q47333; PID:q47334
##experimental_source strain MGAS624 isolate Germany unassigned phage
##note          the nucleotide sequence was submitted to the EMBL data
                  Library, September 1991
#accession      S18798
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues      1-236 ##label NEO
##crosstalk-references EMBL:X61571; NID:q47323; PID:q47324
##experimental_source strain MGAS495 isolate Germany unassigned phage
##note          the nucleotide sequence was submitted to the EMBL data
                  Library, September 1991
GENETICS
#gene           speA3
CLASSIFICATION  #superfamily enterotoxin B
KEYWORDS        exotoxin
FEATURE
1-22
23-236
#domain signal sequence (fragment) #status predicted
#label SIG\
#product exotoxin type A (fragment) #status predicted
#label MAT
#length 236 #checksum 612
SUMMARY
Query Match      44.4%; Score 72; DB 2; Length 236;
Best Local Similarity 62.5%; P-Id. No. 5,98e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 158 NKKMTAQELDYKVR 173
OY 2 NKKMTAQELDYKVR 17
RESULT 2
ENTRY 2
TITLE S18786 #type fragment
       exotoxin type A precursor (allele 2) - Streptococcus pyogenes
       phage (strain MGAS250 isolate California and others)
       (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#variety strain MGAS250 isolate California; strain MGAS251 isolate
          California; strain MGAS256 isolate California; strain
          MGAS285 isolate Colorado; strain MGAS480 isolate
          Yugoslavia; strain MGAS492 isolate United Kingdom; strain
          MGAS496 isolate Germany
DATE 29-Jan-1993 #sequence-revision 29-Jan-1993 #text-change
02-Jul-1998
ACCESSIONS S18786; S18787; S18788; S18790; S18792; S18795; S18799
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
        the speA gene encoding pyrogenic exotoxin A (scarlet fever
        toxin) in Streptococcus pyogenes.
#cross-references MIM:92044323
#accession      S18786
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues      1-236 ##label NEL
##crosstalk-references EMBL:X61561; NID:q47297; PID:q47298
##experimental_source strain MGAS250 isolate California unassigned phage
##note          the nucleotide sequence was submitted to the EMBL data
                  Library, September 1991
#accession      S18787
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues      1-236 ##label NEA
##crosstalk-references EMBL:X61562; NID:q47299; PID:q47300
##experimental_source strain MGAS251 isolate California unassigned phage
##note          the nucleotide sequence was submitted to the EMBL data
                  Library, September 1991
#accession      S18788

```

```

#status      nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues    1-236 ##label NEZ
##cross-references EMBL:X61563; NID:q47301; PID:q47302
##experimental_source strain MGAS256 isolate California unassigned phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession   S18790
#status      nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues    1-236 ##label NEX
##cross-references EMBL:X61564; NID:q47305; PID:q47306
##experimental_source strain MGAS285 isolate Colorado unassigned phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession   S18792
#status      nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues    1-236 ##label NEO
##cross-references EMBL:X61565; NID:q47311; PID:q47312
##experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession   S18795
#status      nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues    1-236 ##label NEH
##cross-references EMBL:X61566; NID:q47317; PID:q47318
##experimental_source strain MGAS492 isolate United Kingdom unassigned
              phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession   S18799
#status      nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues    1-236 ##label NES
##cross-references EMBL:X61567; NID:q47325; PID:q47326
##experimental_source strain MGAS496 isolate Germany unassigned phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

GENETICS
#gene        SPEA2
CLASSIFICATION
#superfamily enterotoxin B
KEYWORDS
#exotoxin
FEATURE
1-22
23-236      #domain signal sequence (fragment) #status predicted
              #label SIG\
              #product exotoxin type A (fragment) #status predicted
              #label MAT
SUMMARY
#length 236 #checksum 1685

Query Match      44.4%; Score 72; DB 2; Length 236;
Best Local Similarity 62.5%; Pred. No. 5,98e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 158 NKKKVTAEQELDYVRK 173
      |||:| |||||:|
OY 2 NKKKATVQELDYNNKK 17

RESULT 3
ENTRY S29659 #type complete
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes
      phase 112
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phase 112
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change
      25-Mar-1998
ACCESSIONS S29659; S18782; S18784; S18785; S18791; S18796; S18797;
      S18800
REFERENCE S29659
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150

```

| | |
|----------------------|--|
| #title | Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12. |
| #cross-references | MUID:8616804 |
| #accession | S29659 |
| #molecule_type | DNA |
| #residues | 1-251 ##label WE |
| #cross-references | GB:U04053; EMBL:M19350; NID:g1877426; PID:g1877430 |
| REFERENCE | |
| #authors | Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. |
| #journal | J. Exp. Med. (1991) 174:1271-1274 |
| #title | Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes. |
| #cross-references | MUID:92044323 |
| #accession | S18782 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-244 ##label NEL |
| #cross-references | EMBL:X61560; NID:g47287; PID:g47288 |
| #experimental_source | Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18784 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-244 ##label NEA |
| #cross-references | EMBL:X61556; NID:g47291; PID:g47292 |
| #experimental_source | Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18785 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-244 ##label NEZ |
| #cross-references | EMBL:X61559; NID:g47293; PID:g47294 |
| #experimental_source | Streptococcus pyogenes strain MGAS167 isolate Texas unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18791 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-244 ##label NEY |
| #cross-references | EMBL:X61555; NID:g47309; PID:g47310 |
| #experimental_source | Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18796 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-244 ##label NEO |
| #cross-references | EMBL:X61557; NID:g47319; PID:g47320 |
| #experimental_source | Streptococcus pyogenes strain MGAS493 isolate France unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18797 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-244 ##label NEH |
| #cross-references | EMBL:X61558; NID:g47321; PID:g47322 |
| #experimental_source | Streptococcus pyogenes strain MGAS494 isolate France unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18800 |
| #status | nucleic acid sequence not shown; translation not shown |
| #molecule_type | DNA |
| #residues | 9-228 ##label NES |

```

##cross-references EMBL:X61554, NID:g473373, PID:g473328
##experimental_source Streptococcus pyogenes strain M6A5500 isolate New Zealand unassigned phage
the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#note

#gene
GENES
#classification
CLASSIFICATION
#superfamily enterotoxin B
KEYWORDS
FEATURES
1-30
31-251
SUMMARY
#domain signal sequence #status predicted #label sig\
#product exotoxin type A #status predicted #label MAT
#length 251 #molecular-weight 29246 #checksum 1475

Query Match
Best Local Similarity 62.5%; Pred. No. 5,99e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 166 NKKMTAQVELDYKVK 181
OY 2 NKKKATVQELDYNNKK 17
||||:| |||||:|

RESULT 4
ENTRY S24453 #type complete
TITLE hypothetical protein 4 - phage SPPI
ORGANISM #formal_name phage SPPI
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
ACCESSIONS S24453
REFERENCE S24450
#authors Chal, S.; Bravo, A.; Lueder, G.; Nedlin, A.; Trautner, T.A.; Alonso, J.C.
#journal J. Mol. Biol. (1992) 224:87-102
#title Molecular analysis of the Bacillus subtilis bacteriophage . SPPI region encompassing genes 1 to 6. The products of gene 1 and gene 2 are required for pac cleavage.
#cross-references EMBL:X56064; NID:g15464; PID:g15468
#accession S24453
#status preliminary
##molecule_type DNA
##residues 1-85 #label CHN
#cross-references EMBL:X56064; NID:g15464; PID:g15468
SUMMARY #length 85 #molecular_weight 10206 #checksum 5408

Query Match
Best Local Similarity 27.3%; Pred. No. 8.48e-01;
Matches 6; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Db 7 RKKNRIOIEYKKNLTQDIE 28
OY 3 KKKATVQELDYNNKKATVQELD 24
||||:| |||||:|

RESULT 5
ENTRY S73935 #type complete
TITLE hypothetical protein yaca homolog G07_orf289 - Mycoplasma pneumoniae (ATCC 29342) (SGC)
ALTERNATE_NAMES hypothetical protein G07_orf289
ORGANISM #formal_name Mycoplasma pneumoniae
VARIETY ATCC 29342
DATE 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 17-Jul-1998
ACCESSIONS S73935
REFERENCE S73932
#authors Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkil, E.; Li, B.C.; Herrmann, R.
#journal Nucleic Acids Res. (1996) 24:4420-4449
#title Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
#cross-references MUID:97105885
#accession S73935
preliminary; nucleic acid sequence not shown;

```


| | | |
|---|---|--|
| | 23-236 | #product exotoxin A (fragment) #status predicted #label #accession A64714 |
| SUMMARY | #length 236 #checksum 3493 | |
| Query Match | 42.0%; Score 68; DB 2; Length 236; | |
| Best Local Similarity | Pred. No. 2.38e+00; | |
| Matches | 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0; | |
| Dn | 158 SKKWTAQVLDYKVRK 173 | |
| Oy | 2 NKKKAQVLELNNKK 17 | |
| RESULT 12 | \$S4O91 #type complete | |
| ENTRY | hypothetical protein YPR070w - yeast (<i>Saccharomyces cerevisiae</i>) | |
| TITLE | cerevstae) | |
| ALTERNATE_NAMES | hypothetical protein ypr949g.25 | |
| ORGANISM | #formal_name Saccharomycetes cerevistae | |
| DATE | 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 12-Dec-1997 | |
| ACCESSIONS | \$S4O91: S69058 | |
| REFERENCE | Baddock, K.; Churcher, C.M. | |
| #authors | submitted to the EMBL Data Library, May 1995 | |
| #submission | \$S4O91 | |
| #accession | #molecule_type DNA | |
| #residues | 1-566 ##label BAD | |
| ##cross-references | EML:249219; NID:g805025; PID:g805050; MIPS:YPR070W | |
| ##experimental_source strain AB972 | | |
| REFERENCE | Couch, J. | |
| #authors | Submitted to the EMBL Data Library, March 1996 | |
| #description | The sequence of s. cerevistae consmd 9513. | |
| #accession | S69058 | |
| #molecule_type | DNA | |
| #residues | 1-566 ##label COU | |
| ##cross-references | EML:US1033; NID:g1230676; PID:g1230678; MIPS:YPR070W | |
| GENTICS | | |
| #map_position | 16R | |
| SUMMARY | #length 566 #molecular_weight 64251 #checksum 1300 | |
| Query Match | 42.0%; Score 68; DB 2; Length 566; | |
| Best Local Similarity | Pred. No. 2.38e+00; | |
| Matches | 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0; | |
| Dn | 59 KIIVDVNKKODRIDOV 77 | |
| Oy | 5 KAIVOELDYNNKKAQVOEL 23 | |
| RESULT 13 | A64714 #type complete | |
| ENTRY | helicase - Helicobacter pylori (strain 26695) | |
| TITLE | #formal_name Helicobacter pylori | |
| ORGANISM | 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 10-Oct-1997 | |
| ACCESSIONS | A64714 | |
| REFERENCE | A64520 | |
| #authors | Tomlinson, F.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klein, H.P.; Gillis, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khakhria, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, W.D.; Hickley, E.K.; Berg, D.E.; Gokey, J.D.; Uitterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weisman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.; Mallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C. | |
| Nature (1997) 388:539-547 | | |
| The complete genome sequence of the gastric pathogen Helicobacter pylori. | | |

| | | |
|--|--|--|
| | #cross-references MDI:97394467 | |
| #accession | A64714 | |
| #status | translational not shown | |
| #molecule_type | DNA | |
| #residues | 1-945 ##label TOM | |
| ##cross-references | GB:AE000653; GB:AE000511; NID:g2314733; PID:g2314736; TIGR:HP1553 | |
| SUMMARY | #length 945 #molecular-weight 108880 #checksum 6304 | |
| Query Match | 42.0%; Score 68; DB 2; Length 945; | |
| Best Local Similarity | Pred. No. 2.38e+00; | |
| Matches | 7; Conservative 7; Mismatches 9; Indels 0; Gaps 0; | |
| Dn | 303 YDNATSKIALPDFAIKDKRVHL 325 | |
| Oy | 1 YNKKAQVLELNNKKAQVOEL 23 | |
| RESULT 14 | A71805 #type complete | |
| ENTRY | probable ATP-dependent helicase - Helicobacter pylori (strain J99) | |
| TITLE | #formal_name Helicobacter pylori | |
| ORGANISM | #variety strain J99 | |
| DATE | 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 12-Feb-1999 | |
| ACCESSIONS | A71805 | |
| REFERENCE | A71800 | |
| #authors | Allm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonghe, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uribe-Nicholsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Meiberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voyts, G.F.; Trust, T.J. | |
| Nature (1999) 397:176-180 | | |
| Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori. | | |
| #cross-references | MIMD:99120557 | |
| #accession | A71805 | |
| #status | preliminary | |
| #molecule_type | DNA | |
| #residues | 1-946 ##label ARN | |
| ##cross-references | GB:AE001567; GB:AE001439; NID:g4156065; PID:g4156072 | |
| ##experimental_source strain J99 | | |
| GENTICS | | |
| #gene | pCRA | |
| SUMMARY | #length 946 #molecular-weight 109364 #checksum 9318 | |
| Query Match | 42.0%; Score 68; DB 2; Length 946; | |
| Best Local Similarity | Pred. No. 2.38e+00; | |
| Matches | 7; Conservative 7; Mismatches 9; Indels 0; Gaps 0; | |
| Dn | 303 YDNATSKIALPDFAIKDKRVHL 325 | |
| Oy | 1 YNKKAQVLELNNKKAQVOEL 23 | |
| RESULT 15 | H70914 #type complete | |
| ENTRY | hypothetical protein RV1429 - Mycobacterium tuberculosis (strain H37Rv) | |
| TITLE | #formal_name Mycobacterium tuberculosis | |
| ORGANISM | 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998 | |
| ACCESSIONS | H70914 | |
| REFERENCE | A70500 | |
| #authors | Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry, III, C.E.; Tekala, F.; Baddock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtrold, S.; Horsby, T.; Jacobs, K.; Krogh, A.; McLean, J.; Moule, S. | |

Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
Skellton, S.; Squares, S.; Squires, R.; Sultson, J.E.;
Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature (1998) 393:537-544
Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.
#cross-references MUID:98295987
#accession H70914
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1422 #label COL
#cross-references GB:295844; GB:AL123456; NID:93250713; PID:e318874;
PID:g2131067
#experimental_source strain H37Rv
GENETICS
#gene Rv1429
SUMMARY #length 422 #molecular-weight 46898 #checksum 4542
Query Match 41.4%; Score 67; DB 2; Length 422;
Best Local Similarity 38.9%; Pred. No. 3.34e+00;
Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
DB 28 FDKMKAETIRGLDYDARMA 45
QY 1 YNKKKATVOELDYNNKKA 18

Search completed: Tue Aug 31 19:20:58 1999
Job time : 23 secs.

THIS PAGE BLANK (USPTO)

 MWSEKLEH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MPearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Aug 31 19:19:15 1999; Masspar time 2.62 Seconds
 Tabular output not generated. 256.542 Million cell updates/sec

Title: >US-09-150-947-7
 Description: (1-24) from US09150947.pep
 Perfect Score: 162
 Sequence: 1 INKKKATVQELDYNNKKATVQELD 24

Scoring table:
 PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 28.932; Variance 45.977; scale 0.629

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|-----------|
| 1 | 72 | 44.4 | 251 | 1 | SPEA_STRPY | 1.27e+01 |
| 2 | 71 | 43.8 | 85 | 1 | YOR4_BPSP | 1.88e+01 |
| 3 | 71 | 43.8 | 289 | 1 | YOR4_MYCPN | 1.88e+01 |
| 4 | 70 | 43.2 | 266 | 1 | ETC3_STANU | 2.79e+01 |
| 5 | 70 | 43.2 | 266 | 1 | ETC2_STANU | 2.79e+01 |
| 6 | 70 | 43.2 | 266 | 1 | ETXB_STANU | 2.79e+01 |
| 7 | 70 | 43.2 | 266 | 1 | ETC1_STANU | 2.79e+01 |
| 8 | 69 | 42.6 | 433 | 1 | CP51_USTMA | 4.12e+01 |
| 9 | 67 | 41.4 | 433 | 1 | PR12_CAEEL | 8.90e+01 |
| 10 | 66 | 40.7 | 181 | 1 | YHCE_ECOLI | 1.30e+00 |
| 11 | 64 | 39.5 | 227 | 1 | Y443_METJA | 2.75e+00 |
| 12 | 64 | 39.5 | 258 | 1 | ETXD_STANU | 2.75e+00 |
| 13 | 64 | 39.5 | 782 | 1 | YQ91_CAEEL | 2.75e+00 |
| 14 | 64 | 39.5 | 1284 | 1 | ATI_COMPX | 2.75e+00 |
| 15 | 63 | 38.9 | 205 | 1 | NEF_HV13H | 3.98e+00 |
| 16 | 63 | 38.9 | 452 | 1 | PH4H_HUMAN | 3.98e+00 |
| 17 | 63 | 38.9 | 751 | 1 | YIX5_CAEEL | 3.98e+00 |
| 18 | 62 | 38.3 | 501 | 1 | SCRB_PEPDE | 5.73e+00 |
| 19 | 62 | 38.3 | 560 | 1 | G6PI_ARATH | 5.73e+00 |
| 20 | 61 | 37.7 | 257 | 1 | ETX4_STANU | 8.22e+00 |
| 21 | 61 | 37.7 | 290 | 1 | YOR4_MYCPN | 8.22e+00 |
| 22 | 61 | 37.7 | 870 | 1 | ADH2_ENTHI | 8.22e+00 |
| 23 | 60 | 37.0 | 177 | 1 | NUSG_BACSU | 1.17e+01 |

| | | | | | | | |
|----|----|------|------|---|------------|------------------------|----------|
| 24 | 60 | 37.0 | 218 | 1 | RL1_SUISO | 50S RIBOSOMAL PROTEIN | 1.17e+01 |
| 25 | 60 | 37.0 | 302 | 1 | CEA2_MCTU | CYCLOPROpane-FATTY-ACY | 1.17e+01 |
| 26 | 60 | 37.0 | 663 | 1 | RGPI_YEAST | REDUCED GROWTH PHENOTY | 1.17e+01 |
| 27 | 60 | 37.0 | 670 | 1 | SR72_CANFA | SIGNAL RECOGNITION PAR | 1.17e+01 |
| 28 | 60 | 37.0 | 867 | 1 | RRPO_BYDVI | POTATIVE RNA-DIRECTED | 1.67e+01 |
| 29 | 59 | 36.4 | 205 | 1 | NEF_SIVC2 | NEGATIVE FACTOR (F-PRO | 1.67e+01 |
| 30 | 59 | 36.4 | 205 | 1 | NEF_HV13 | NEGATIVE FACTOR (F-PRO | 1.67e+01 |
| 31 | 59 | 36.4 | 208 | 1 | NEF_HV1S1 | NEGATIVE FACTOR (F-PRO | 1.67e+01 |
| 32 | 59 | 36.4 | 211 | 1 | NEF_HV1OY | NEGATIVE FACTOR (F-PRO | 1.67e+01 |
| 33 | 59 | 36.4 | 216 | 1 | NEF_HV1JR | NEGATIVE FACTOR (F-PRO | 1.67e+01 |
| 34 | 59 | 36.4 | 262 | 1 | YQ52_CAEEL | HYPOTHETICAL 30.9 KD P | 1.67e+01 |
| 35 | 59 | 36.4 | 285 | 1 | RL2_MYGE | 50S RIBOSOMAL PROTEIN | 1.67e+01 |
| 36 | 59 | 36.4 | 610 | 1 | EDD_PSEAE | PHOSPHOGUCCONATE DEHYD | 1.67e+01 |
| 37 | 59 | 36.4 | 707 | 1 | YG3J_YEAST | HYPOTHETICAL 81.7 KD P | 1.67e+01 |
| 38 | 59 | 36.4 | 867 | 1 | RRPO_BYDVR | POTATIVE RNA-DIRECTED | 1.67e+01 |
| 39 | 59 | 36.4 | 989 | 1 | YX14_CAEEL | HYPOTHETICAL 115.3 KD | 1.67e+01 |
| 40 | 59 | 36.4 | 1088 | 1 | RRPO_ROTBU | RNA-DIRECTED RNA POLYM | 1.67e+01 |
| 41 | 59 | 36.4 | 1088 | 1 | RRPO_ROTBR | RNA-DIRECTED RNA POLYM | 1.67e+01 |
| 42 | 59 | 36.4 | 1088 | 1 | RRPO_ROTSL | RNA-DIRECTED RNA POLYM | 1.67e+01 |
| 43 | 59 | 36.4 | 1703 | 1 | SNF2_YEAST | TRANSCRIPTION REGULATO | 1.67e+01 |
| 44 | 59 | 36.4 | 3210 | 1 | CENF_HUMAN | CENP-F KINETOCORE PRO | 1.67e+01 |
| 45 | 59 | 36.4 | 4466 | 1 | DYHC_TRIGR | DYNEIN BETA CHAIN, CIL | 1.67e+01 |

ALIGNMENTS

RESULT 1
 ID SPEA_STRPY STANDARD; PRT: 251 AA.
 AC P08095;
 DT 01-AUG-1988 (REL. 08, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
 DE (SPE A).
 GN SPEA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86166804.
 RA WEEKS C.R., FERRETTI J.J.;
 RT "Nucleotide sequence of the type A streptococcal exotoxin
 RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 RT 112.";
 RL INFECT. IMMUN. 52:144-150(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86284313.
 RA JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 RT related to staphylococcus aureus enterotoxin B.";
 RL MOL. GEN. GENET. 203:354-356(1986).
 CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE 112.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC *****
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC *****
 CC EMBL: U40453; G1877430; -;
 CC EMBL: X03929; G47442; -;
 CC DR EMBL: A26152; A26152.

DR PIR: S29659; S29659.
DR PROSITE: PS00277; STAPH_STRP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STRP_TOXIN_2; 1.
DR PRAM: PF01123; Staph_Strp_Toxin; 1.
DR HSSP: P01532; ISEB.
KW TOXIN: SIGNAL.
FT SIGNAL 1 30 EXOTOXIN TYPE A.
FT CHAIN 31 251 K -> E (IN REF. 2).
FT CONFLICT 6 6 VT -> MK (IN REF. 2).
FT CONFLICT 17 18 SQEFAQDDP -> LKGLCTSPRK (IN REF. 2).
FT CONFLICT 25 35 H -> Q (IN REF. 2).
FT CONFLICT 40 40 S -> N (IN REF. 2).
FT CONFLICT 43 43 NLQNIYFLYEGDP -> TFKIIFEMVTL (IN
FT CONFLICT 47 59 REF. 2).
FT CONFLICT 129 129 I -> L (IN REF. 2).
FT CONFLICT 165 178 TRKMTVAQELDYK -> QIKNGCSRIYST (IN
FT REF. 2).
SQ SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;
Query Match 44.4%; Score 72; DB 1; Length 251;
Best Local Similarity 62.5%; Pred. No. 1.27e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 166 NKKMTVAQELDYK 181
QY 2 NKKKATVQELDYK 17
RESULT 2
ID Y084_BPSP STANDARD; PRT; 85 AA.
AC Q38440;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 13-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 10.2 KD PROTEIN IN GP2-GP6 INTERGENIC REGION (ORF 4).
OS BACTERIOPHAGE SP1.
OC VIRUSES: DSDNA VIRUSES, NO RNA STAGE, TAILED PHAGES; SITHOVIIRIDAE;
OC LAMDA PHAGE GROUP.
CC [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 92194332.
RX CHAI S., BRAVO A., LUEDER G., NEDLIN A., TRAUTNER T.A., ALONSO J.C.;
RT "Molecular analysis of the Bacillus subtilis bacteriophage SP1
RT region encompassing genes 1 to 6. The products of gene 1 and gene 2
RT are required for pac cleavage."
RL J. MOL. BIOL. 224:87-102(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA ALONSO J.C., LUEDER G., STIEGE A.C., CHAI S., WEISE F., TRAUTNER T.A.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: SOME, TO PHAGE SP01 GENE 46 PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56064; G15468; -
DR EMBL: X97918; E244472; -
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 85 AA; 10206 MW; 3500FE7 CRC32;
Query Match 43.8%; Score 71; DB 1; Length 85;
Best Local Similarity 27.3%; Pred. No. 1.88e-01;
Matches 6; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
Db 7 RKNRRIQIEYKNNLTAKDIE 28
QY 1 KKKATVQELDYK 24

RESULT 3
ID Y084_MYCPN STANDARD; PRT; 289 AA.
AC P75549;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN MG084 HOMOLOG.
OS MYCOPLASMA PNEUMONIAE.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
OC MYCOPLASMA TACTACEAE; MYCOPLASMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE: 97105885.
RA HIMMELREICH R., HILBERT H., PLACENS H., PIKRL E., LI B.-C.,
RA HERRMANN R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
CC -1- SIMILARITY: SOME, TO B.SUBTILIS YACA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000058; G1674311; -
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 289 AA; 34385 MW; 22AE00AA CRC32;
Query Match 43.8%; Score 71; DB 1; Length 289;
Best Local Similarity 36.4%; Pred. No. 1.88e-01;
Matches 8; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
Db 23 YHKRIACVHVNNKRTALRD 44
QY 1 YNKKATVQELDYK 22
RESULT 4
ID ETC3_STAUV STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ENT3.
OS BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90220508.
RA HOVDE C.J., HACKERT S.P., BOHACH G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RL MOL. GEN. GENET. 220:329-333(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECP.
RX MEDLINE: 97064178.
RA FIELDS B.A., MALCHIODI E.L., LI H., YSRN X., STAUFFACHER C.V.,
RA SCHLIEVERT P.M., KARULAINEN K., MARIOTZA R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RL NATURE 384:188-192(1996).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.


```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 248164; G663267; -
CC PROSITE: PS00086; CYTOCHROME_P450; 1.
CC PFAM: PF00067; P450; 1.
CC ELECTRON TRANSPORT: OXIDOREDUCTASE; MONOOXYGENASE; MEMBRANE; HEME;
CC STEROL BIOSYNTHESIS
CC BINDING 501 501 HEME (BY SIMILARITY).
CC SEQUENCE 561 AA; 62197 MW; A4/675CA CRC32;
SQ
Query Match 42.6%; Score 69; DB 1; Length 561;
Best Local Similarity 37.5%; Pred. No. 4,12e-01;
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Db 359 YSDGHGRLDYETOKTSVPLLD 382
QY 1 YNKKRATVOELDYNNKKATVOELD 24
RESULT 9
ID PRI2_GAEEL STANDARD: PRT; 433 AA.
AC 002334;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROBABLE DNA PRIMASE LARGE SUBUNIT (EC 2.7.7.-).
GN W02D9.1.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIDA; RHABDITIDA;
OC RHABDITIDA; RHABDITODEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA LENNARD N.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -I- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL
CC RNA PRIMERS FOR THE OKAZAKI FRAGMENTS MADE DURING DISCONTINUOUS
CC DNA REPLICATION (BY SIMILARITY).
CC -I- SUBUNIT: HETERODIMER OF A SMALL SUBUNIT AND A LARGE SUBUNIT.
CC -I- SIMILARITY: BELONGS TO THE EUKARYOTIC PRIMASE LARGE SUBUNIT
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 28137; E134998; -
CC WORMPEP; W02D9.1; CE14454.
CC TRANSFERASE: DNA REPLICATION; DNA-DIRECTED RNA POLYMERASE; PRIMOSOME;
CC DNA-BINDING.
CC SEQUENCE 433 AA; 50218 MW; 33EF58C6 CRC32;
SQ
Query Match 41.4%; Score 67; DB 1; Length 433;
Best Local Similarity 33.3%; Pred. No. 8,90e-01;
Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Db 170 TIEKAGYTEKQAMIELE 187
QY 7 TVOELDYNNKKATVOELD 24
RESULT 10

```

```

ID YHCE_ECOLI STANDARD: PRT; 181 AA.
AC P45421;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 19.2 KD PROTEIN IN GLIF-NANT INTERGENIC REGION.
GN YHCE.
OS ESCHERICHIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RA PLUNKETT G. III;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP CONCEPTUAL TRANSLATION.
RA RUDD K.E.;
RL UNPUBLISHED OBSERVATIONS (APR-1995).
CC -I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THIS PROTEIN IS
CC TRUNCATED BY AN IS5 ELEMENT WHICH IS INSERTED BETWEEN POSITION 123
CC AND 124.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U18997; G606156; ALT_SEQ.
CC DR ECOGENE; EG12811; YHCE.
CC KM HYPOTHETICAL PROTEIN.
CC SEQUENCE 181 AA; 19192 MW; C07A79A4 CRC32;
SQ
Query Match 40.7%; Score 66; DB 1; Length 181;
Best Local Similarity 31.6%; Pred. No. 1,30e+00;
Matches 6; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
Db 25 SSIONIDYGRSARAOVD 43
QY 6 ATVOELDYNNKKATVOELD 24
RESULT 11
ID Y443_METJA STANDARD: PRT; 227 AA.
AC 05785;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN MJ0443.
GN MJ0443.
OS METHANOCOCCUS JANNASCHII.
OC ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
OC METHANOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE: 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.F., ADAMS M.D., REICH C.I.,
RA OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODER A.,
RA SCOTT J.L., GEOGHAGEN S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., RAINE B.P., BORODOVSKI M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOSE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
CC -I- SIMILARITY: SOME. TO S.CEREVISIAE YCL59C.
CC -----

```



```

RC STRAIN-CPRO6:
RX MEDLINE: 88089536.
RA FUNAHASHI S., SATO T., SHIDA H.;
RT "Cloning and characterization of the gene encoding the major protein
RT of the A-type inclusion body of cowpox virus."
RL J. GEN. VIROL. 69:35-47(1988).
RN [2]
RP SEQUENCE OF 1-109 FROM N.A.
RX MEDLINE: 88111568.
RA PATEL D.D., PICKUP D.J.;
RT "Messenger RNAs of a strongly-expressed late gene of cowpox virus
RT contain 5'-terminal poly(A) sequences."
RL EMBO J. 6:3787-3794(1987).
CC -1- FUNCTION: MATURE VIRUSES ARE OCCCLUDED INTO THE ATI, AND IT HAS
CC BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING
CC DISSEMINATION FROM ANIMAL TO ANIMAL.
CC -1- A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION OF LARGE MASSES
CC WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF INFECTED CELLS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D00319; G221141; -
DR EMBL: X06343; G60711; -
DR PIR: J00006; MWYZAI.
KW LATE PROTEIN; REPEAT.
FT DOMAIN 611 912 10 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 611 637 1.
FT REPEAT 638 665 2.
FT REPEAT 666 689 3.
FT REPEAT 690 720 4.
FT REPEAT 721 751 5.
FT REPEAT 752 780 6.
FT REPEAT 781 811 7.
FT REPEAT 812 842 8.
FT REPEAT 843 871 9.
FT REPEAT 872 912 10.
SQ SEQUENCE 1284 AA; 150329 MW; 66262753 CRC32;

Query Match 39.5%; Score 64; DB 1; Length 1284;
Best Local Similarity 25.0%; Pred. No. 2.75e+00;
Matches 6; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Db 1036 FERRIANLEVEKSMETISLE 1059
Oy 1 YNKKRAIVQELDYNKKRAIVQELD 24

RESULT 15
ID NEF_HYLZH STANDARD: PRT: 205 AA.
AC P05859;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KD PROTEIN) (3'ORF).
GN NEF.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE H2321 ISOLATE) (HIV-1).
OC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89228766.
RA SRINIVASAN A., YORK D., BUTLER D. JR., JANNOUN-NASR R., GETCHELL J.,
RA MCCORMICK J., OU C.Y., MYERS G., SMITH T., CHEN E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
RT in 1976: nucleotide sequence comparison to recent isolates and
RT generation of hybrid HIV."
RL AIDS RES. HUM. RETROVIRUSES 5:121-129(1989).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING

```

```

CC ACTIVITIES, IT SEEM TO DOWN REGULATE THE CD4(T4) ANTIGEN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M15896; G329397; -
DR PIR: B44963; B44963.
DR HIV: M15896; NEPS2321.
DR PRAM: PF00469; F-protein; 1.
DR HSSP: P03406; IEFN.
KW AIDS; MYRISTYLATION; GTP-BINDING.
FT LIPID 2 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 205 AA; 23306 MW; BD983BE2 CRC32;

Query Match 38.9%; Score 63; DB 1; Length 205;
Best Local Similarity 30.4%; Pred. No. 3.98e+00;
Matches 7; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Db 90 FLKRGGLDGLYSKKROEILDL 112
Oy 1 YNKKRAIVQELDYNKKRAIVQEL 23

```

Search completed: Tue Aug 31 19:19:25 1999
 Job time : 10 secs.

THIS PAGE BLANK (USPTO)


```

RESULT 2
ID 057453 PRELIMINARY; PRT: 236 AA.
AC 057453;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPCA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS496;
RX MEDLINE: 92044323.
RA NELSON K., SCHLEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL: X61563; G47300; -
DR EMBL: X61563; G47302; -
DR EMBL: X61567; G47326; -
DR EMBL: X61561; G47298; -
DR EMBL: X61564; G47306; -
DR EMBL: X61565; G47312; -
DR EMBL: X61566; G47318; -
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; A5EB1ECD CRC32;

Query Match 44.4%; Score 72; DB 2; Length 236;
Best Local Similarity 62.5%; Pred. No. 5.59e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 158 NKKKATVOELDYKK 173
|||:| |||||:|
QY 2 NKKKATVOELDYKK 17

RESULT 3
ID P97163 PRELIMINARY; PRT: 236 AA.
AC P97163; P97164;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPCA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, AND MGAS500;
RX MEDLINE: 92044323.
RA NELSON K., SCHLEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. EXP. MED. 174:1271-1274(1991).
DR EMBL: X61556; G47292; -
DR EMBL: X61557; G47320; -
DR EMBL: X61560; G47288; -
DR EMBL: X61555; G47310; -
DR EMBL: X61558; G47322; -
DR EMBL: X61559; G47294; -
DR EMBL: X61554; G47328; -

```

```

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 81A0C2FE CRC32;

Query Match 44.4%; Score 72; DB 2; Length 236;
Best Local Similarity 62.5%; Pred. No. 5.59e-01;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 158 NKKKATVOELDYKK 173
|||:| |||||:|
QY 2 NKKKATVOELDYKK 17

RESULT 4
ID 054739 PRELIMINARY; PRT: 260 AA.
AC 054739; 054737;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL INFECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE: 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT streptococcus pyogenes."
RL INFECT. IMMUN. 64:1161-1165(1996).
DR EMBL: U48794; G1245176; -
DR EMBL: U48792; G1245172; -
DR PFAM: PF01123; Staph_strep_toxin; 1.
SQ SEQUENCE 260 AA; 29767 MW; C81448C1 CRC32;

Query Match 44.4%; Score 72; DB 2; Length 260;
Best Local Similarity 57.9%; Pred. No. 5.59e-01;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 173 NKKKATVOELDYCKTKILV 191
||| |||||:| |
QY 2 NKKKATVOELDYKKATV 20

RESULT 5
ID 054971 PRELIMINARY; PRT: 260 AA.
AC 054971;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SUPERANTIGEN.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
CC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.

```


THIS PAGE BLANK (USPTO)

WIDEORH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:24:14 1999; MasPar time 4.87 Seconds

Tabular output not generated. 152.931 Million cell updates/sec

Title: >US-09-150-947-8

Description: (1-35) from US09150947.pep

Perfect Score: 236

Sequence: 1 YNKKKATVQELDYNKKKATVQELDYNKKKATVEID 35

Scoring table: PAM 150

Gap 11

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 20.250; Variance 92.901; scale 0.218

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|-------------|--------------------------------|
| 1 | 236 | 100.0 | 35 | 34 | W64643 | Synthetic SEB peptide 5.61e-13 |
| 2 | 162 | 68.6 | 24 | 34 | W64642 | Synthetic SEB peptide 1.62e-06 |
| 3 | 88 | 37.3 | 36 | 36 | W72426 | Peptide #5 for reduci 2.22e+00 |
| 4 | 88 | 37.3 | 38 | 36 | W72427 | Peptide #6 for reduci 2.22e+00 |
| 5 | 81 | 34.3 | 12 | 34 | W64637 | Synthetic SEB peptide 7.83e+00 |
| 6 | 81 | 34.3 | 13 | 34 | W64646 | Synthetic SEB peptide 7.83e+00 |
| 7 | 81 | 34.3 | 13 | 34 | W64641 | Synthetic SEB peptide 7.83e+00 |
| 8 | 81 | 34.3 | 14 | 34 | W64644 | Synthetic SEB peptide 7.83e+00 |
| 9 | 81 | 34.3 | 14 | 34 | W64645 | Synthetic SEB peptide 7.83e+00 |
| 10 | 80 | 33.9 | 221 | 8 | R45017 | Staphylococcal entero 9.36e+00 |
| 11 | 80 | 33.9 | 221 | 3 | R13209 | Streptococcus pyogen 9.36e+00 |
| 12 | 80 | 33.9 | 250 | 24 | W12145 | Streptococcus pyogen 9.36e+00 |
| 13 | 80 | 33.9 | 251 | 33 | W59781 | Amino acid sequence o 9.36e+00 |
| 14 | 80 | 33.9 | 251 | 33 | W59798 | Amino acid sequence o 9.36e+00 |
| 15 | 80 | 33.9 | 251 | 24 | W12150 | Streptococcus pyogen 9.36e+00 |
| 16 | 80 | 33.9 | 251 | 33 | W59780 | Amino acid sequence o 9.36e+00 |

| | | | | | | |
|----|----|------|------|----|--------|--------------------------------|
| 17 | 80 | 33.9 | 251 | 24 | W12153 | Streptococcus pyogen 9.36e+00 |
| 18 | 80 | 33.9 | 251 | 24 | W12149 | Streptococcus pyogen 9.36e+00 |
| 19 | 80 | 33.9 | 251 | 24 | W12148 | Streptococcus pyogen 9.36e+00 |
| 20 | 80 | 33.9 | 251 | 24 | W12154 | Streptococcus pyogen 9.36e+00 |
| 21 | 80 | 33.9 | 251 | 24 | W12151 | Streptococcus pyogen 9.36e+00 |
| 22 | 80 | 33.9 | 251 | 24 | W12152 | Streptococcus pyogen 9.36e+00 |
| 23 | 80 | 33.9 | 251 | 24 | W12147 | Streptococcus pyogen 9.36e+00 |
| 24 | 80 | 33.9 | 251 | 24 | W12146 | Streptococcus pyogen 9.36e+00 |
| 25 | 80 | 33.9 | 251 | 24 | W12097 | Streptococcus pyogen 9.36e+00 |
| 26 | 79 | 33.5 | 24 | 36 | W72423 | Peptide #2 for reduci 1.12e+01 |
| 27 | 79 | 33.5 | 28 | 36 | W72425 | Peptide #4 for reduci 1.12e+01 |
| 28 | 75 | 31.8 | 1254 | 2 | R07503 | Merozoite apical-end 2.26e+01 |
| 29 | 75 | 31.8 | 1254 | 24 | W24575 | Merozoite apical-end 2.26e+01 |
| 30 | 74 | 31.4 | 238 | 8 | R45016 | Staphylococcal entero 2.70e+01 |
| 31 | 74 | 31.4 | 238 | 3 | R13208 | Staphylococcal entero 2.70e+01 |
| 32 | 74 | 31.4 | 239 | 3 | R13207 | Staphylococcal entero 2.70e+01 |
| 33 | 74 | 31.4 | 239 | 8 | R45015 | Staphylococcal entero 2.70e+01 |
| 34 | 73 | 30.9 | 239 | 34 | W64647 | Synthetic SEB protein 3.21e+01 |
| 35 | 73 | 30.9 | 239 | 8 | R45014 | Staphylococcal entero 3.21e+01 |
| 36 | 73 | 30.9 | 239 | 3 | R13206 | Staphylococcal entero 3.21e+01 |
| 37 | 73 | 30.9 | 255 | 20 | W06737 | Staphylococcus entero 3.21e+01 |
| 38 | 71 | 30.1 | 230 | 32 | W37993 | Mutant Aspergillus or 4.55e+01 |
| 39 | 70 | 29.7 | 365 | 28 | W43005 | Truncated transferrin 5.41e+01 |
| 40 | 70 | 29.7 | 404 | 28 | W43006 | Truncated transferrin 5.41e+01 |
| 41 | 70 | 29.7 | 411 | 28 | W43007 | Truncated transferrin 5.41e+01 |
| 42 | 70 | 29.7 | 417 | 28 | W43008 | Truncated transferrin 5.41e+01 |
| 43 | 70 | 29.7 | 425 | 28 | W43009 | Truncated transferrin 5.41e+01 |
| 44 | 70 | 29.7 | 463 | 28 | W43010 | Truncated transferrin 5.41e+01 |
| 45 | 70 | 29.7 | 660 | 30 | W53047 | H. influenzae strain 5.41e+01 |

ALIGNMENTS

RESULT 1
ID W64643 standard; peptide: 35 AA.
AC W64643:
DE 23-OCT-1998 (first entry)
KW Synthetic SEB peptide trimer.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09629444-A1.
PD W09629444-A1.
PE 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kademler R.
DR WPT-98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 19: Page 41: 68pp: English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 35 AA:
Query Match 100.0%; Score 236; DB 34; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.61e-13;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ynkktatvqeldynkkkatvqeldynkkkatveid 35

QY 1 YNKKKATVQELDYNKKKATVQELDYNKKKATVQELD 35

RESULT 2
ID W64642 standard; peptide: 24 AA.

AC W64642;
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide dimer.
KM Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
KM Toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KM Therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.

PN W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT Antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 18; Page 41; 68pp; English.

CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PERT or by a mixture of PERTs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PERTs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PERT.
SQ Sequence 24 AA;

Query Match 68.6%; Score 162; DB 34; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.62e-06;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YNKKKATVQELDYNKKKATVQELD 24
1 YNKKKATVQELDYNKKKATVQELD 24

RESULT 3
ID W72426 standard; peptide: 36 AA.

AC W72426;
DT 22-DEC-1998 (first entry)
DE Peptide #5 for reducing symptoms of toxic shock syndrome.
KM Toxic shock syndrome; immunogenic response; bacterial infection;
KM Staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KM Autoimmune disease.
OS Synthetic.

OS Staphylococcus sp.
OS Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.

PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
PS Claim 4; Page 54; 69pp; English.

CC The present invention describes peptides having consensus sequences #1
CC or #2, optionally as part of a larger molecule of size at least 6-8 kd.
CC Where consensus sequence #1 and #2 are: X25X26YGX1RX23X4X5N #1,

CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 - L, I or V; X3, X25 and X26 - any amino acid (aa)
CC or are absent; X27 - L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
CC are used: (i) for diagnostic detection of SPSA or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit biogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
SQ Sequence 36 AA;

Query Match 37.3%; Score 88; DB 36; Length 36;
Best Local Similarity 53.8%; Pred. No. 2.22e+00;

Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

6 VTEHGNKKHVTQGLDYKIRYLVd 31
8 VOELDYNKKKATVQELDYNKKKATVE 33

RESULT 4
ID W72427 standard; peptide: 38 AA.

AC W72427;
DT 22-DEC-1998 (first entry)
DE Peptide #6 for reducing symptoms of toxic shock syndrome.
KM Toxic shock syndrome; immunogenic response; bacterial infection;
KM Staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KM Autoimmune disease.
OS Synthetic.

OS Staphylococcus sp.
OS Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PF 01-APR-1998; U06663.
PR 07-APR-1997; US-838413.
PA (UYRO) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.

PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
PS Claim 4; Page 54; 69pp; English.

CC The present invention describes peptides having consensus sequences #1
CC or #2, optionally as part of a larger molecule of size at least 6-8 kd.
CC Where consensus sequence #1 and #2 are: X25X26YGX1TX23X4X5N #1,
CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 - L, I or V; X3, X25 and X26 - any amino acid (aa)
CC or are absent; X27 - L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
CC are used: (i) for diagnostic detection of SPSA or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit biogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
SQ Sequence 38 AA;

Query Match 37.3%; Score 88; DB 36; Length 38;
Best Local Similarity 53.8%; Pred. No. 2.22e+00;

Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

6 VTEHGNKKHVTQGLDYKIRYLVd 31
8 VOELDYNKKKATVQELDYNKKKATVE 33

RESULT 5
ID W64637 standard; peptide; 12 AA.
AC W64637:
U1 23-OCT-1998 (first entry)
U2 Synthetic SEB peptide p12(151-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 8; Page 41; 68pp; English.
CC W64636-W64637 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 12 AA:

Query Match 34.3%; Score 81; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.83e+00;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkkratvgeid 12
|||||
QY 1 YNKKRATVGEID 12

RESULT 6
ID W64646 standard; peptide; 13 AA.
AC W64646:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide Ac-p12(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
FH Key location/Qualifiers
FT Modified_site 1
FT /note= "N-terminal Tyr modified by N-acetyl group"
FT Misc_difference 14
FT /note= "D-form residue"
PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 24; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by

CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA:

Query Match 34.3%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.83e+00;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkkratvgeid 12
|||||
QY 1 YNKKRATVGEID 12

RESULT 7
ID W64641 standard; peptide; 13 AA.
AC W64641:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide p12LC(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
FH Key location/Qualifiers
FT Modified_site 1
FT /note= "N-terminal Tyr modified by presence of
FT N-lauryl-cysteine!"
PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 16; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA:

Query Match 34.3%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.83e+00;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkkratvgeid 13
|||||
QY 1 YNKKRATVGEID 12

RESULT 8
ID W64644 standard; peptide; 14 AA.
AC W64644:
DT 23-OCT-1998 (first entry)
DE Synthetic SEB peptide Cys-p12(150-161).

KM Enterotoxin B: SEB; pyrogenic exotoxin; PET; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KM therapeutic; vaccine; food poisoning.
 OS Synthetic.
 OS Staphylococcus aureus.
 PN WO9829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 21; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 14 AA;

Query Match 34.3%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.83e+00;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvgeld 13
 |||||
 QY 1 YNKKRATVQELD 12

RESULT 9

ID W64645; standard; peptide; 14 AA.

AC 23-OCT-1998 (first entry)

DE Synthetic SEB peptide D-Ala.

KM Enterotoxin B: SEB; pyrogenic exotoxin; PET; protective immunity;

KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;

KM therapeutic; vaccine; food poisoning.
 OS Synthetic.

OS Staphylococcus aureus.

FM Key Location/Qualifiers

FT Misc_difference 1 /note= "D-form residue"

FT Misc_difference 14 /note= "D-form residue"

PN WO9829444-A1.

PD 09-JUL-1998.

PF 30-DEC-1997; IL0438.

PR 30-DEC-1996; IL-119938.

PA (YISS) YISSUM RES & DEV CO.

PI Arad G, Kaempfer R;

DR WPI: 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)

PS Claim 23; Page 41; 68pp; English.

CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation

CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 14 AA;

Query Match 34.3%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.83e+00;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvgeld 13
 |||||
 QY 1 YNKKRATVQELD 12

RESULT 10

ID R45017 standard; protein; 221 AA.

AC R45017.

DE 08-JUN-1994 (first entry)

DE Staphylococcal enterotoxin SPE A.

KM Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;

KM autoimmune disease; toxicity; Protein A; perfusion system.

OS Staphylococcus aureus.

PN WO9324136-A.

PD 09-DEC-1993.

PF 01-JUN-1993; 005213.

PR 01-JUN-1992; US-891718.

PA (STON/) STONE J L.

PI (TERM/) TERMAN D S.

DR Stone JL, Terman DS;

DR WPI: 93-405418/50.

PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases

PS Disclosure: Fig 1: 90pp; English.

CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.

CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.

SQ Sequence 221 AA;

Query Match 33.9%; Score 80; DB 8; Length 221;
 Best Local Similarity 50.0%; Pred. No. 9.36e+00;

Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 132 dietnkkmtatgaldykyrk 151
 ::|||:|||||:|

QY 10 ELDYNKKRATVQELDYNNKK 29

RESULT 11

ID R13209 standard; Protein; 221 AA.

AC R13209.

DE 15-OCT-1991 (first entry)

DE Streptococcal pyrogenic enterotoxin A.

KM SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.

OS Streptococcus Nr-5 strain.

PN WO9110680-A.

PD 25-JUL-1991.

PF 17-JAN-1991; 000342.

PR 17-JAN-1990; US-466577.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI: 91-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumouricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure: Fig 1: 74pp; English.

CC SPE A can be used for tumouricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to Streptococcal

CC wild type SPE-A toxin. The mutant SPE-A toxins are nontoxic and can
CC produce antibodies that neutralise wild type SPE-A toxin activity. The
CC toxins can be used in vaccines and therapeutics to generate a protective
CC immune response against streptococcal infection. They can be used to
CC protect against the development of streptococcal toxic shock syndrome
CC (STSS). In addition, the toxins can be used for treating animals with
CC symptoms of streptococcal infection or STSS and in methods for
CC stimulating T cell proliferation and in the treatment of cancer. In
CC particular they can be used for treating T cell lymphomas, and ovarian
CC and uterine cancer.
CC This sequence was not present in the specification but was created
CC using information given.
CC Sequence 251 AA;

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 33.98; | Score 80; | DB 33; | Length 251; |
| Best Local Similarity | 50.08; | Pred. No. 9.36e+00; | | |
| Matches 10; | Conservative 6; | Mismatches 4; | Indels 0; | Gaps 0; |

```
Db 162 d!etnkmvtageldykvrk 181
::: | | | | | : : |
QY 10 ELDYNNKKKATVQELDYNNKK 29
```

| RESULT | 15 | |
|--------|--|---------------------------|
| ID | W12150 | standard;Protein: 251 AA. |
| AC | W12150: | |
| DT | 04-NOV-1997 | (first entry) |
| DE | Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn. | |
| KW | Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; | |
| KW | vaccine; protection; treatment; cancer; neutralising antibody; | |
| KW | streptococcal toxic shock syndrome; STSS; symptom; amelioration; | |
| KW | fever; hypotension; group A streptococcal infection; myositis; | |
| KW | fasciitis; liver damage; T cell; lymphoma; ovarian; uterine. | |
| OS | Streptococcus pyogenes. | |
| OS | Synthetic. | |
| FH | Key | Location/Qualifiers |
| FT | peptide | 1..30 |
| FT | /label= | sig-peptide |
| FT | peptide | 31..251 |
| FT | /label= | mat-peptide |
| FT | Misc.difference | 46 |
| FT | /note= "wild type Lys replaced by Asn" | |
| PN | W09640930-A1. | |
| PD | 19-DEC-1996. | |
| PE | 07-JUN-1996: U10252. | |
| PR | 07-JUN-1995: US-480261. | |
| PA | (MNU) UNIV MINNESOTA. | |
| PI | Oehlendorf D, Rोगgiani M, Schlievert PM, Stoehr J; | |
| DR | WPI: 97-099936/09. | |
| PT | Mutant SPE-A toxin with at least one amino acid change is | |
| PT | substantially non-lethal - used in vaccine composition for | |
| PT | treatment of cancer and streptococcal toxic shock syndrome etc. | |
| PS | Example 4: Page -: 102pp; English. | |
| CC | The present sequence is a non-lethal Streptococcus pyogenes | |
| CC | Streptococcal toxin A (SPE-A) mutant, which can be used to produce | |
| CC | vaccines to protect animals against wild type SPE-A and to treat | |
| CC | cancer and streptococcal toxic shock syndrome (STSS). The mutant | |
| CC | SPE-A causes neutralising antibodies (Ab) to be produced, which | |
| CC | may be used to ameliorate STSS symptoms, e.g. fever, hypotension, | |
| CC | group A streptococcal infection, myositis, fasciitis and liver | |
| CC | damage. The neutralising Ab is preferably administered in | |
| CC | conjunction with antibiotic therapy. The mutant SPE-A is | |
| CC | especially useful for treating T cell lymphomas, and ovarian and | |
| CC | uterine cancer. It is thought that mutant SPE-A can be selectively | |
| CC | toxic to T cell lymphoma cells. | |
| CC | N.B. Sequence not given in the specification, but constructed | |
| CC | using the wild type SPE-A sequence given on pages 77-79. | |
| Q | Sequence 251 AA: | |

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 33.98; | Score 80; | DB 24; | Length 251; |
| Best Local Similarity | 50.08; | Pred. No. 9.36e+00; | | |
| Matches | 10; Conservative | 6; Mismatches | 4; Indels | 0; Gaps |

```
Db 162 dietnkmvtageldykvrk 181
    :: |||: | ||||: :|
QY 10 ELDYNNKKATVQELDYNNKK 29
```

Search completed: Tue Aug 31 19:24:48 1999
Job time : 34 secs.

(TM)

Distribution rights by Oxford Molecular Ltd

INKKKATVEID 35

Issues

-I 4

35; scale 0.437

score distribution.

| Description | Pred. No. |
|------------------------|-----------|
| exotoxin type A precu | 1.08e+00 |
| exotoxin type A precu | 1.08e+00 |
| exotoxin type A precu | 1.08e+00 |
| hypothetical protein | 1.45e+00 |
| hypothetical protein | 1.45e+00 |
| exotoxin A precursor | 3.41e+00 |
| adenosinetriphosphata | 3.41e+00 |
| reticulocyte-binding | 4.52e+00 |
| enterotoxin C3 - Stap | 5.98e+00 |
| enterotoxin C-1 precu | 5.98e+00 |
| enterotoxin C-2 precu | 5.98e+00 |
| hypothetical protein | 5.98e+00 |
| SMC2 protein - yeast | 5.98e+00 |
| enterotoxin B precurs | 7.90e+00 |
| hypothetical protein | 7.90e+00 |
| glutamate synthase (N | 7.90e+00 |
| dynen beta heavy cha | 7.90e+00 |
| hypothetical protein | 1.04e+00 |
| conserved hypothetical | 1.04e+00 |
| hypothetical protein | 1.04e+00 |
| hypothetical protein | 1.04e+00 |
| unspecific monooxygen | 1.04e+00 |
| hypothetical protein | 1.37e+00 |

| | | | | | | |
|----|----|------|------|---|--------|-------------------------|
| 15 | 68 | 28.8 | 4466 | 1 | S17231 | |
| 16 | 68 | 28.8 | 2380 | 2 | A71604 | dynein beta heavy chain |
| 17 | 68 | 28.8 | 1104 | 2 | A36865 | microbial collagenase |
| 18 | 68 | 28.8 | 946 | 2 | A71805 | probable ATP-depend |
| 19 | 68 | 28.8 | 493 | 2 | S72196 | X-Pro dipeptidase (EC |
| 20 | 68 | 28.8 | 262 | 2 | C70372 | flagellar hook basal |
| 21 | 68 | 28.8 | 248 | 2 | C50179 | indole-3-glycerol-pi |
| 22 | 68 | 28.8 | 248 | 2 | C40635 | probable membrane pro |
| 23 | 68 | 28.8 | 880 | 2 | S51473 | cation efflux system |
| 24 | 69 | 29.2 | 342 | 2 | S70415 | inner layer protein V |
| 25 | 69 | 29.2 | 135 | 2 | PNO494 | inner layer protein V |
| 26 | 70 | 29.7 | 1088 | 1 | P1XRBR | inner layer protein V |
| 27 | 70 | 29.7 | 1088 | 1 | P1XRBR | inner layer protein V |
| 28 | 70 | 29.7 | 834 | 2 | S44866 | R05D3.4 protein - Cae |
| 29 | 70 | 29.7 | 793 | 2 | E64545 | hypothetical protein |
| 30 | 70 | 29.7 | 660 | 2 | S70904 | transferrin-binding p |
| 31 | 70 | 29.7 | 884 | 2 | S44866 | R05D3.4 protein - Cae |
| 32 | 70 | 29.7 | 1088 | 2 | S13558 | VPI protein - bovine |
| 33 | 70 | 29.7 | 1088 | 1 | P1XRBR | inner layer protein V |
| 34 | 70 | 29.7 | 1088 | 1 | P1XRBR | inner layer protein V |
| 35 | 69 | 29.2 | 135 | 2 | PNO494 | NAD+ ADP-ribosyltrans |
| 36 | 69 | 29.2 | 342 | 2 | S70415 | probable membrane pro |
| 37 | 69 | 29.2 | 880 | 2 | S51473 | cation efflux system |
| 38 | 68 | 28.8 | 248 | 2 | C40635 | probable membrane pro |
| 39 | 68 | 28.8 | 248 | 2 | C50179 | indole-3-glycerol-pi |
| 40 | 68 | 28.8 | 262 | 2 | C70372 | flagellar hook basal |
| 41 | 68 | 28.8 | 493 | 2 | S72196 | X-Pro dipeptidase (EC |
| 42 | 68 | 28.8 | 946 | 2 | A71805 | probable ATP-depend |
| 43 | 68 | 28.8 | 1104 | 2 | A36865 | microbial collagenase |
| 44 | 68 | 28.8 | 2380 | 2 | A71604 | microbial protein |
| 45 | 68 | 28.8 | 4466 | 1 | S17231 | dynein beta heavy chain |

ALIGNMENTS

| RESULT | 1 |
|-----------------------|---|
| ENTRY | S18783 |
| TITLE | exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isolate Nebraska and others) (fragment) |
| ALTERNATE_NAMES | scarlet fever toxin |
| ORGANISM | #formal name Streptococcus pyogenes phage strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS824 isolate Germany; strain MGAS495 isolate Germany |
| variety | 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998 |
| DATE | |
| ACCESSIONS | S18783; S18793; S18794; S18801; S18798 |
| REFERENCE | S18782 |
| authors | Nelson, K.; Schlivert, P.M.; Selander, R.K.; Musser, J.M. |
| journal | J. Exp. Med. (1991) 174:1271-1274 |
| #title | Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes. |
| #cross-references | MU01:92044333 |
| #accession | S18783 |
| #status | nucleic acid sequence not shown; translation not shown |
| ##molecule_type | DNA |
| ##residues | 1-236 #label NE1 |
| ##cross-references | EMBL:X61568; NID:947289; PID:947290 |
| ##experimental_source | strain MGAS158 isolate Nebraska unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18793 |
| #status | nucleic acid sequence not shown; translation not shown |
| ##molecule_type | DNA |
| ##residues | 1-236 #label NEA |
| ##cross-references | EMBL:X61566; NID:947313; PID:947314 |
| ##experimental_source | strain MGAS485 isolate Yugoslavia unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18794 |
| #status | nucleic acid sequence not shown; translation not shown |
| ##molecule_type | DNA |
| ##residues | 1-236 #label NEZ |
| ##cross-references | EMBL:X61570; NID:947315; PID:947316 |
| ##experimental_source | strain MGAS491 isolate United Kingdom unassigned phage |
| #note | the nucleotide sequence was submitted to the EMBL Data Library, September 1991 |
| #accession | S18801 |
| #status | nucleic acid sequence not shown; translation not shown |

```
#molecule-type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61572; NID:q47333; PID:q47334
##experimental_source strain MGAS24 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18798
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61571; NID:q47323; PID:q47324
##experimental_source strain MGAS495 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA3
#superfamily enterotoxin B
#keywords exotoxin
FEATURE
1-22
23-236
#domain signal sequence (fragment) #status predicted
#label SIG\
#product exotoxin type A (fragment) #status predicted
#label MAT
#length 236 #checksum 612
SUMMARY
Query Match 33.9%; Score 80; DB 2; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.08e+00;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Db 154 DIETNKKMTAQLDYKVRK 173
::: |||: | |||||: |
UY 10 ELDYNNKKATVQELDYNNKK 29

RESULT 2
ENTRY
TITLE exotoxin type A precursor (allele 2) - Streptococcus pyogenes
ALTERNATE_NAMES (fragment)
#formal_name Streptococcus pyogenes phage
#strain MGAS250 isolate California; strain MGAS251 isolate
California; strain MGAS256 isolate California; strain
MGAS285 isolate Colorado; strain MGAS480 isolate
Yugoslavia; strain MGAS492 isolate United Kingdom; strain
MGAS496 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
02-Jul-1998
S18786; S18787; S18788; S18790; S18792; S18795; S18799
S18782
#authors Nelson, K.; Schlievert, P.M.; Seldander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of
the speA gene encoding pyrogenic exotoxin A (scarlet fever
toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18786
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEL
##cross-references EMBL:X61561; NID:q47297; PID:q47298
##experimental_source strain MGAS250 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18787
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61562; NID:q47299; PID:q47300
##experimental_source strain MGAS251 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18788
```

```
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEZ
##cross-references EMBL:X61563; NID:q47301; PID:q47302
##experimental_source strain MGAS256 isolate California unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18790
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61564; NID:q47305; PID:q47306
##experimental_source strain MGAS285 isolate Colorado unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18792
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61565; NID:q47311; PID:q47312
##experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18795
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61566; NID:q47317; PID:q47318
##experimental_source strain MGAS492 isolate United Kingdom unassigned
phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18799
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-236 ##label NES
##cross-references EMBL:X61567; NID:q47325; PID:q47326
##experimental_source strain MGAS496 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
GENETICS
#gene speA2
#superfamily enterotoxin B
#keywords exotoxin
FEATURE
1-22
23-236
#domain signal sequence (fragment) #status predicted
#label SIG\
#product exotoxin type A (fragment) #status predicted
#label MAT
#length 236 #checksum 1685
SUMMARY
Query Match 33.9%; Score 80; DB 2; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.08e+00;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Db 154 DIETNKKMTAQLDYKVRK 173
::: |||: | |||||: |
UY 10 ELDYNNKKATVQELDYNNKK 29

RESULT 3
ENTRY
TITLE erythrogenic toxin: scarlet fever toxin
ALTERNATE_NAMES #type complete
#formal_name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change
25-Mar-1998
ACCESSIONS S29659; S18782; S18784; S18785; S18791; S18796; S18797;
S18800
REFERENCE S29659
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150
```


#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage 112.
#cross-references MUID:86168604
#accession S29659
#molecule-type DNA
#residues 1-251 #label MEE
#cross-references GB:U40453; EMBL:M19350; NID:g1877426; PID:g1877430
REFERENCE
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18782
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 #label NEL
#cross-references EMBL:X61560; NID:g47287; PID:g47288
#experimental_source Streptococcus pyogenes strain MGAS156 isolate
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
#accession S18784
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 #label NEA
#cross-references EMBL:X61556; NID:g47291; PID:g47292
#experimental_source Streptococcus pyogenes strain MGAS165 isolate
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
#accession S18785
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 #label NEZ
#cross-references EMBL:X61559; NID:g47293; PID:g47294
#experimental_source Streptococcus pyogenes strain MGAS167 isolate
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
#accession S18791
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 #label NEY
#cross-references EMBL:X61555; NID:g47309; PID:g47310
#experimental_source Streptococcus pyogenes strain MGAS327 isolate
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
#accession S18796
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 #label NEO
#cross-references EMBL:X61557; NID:g47319; PID:g47320
#experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
#accession S18797
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-244 #label NEH
#cross-references EMBL:X61558; NID:g47321; PID:g47322
#experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
#accession S18800
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 9-228 #label NES

##cross-references EMBL:X61554; NID:g47327; PID:g47328
#experimental_source Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991
GENETICS
#gene speA
CLASSIFICATION
KEYWORDS #superfamily enterotoxin B
FEATURE
1-30
31-251
SUMMARY #domain signal sequence #status predicted #label SIG
#product exotoxin type A #status predicted #label MAT
#length 251 #molecular-weight 29246 #checksum 1475
Query Match 33.9%; Score 80; DB 2; Length 251;
Best Local Similarity 50.0%; Pred. No. 1.08e+00;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
DB 162 DIETNKKKWTQDELNYKVRK 181
QY 10 ELDYNNKKRATVOELDYNNKK 29
RESULT 4
ENTRY E70109 #type complete
TITLE hypothetical protein BB0077 - Lyme disease spirochete
ORGANISM #formal_name Borrelia burgdorferi #common_name Lyme disease spirochete
DATE 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998
ACCESSIONS E70109
REFERENCE A70100
#authors Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickley, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gokeyne, J.; Weidman, J.; Utechtack, T.; Matthey, L.; McDonald, L.; Artlach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
#journal Nature (1997) 390:580-586
#title Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
#cross-references MUID:98065943
#accession E70109
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-342 #label KLE
#cross-references GB:AE001120; GB:AE000783; NID:g2687951; PID:g2687958; TIGR:BB0077
SUMMARY #experimental_source strain B31
#length 342 #molecular-weight 41049 #checksum 299
Query Match 33.5%; Score 79; DB 2; Length 342;
Best Local Similarity 30.3%; Pred. No. 1.45e+00;
Matches 10; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
DB 81 YDTKDKRRELYDNLNNKIOEIEYDKSKTLE 113
QY 1 YNNKKRATVOELDYNNKKRATVOELDYNNKKATVE 33
RESULT 5
ENTRY T00263 #type complete
TITLE hypothetical protein KIAA0480 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
ACCESSIONS T00263
REFERENCE 214085
#authors Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.;

```

#journal      Nakajima, D.; Nomura, N.; Ohara, O.
#title        DNA Res. (1997) 4:345-349
               Characterization of cDNA clones in size-fractionated cDNA
               libraries from human brain.
#accession    T00263
               Preliminary; translated from GB/EMBL/DBJ
#status       ##molecule_type mRNA
               ##residues     1-1252 ##label SEK
               ##cross-references EMBL:AB007949; NID:d1225358; PID:d1033287
               ##experimental_source brain
GENETICS
#map_position 1
#note         KIAA0480
SUMMARY       #length 1252 #molecular-weight 142461 #checksum 6996

Query Match          33.5%; Score 79; DB 2; Length 1252;
Best Local Similarity 33.3%; Pred. No. 1.45e+00;
Matches 11; Conservative 11; Mismatches 8; Indels 3; Gaps 3;

Db   389 KKSEIKETIYTKLKSKIED-AFSGEGKSDVLL 420
Qy   4 KKATVQELDYNK-KKATVQELDYNNK-KATVEL 34
              ||::||::| ||:::||::||
RESULT      6
ENTRY       S18789 #type fragment
TITLE       exotoxin A precursor (allele 4) - Streptococcus pyogenes
             (strain MGAS262 isolate California) (fragment)
ALTERNATE_NAMES
ORGANISM    scarlet fever toxin
            #formal_name Streptococcus pyogenes
            strain MGAS262 isolate California
            29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
            25-Mar-1998
ACCESSIONS S18789
REFERENCE   S18782
            Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
            J. Exp. Med. (1991) 174:1271-1274
            Characterization and clonal distribution of four alleles of
            the speA gene encoding pyrogenic exotoxin A (scarlet fever
            toxin) in Streptococcus pyogenes.
            PMID:92044323
            #cross-references M01D:92044323
            #accession S18789
            #status     nucleic acid sequence not shown; translation not shown
            ##molecule_type DNA
            ##residues  1-236 ##label NEL
            ##cross-references EMBL:X61573; NID:g47303; PID:g47304
            ##note      the nucleotide sequence was submitted to the EMBL Data
                        Library, September 1991
GENETICS
#gene        speA
CLASSIFICATION
KEYWORDS     #superfamily enterotoxin B
FEATURE      exotoxin
            1-22
                #domain signal sequence (fragment) #status predicted
                #label SIC\
                #product exotoxin A (fragment) #status predicted #label
                Mat
SUMMARY       #length 236 #checksum 3493

Query Match          32.2%; Score 76; DB 2; Length 236;
Best Local Similarity 45.0%; Pred. NO. 3.4e+00;
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db   154 DIETSKMKWTAQGLDYKVR 173
Qy   10 ELDTNKKKATVQELDYNNKK 29

```

```

DATE 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change
13-Mar-1997
ACCESSIONS S67483
REFERENCE S67483
#authors Trottein, F.; Cowman, A.F.
#journal Eur. J. Biochem. (1995) 227:214-225
#title Molecular cloning and sequence of two novel P-type
adenosinetriphosphatases from Plasmodium falciparum.
#cross-references M3D:95154293
#accession S67483
#status Preliminary
##molecule_type DNA
##residues 1-1553 ##label TRO
##cross-references EMBL:U16955
GENETICS
#introns 17/2
SUMMARY #length 1553 #molecular-weight 178919 #checksum 8281
Query Match 32.2%; Score 76; DB 2; Length 1553;
Best Local Similarity 32.4%; Pred. No. 3,41e+00;
Matches 12; Conservative 12; Mismatches 10; Indels 3; Gaps 3;
Db 292 FEKDKIDVENIGIOELKKTTEIEYKRRKLSVDL 328
::|||::: |||:::|
Oy 1 YNK-KKATVQELDYNNK-KATVQELDYNNKK-ATVEL 34
RESULT 8
ENTRY #type fragment
TITLE reticulocyte-binding protein 2 - Plasmodium vivax (fragment)
ORGANISM #formal_name Plasmodium vivax
DATE 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
09-Sep-1997
ACCESSIONS B42771
REFERENCE A42771
#authors Galinski, M.R.; Medina, C.C.; Inravallo, P.; Barnwell, J.W.
#journal Cell (1992) 69:1213-1226
#title A reticulocyte-binding protein complex of Plasmodium vivax
merozoites.
#cross-references M3D:92315338
#accession B42771
#status preliminary; nucleic acid sequence not shown;
translational not shown
##molecule_type DNA
##residues 1-1252 ##label GAL
##cross-references GB:M88098; NID:g160627; PID:g160628
##experimental_source strain Belen, merozoites
GENETICS
#gene RBP2
SUMMARY #length 1252 #checksum 7885
Query Match 31.8%; Score 75; DB 2; Length 1252;
Best Local Similarity 44.8%; Pred. No. 4,52e+00;
Matches 13; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
Db 753 TAOELKESKNNVLETE-NMSKNTNELD 780
||||:::| |:::| |
Oy 7 TYQELDYNNKKATVQELDYNNKKATVELD 35
RESULT 9
ENTRY #type complete
TITLE enterotoxin C3 - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
20-Mar-1998
ACCESSIONS S11885
REFERENCE S11885
#authors Howde, C.J.; Hackett, S.P.; Bohach, G.A.
#journal Mol. Gen. Genet. (1990) 220:329-333
#title Nucleotide sequence of the staphylococcal enterotoxin C3
gene: sequence comparison of all three type C
staphylococcal enterotoxins.

```


Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
Murphy, L.; Oliver, S.; Osborne, J.; Oual, M.A.;
Rajandream, M.A.; Rogers, J.; Rutler, S.; Seeger, K.;
Skellon, S.; Squares, S.; Squires, R.; Sulston, J.E.;
Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature (1998) 393:537-544
#journal
#title Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.
#cross-references MUID:98295987
#accession H70914
#status preliminary; nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-422 ##label COL
##cross-references GB:Z95844; GB:AL123456; NID:93250713; PID:e318874;
PID:g2131067
##experimental_source strain H37Rv
GENETICS
#gene Rv1429
SUMMARY #length 422 #molecular_weight 46898 #checksum 4542
Query Match 30.9%; Score 73; DB 2; Length 422;
Best Local Similarity 39.1%; Pred. No. 7.90e+00;
Matches 9; Conservative 9; Mismatches 4; Indels 1; Gaps 1;
Db 24 ISEL-FDKMKAIRGLDYDARMA 45
 : ||:::||||::|||:::
OY 8 VOELDYNKKKATVOELDYNKKKA 30

Search completed: Tue Aug 31 19:23:56 1999
Job time : 26 secs.

THIS PAGE BLANK (USPTO)

[W] [E] [R] [E] [I] (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:21:52 1999; Maspar time 3.04 Seconds

Tabular output not generated. 324.975 Million cell updates/sec

Title: >US-09-150-947-8

Description: (1-35) from US09150947.pep

Sequence: 1 YNKKKATVQELDYNNKKATVQELDYNNKKATVELD 35

Scoring table: PAM 150

Gap 11

Searched: 77977 segs, 28268293 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot37

1:swissprot

Statistics: Mean 31.279; Variance 62.483; scale 0.501

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 80 | 33.9 | 251 | 1 | SPEA_STRPY EXOTOXIN TYPE A PRECUR | 2.94e+01 |
| 2 | 75 | 31.8 | 1251 | 1 | RBP2_PLAVB RETICULOCYTE BINDING P | 1.44e+00 |
| 3 | 74 | 31.4 | 266 | 1 | ETC3_STPAU ENTEROTOXIN TYPE C-3 P | 1.97e+00 |
| 4 | 74 | 31.4 | 266 | 1 | ETC1_STPAU ENTEROTOXIN TYPE C-1 P | 1.97e+00 |
| 5 | 74 | 31.4 | 266 | 1 | ETC2_STPAU ENTEROTOXIN TYPE C-2 P | 1.97e+00 |
| 6 | 74 | 31.4 | 459 | 1 | THIC_STVY3 THIAMIN BIOSYNTHESIS P | 1.97e+00 |
| 7 | 74 | 31.4 | 641 | 1 | SAC2_YEAST SAC2 PROTEIN. | 1.97e+00 |
| 8 | 73 | 30.9 | 266 | 1 | ETXB_STPAU ENTEROTOXIN TYPE B PRE | 2.69e+00 |
| 9 | 73 | 30.9 | 751 | 1 | YLX5_CAEEL HYPOTHETICAL 84.8 KD P | 2.69e+00 |
| 10 | 73 | 30.9 | 2194 | 1 | GLSN_MEDSA GLUTAMATE SYNTHASE [NA | 2.69e+00 |
| 11 | 73 | 30.9 | 4466 | 1 | DYHC_TRIGR DYNEIN BETA CHAIN, CIT | 2.69e+00 |
| 12 | 72 | 30.5 | 130 | 1 | Y04M_BP14 HYPOTHETICAL 15.2 KD P | 3.65e+00 |
| 13 | 72 | 30.5 | 227 | 1 | Y443_METJA HYPOTHETICAL PROTEIN M | 3.65e+00 |
| 14 | 72 | 30.5 | 290 | 1 | YABG_BACSU HYPOTHETICAL 33.3 KD P | 3.65e+00 |
| 15 | 72 | 30.5 | 340 | 1 | YHVG_YEAST HYPOTHETICAL 40.4 KD P | 3.65e+00 |
| 16 | 72 | 30.5 | 511 | 1 | RT04_PROMI MITOCHONDRIAL RIBOSOMA | 3.65e+00 |
| 17 | 72 | 30.5 | 561 | 1 | CP51_USTMA CYTOCHROME P450 51 (EC | 3.65e+00 |
| 18 | 71 | 30.1 | 85 | 1 | Y084_BESP1 HYPOTHETICAL 10.2 KD P | 4.95e+00 |
| 19 | 71 | 30.1 | 289 | 1 | Y084_MYCPN HYPOTHETICAL PROTEIN M | 4.95e+00 |
| 20 | 71 | 30.1 | 946 | 1 | RGCI_HUMAN RHO-GAP HEMATOPOIETIC | 4.95e+00 |
| 21 | 70 | 29.7 | 135 | 1 | ATPE_MARPO ATP SYNTHASE EPSILON C | 6.69e+00 |
| 22 | 70 | 29.7 | 281 | 1 | Y054_METJA HYPOTHETICAL PROTEIN M | 6.69e+00 |
| 23 | 70 | 29.7 | 415 | 1 | IL5R_MOUSE INTERLEUKIN-5 RECEPTOR | 6.69e+00 |

| RESULT | 1 | ALIGNMENTS |
|--------|--|------------------------|
| ID | SPEA_STRPY | STANDARD: PRT: 251 AA. |
| AC | P08095; | |
| DT | 01-AUG-1988 (REL. 08, CREATED) | |
| DT | 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) | |
| DT | 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) | |
| DE | EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN) | |
| DE | (SPE A). | |
| GN | SPEA. | |
| OS | STREPTOCOCCUS PYOGENES. | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; | |
| OC | STREPTOCOCCUS. | |
| RN | (1) | |
| RP | SEQUENCE FROM N.A. | |
| RX | MEDLINE: 86166804. | |
| RA | WEEKS C.R., FERRETTI J.J.; | |
| RT | "Nucleotide sequence of the type A streptococcal exotoxin | |
| RT | (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage | |
| RT | 112." | |
| RL | INFECT. IMMUN. 52:144-150(1986). | |
| RN | [2] | |
| RP | SEQUENCE FROM N.A. | |
| RX | MEDLINE: 86284313. | |
| RA | JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.; | |
| RT | "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is | |
| RT | related to staphylococcus aureus enterotoxin B." | |
| RL | MOL. GEN. GENET. 203:354-356(1986). | |
| CC | -1- DISEASE: THE STREPTOCOCCAL PYOGENIC TOXINS A, B, AND C ARE | |
| CC | THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET | |
| CC | FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE | |
| CC | DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC | |
| CC | FEVER. | |
| CC | -1- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE 112. | |
| CC | -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES | |
| CC | PYROGENIC EXOTOXINS ARE ALL RELATED. | |
| CC | ***** | |
| CC | THIS SWISS-PROT entry is copyright. It is produced through a collaboration | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - | |
| CC | the European Bioinformatics Institute. There are no restrictions on its | |
| CC | use by non-profit institutions as long as its content is in no way | |
| CC | modified and this statement is not removed. Usage by and for commercial | |
| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | |
| CC | or send an email to license@sib-sib.ch). | |
| CC | ***** | |
| CC | EMBL: U0453; G1877430; .. | |
| CC | EMBL: X03929; G47442; .. | |
| CC | DR PIR: A26152; A26152. | |

DR PIR: S29659; S29659.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PRAM: PF01123; STAP_STRP_TOXIN; 1.
 DR HSP: P01552; 1SER.
 KW TOXIN; SIGNAL.
 FT SIGNAL 1 30
 FT CHAIN 31 251
 FT CONFLICT 6 6
 FT CONFLICT 17 18
 FT CONFLICT 25 35
 FT CONFLICT 40 40
 FT CONFLICT 43 43
 FT CONFLICT 47 59
 FT CONFLICT 129 129
 FT CONFLICT 165 178
 FT CONFLICT 251 AA; 29246 MW; 535FE465 CRC32;
 FT SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;
 FT REF. 2).

Query Match 33.9%; Score 80; DB 1; Length 251;
 Best Local Similarity 50.0%; Pred. No. 2.94e-01;
 Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 162 DIETNKKMTAQLDYVVRK 181
 10 ELDYNNKKATVQELDYNNKK 29

RESULT 2
 ID RBP2_PLAVB STANDARD; PRT; 1251 AA.
 AC 000799;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).
 GN RBP2.
 OS PLASMODIUM VIVAX (STRAIN BELEM).
 OC EUKARYOT: ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92315338.
 RA GALINSKI M.R., MEDINA C.C., INGRAVALLO P., BARNWELL J.W.;
 RT "A reticulocyte-binding protein complex of Plasmodium vivax
 merozoites".
 RL CELL 69:1213-1226(1992).
 CC -1- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO
 CC HUMAN RETICULOCYTE CELLS.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M88098; G160628; .
 KW MALARIA; RECEPTOR; MEMBRANE.
 FT NON TER 1 1
 FT NON TER 1 1
 FT SEQUENCE 1251 AA; 143741 MW; C53767B7 CRC32;
 SQ

Query Match 31.8%; Score 75; DB 1; Length 1251;
 Best Local Similarity 44.8%; Pred. No. 1.44e+00;
 Matches 13; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

DB 753 TAQLKFEESKNNVLETE-NKSKNTNEID 780
 1 111 111 111 111 111 111 111 111 111 111 111 111
 QY 7 TVALDYNNKKATVQELDYNNKKATVEID 35

RESULT 3
 ID ETC3_STAUV STANDARD; PRT; 266 AA.
 AC P23313;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
 GN ETC3.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90220508.
 RA HOVDE C.J., HACKETT S.P., BOHACH G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 RT sequence comparison of all three type C staphylococcal
 RT enterotoxins".
 RL MOL. GEN. GENET. 220:329-333(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECEPT.
 RX MEDLINE: 97064178.
 RA FIELDS B.A., MALCHIODI E.L., LI H., YSEHN X., STAUFFACHER C.V.,
 RA SCHLEIBERT P.M., KARJALAINEN K., MARTIUSZAK R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen".
 RL NATURE 384:188-192(1996).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: X51661; G46571; .
 DR PIR: S11885; S11885.
 DR PDB: 1JCK; 12-NOV-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PRAM: PF01123; STAP_STRP_TOXIN; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 28 266
 FT DISUFID 120 137
 FT SEQUENCE 266 AA; 30671 MW; 27B4DDDA CRC32;
 SQ

Query Match 31.4%; Score 74; DB 1; Length 266;
 Best Local Similarity 44.0%; Pred. No. 1.97e+00;
 Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 DB 163 YENKNTISEVOTDKRSVTAQELD 187
 1 111 111 111 111 111 111 111 111 111 111 111 111
 QY 1 YNNKKATVQ-ELDYNNKKATVQELD 24

RESULT 4
 ID ETC1_STAUV STANDARD; PRT; 266 AA.
 AC P01553;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).
 GN ETC1.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 RN [1]


```

RP SEQUENCE FROM N.A.
RX MEDLINE: 88038352.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RL relatedness to other pyrogenic toxins."
RM MOL. GEN. GENET. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE: 83213327.
RA SCHMIDT J.J., SPERO L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1."
RL J. BIOL. CHEM. 258:6300-6306(1983).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X05815; G46567; -
DR PIR: A01816; ENSACL.
DR PIR: S06356; S06356.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph-Strep-toxin; 1.
DR HSP: P34071; ISE2.
DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN.
KW CHAIN 1 27
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-1.
FT DISULFID 120 137
FT CONFLICT 177 177
FT SEQUENCE 266 AA; 30546 MW; FE00255A CRC32.
SQ
Query Match 31.4%; Score 74; DB 1; Length 266;
Best Local Similarity 44.0%; Pred. No. 1.97e+00;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
Db 163 YENKNTISFEVOTDKSVTAQELD 187
Oy 1 YNKKKATVQ-ELDYNKKKATVQELD 24

RESULT 5
ID ETC2_STAUB STANDARD: PRT: 266 AA.
AC P34071;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ETC2.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE: 89277549.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RL enterotoxins C1 and C2."
RL INFECT. IMMUN. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE: 96027099.
RA PARAGORGIU A.C., ACHARYA K.R., SHAPIRO R., PASSALACQUA E.F.,
RA BREHM R.D., TRAMER H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT staphylococcus aureus reveals a zinc-binding site."

```

```

RL STRUCTURE 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE: 96022987.
RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
RL enterotoxins."
RL NAT. STRUCT. BIOL. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE: 97334373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. MOL. BIOL. 269:270-280(1997).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC PIR: A60114; A60114.
DR PDB: 1STE; 23-DEC-96.
DR PDB: 1SE2; 08-MAR-96.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph-Strep-toxin; 1.
DR ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
KW CHAIN 1 27
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; A115FD37 CRC32.
Query Match 31.4%; Score 74; DB 1; Length 266;
Best Local Similarity 44.0%; Pred. No. 1.97e+00;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
Db 163 YENKNTISFEVOTDKSVTAQELD 187
Oy 1 YNKKKATVQ-ELDYNKKKATVQELD 24

RESULT 6
ID THIC_SYNY3 STANDARD: PRT: 459 AA.
AC O55894;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE THIAMIN BIOSYNTHESIS PROTEIN THIC.
GN THIC OR SLR0118.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA: CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96127529.
RA KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
RA SUGIURA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 648 to 928 of the genome."
RL DNA RES. 2:153-166(1995).
CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF THE HYDROMETHYLPYRIMIDINE.
CC (HMP) MOETY OF THIAMIN (4-AMINO-2-METHYL-5-
CC HYDROXYMETHYLPYRIMIDINE) (BY SIMILARITY).
CC -1- PATHWAY: THIAMIN BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: D64004; G1208488; -
KW THIAMIN BIOSYNTHESIS.
SQ SEQUENCE 459 AA; 51137 MW; 6233819E CRC32;

Query Match 31.4%; Score 74; DB 1; Length 459;
Best Local Similarity 23.3%; Pred. No. 1.97e+00;
Matches 7; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Db 13 TNSQMHYARKGVITEEDVAKRENLPVE 42
QY 6 ATYQELDYNNKKTATVQELDYNNKKTATVELD 35

RESULT 7 STANDARD: PRT: 641 AA.

AC P39904: 003379;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE SAC2 PROTEIN.
GN SAC2 OR YDR484W OR D8035.27.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCHAROMYCETALES;
RN SACCHAROMYCETACEAE; SACCHAROMYCES.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-S288C;
RX MEDLINE: 95274323.

RA KOELLING R., LEE A., CHEN E.Y., BOTSTEIN D.;
RT "Nucleotide sequence of the SAC2 gene of *Saccharomyces cerevisiae*.";
RL YEAST 10:1211-1216(1994).
RL [2]
RN SEQUENCE FROM N.A.
RP DIETRICH F.S., MULLIGAN J., ALLEN E., ARAUJO R., AVILES E.,
RA BERNI A., CARPENTER J., CHEN E., CHERRY J.M., CHUNG E., DUNCAN M.,
RA HUNNICKE-SMITH S., HIMAN R., KOMP C., LASHKARI D., LEW H., LIN D.,
RA MOSDALE D., NAKAHARA K., NAMATH A., OEFNER P., OH C., PETEL F.X.,
RA ROBERTS D., SCHRAMM S., SCHROEDER M., SHOGREN T., SHROFF N.,
RA WINANT A., YELTON M., BOTSTEIN D., DAVIS R.W.;
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: 229988; G454893; -
DR EMBL: U33050; G927740; -
DR PIR: S42036; S42036.
DR PIR: S46603; S46602.
DR SGD: L0001791; SAC2.
KW CYTOSKELETON.

FT CONFLICT 204 KRLIIS -> EKYTYF (IN REF. 1).
SQ SEQUENCE 641 AA; 74332 MW; EDD81473 CRC32;

Query Match 31.4%; Score 74; DB 1; Length 641;
Best Local Similarity 47.8%; Pred. No. 1.97e+00;
Matches 11; Conservative 5; Mismatches 5; Indels 2; Gaps 2;

Db 93 QDLDFIKKSNLEQSLFENSTK 115
QY 9 QELDYNNKKTATVQELDYNNKKTAT 29

RESULT 8

ID ETXB STAAU STANDARD: PRT: 266 AA.
AC P01552;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN ENTB.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN STAPHYLOCOCCUS.
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE: 86168029.
RA JONES C.L., KHAN S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from *Staphylococcus aureus*.";
RL J. BACTERIOL. 166:29-33(1986).
RN [2]
RN SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE: 85298255.
RA RANELLI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in *Escherichia coli* and staphylococcus aureus.";
RL PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985).
RN [3]
RN SEQUENCE OF 28-266 (S-6).
RX MEDLINE: 71007902.
RA HUANG I.-Y., BERGDOLL M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";
RL J. BIOL. CHEM. 245:3518-3525(1970).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE: 93063291.
RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL NATURE 359:801-806(1992).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE: 94203282.
RA JARDETEK T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G.,
RA CHI Y.I., STAEFFACHER C., STROMINGER J.L., WILEY D.C.;
RT "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";
RL NATURE 368:711-718(1994).
RN [6]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE: 98181012.
RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
RT "Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors.";
RL J. MOL. BIOL. 277:61-79(1998).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOCENES PYROGENIC EXOTOXINS ARE ALL RELATED.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M1118; G153000; -
DR PIR: A01815; ENSAB6.
DR PIR: S27360; S27360.
DR PDB: 1SEB; 20-JUN-96.
DR PDB: 2SEB; 28-JAN-98.
DR PDB: 3SEB; 27-MAY-98.

```

FT TRANSMEM 583 603 POTENTIAL.
FT TRANSMEM 614 634 POTENTIAL.
FT TRANSMEM 678 698 POTENTIAL.
SQ SEQUENCE 751 AA; 84832 MW; 9EBA4F9E CRC32:

Query Match 30.9%; Score 73; DB 1; Length 751;
Best Local Similarity 31.8%; Pred. No. 2,696+00;
Matches 7; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Db 713 EELVDYDRKKSMTENTVIOKRRT 734
OY 9 OELDYNNKKATVOELDYNNKKKA 30

RESULT 10
ID GLSN MEDSA STANDARD; PRT; 2194 AA.
AC Q03460.
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14) (NADH-GOGAT).
OS MEDICAGO SATIVA (ALPULFA)
OC EUCARIOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMERIOPHYTA; TRACHEOPHYTA;
OC EUHYALLOPHYTES; SPEMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC FABALES; FABACEAE; PAPILIONOIDEAE; MEDICAGO.
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 102-114.
RX MEDLINE: 93200806.
RA GREGGERSON R.G., MILLER S.S., TWARY S.N., GANTT J.S., VANCE C.P.;
RT "Molecular characterization of NADH-dependent glutamate synthase from
RT alfalfa nodules.";
RL PLANT CELL 5:215-226(1993).
CC -1- CATALYTIC ACTIVITY: 2 L-GLUTAMATE + NAD(+) = L-GLUTAMINE +
CC -2- OXOSULFURATE + NADH.
CC -3- COFACTOR: IRON-SULFUR; FAD AND FMN FLAVOPROTEIN.
CC -4- PATHWAY: GLUTAMINE SYNTHETASE/GOGAT PATHWAY WHICH IS INVOLVED
CC IN THE ASSIMILATION OF AMMONIA.
CC -5- SUBUNIT: MONOMER.
CC -6- SUBCELLULAR LOCATION: AMYLOPLAST (POTENTIAL).
CC -7- TISSUE SPECIFICITY: ROOT NODULE.
CC -8- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
-----
CC -9- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/sib.ch).
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: L01660; G166412; -.
DR PIR: J01977; J01977.
KW OXIDOREDUCTASE; IRON-SULFUR; 3FE-4S; FLAVOPROTEIN; FAD; FMN;
KW CHLOROPLAST; AMYLOPLAST; TRANSIT PEPTIDE; GLUTAMATE BIOSYNTHESIS.
FT TRANSIT 1 101
FT CHAIN 102 2194 GLUTAMATE SYNTHASE [NADH].
FT DOMAIN 102 456 GLUTAMINE AMIDOTRANSFERASE (POTENTIAL).
FT NP_BIND 1193 1250 FMN (BY SIMILARITY).
FT METAL 1246 1246 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT METAL 1252 1252 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT METAL 1257 1257 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT NP_BIND 1974 1988 NAD (POTENTIAL).
SQ SEQUENCE 2194 AA; 240373 MW; A1397C5B CRC32:

Query Match 30.9%; Score 73; DB 1; Length 2194;
Best Local Similarity 21.2%; Pred. No. 2,696+00;
Matches 7; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Db 678 KEMBAIKKMNIRGMRSKYIDITYSKERGKGLCE 710
OY 3 KKKATVOELDYNNKKKATVOELDYNNKKKATVELD 35

```

```

RESULT 11
ID DYNC TRIGR STANDARD: PRT: 4466 AA.
AC P23096.
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE DYNEIN BETA CHAIN, CILIARY
OS TRIPNEUSTES GRATILDA (HAWAIIAN SEA URCHIN).
OC EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA.
OC EUCHEILINOIDEA; ECHINACEA; TEMNOPLEROIDA; TOXOPNEUSTIDAE; TRIPNEUSTES.
(1)
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RF TISSUE-BLASTULA:
RX MEDLINE: 91326103.
RA GIBBONS I.R., GIBBONS B.H., MCCZ G., ASAI D.J.:
RT "Multiple nucleotide-binding sites in the sequence of dynein beta
RT heavy chain".
RL NATURE 352:640-643(1991).
(2)
RN SEQUENCE FROM N.A.
RX MEDLINE: 92020893.
RA GIBBONS I.R., ASAI D.J., CHING N.S., DOLECKI G.J., MCCZ G.,
RA PHILLIPSON C.A., REN H., TANG W.Y., GIBBONS B.H.:
RT "A PCR procedure to determine the sequence of large polypeptides by
RT rapid walking through a cDNA library".
RL PROC. NATL. ACAD. SCI. U.S.A. 88:8563-8567(1991).
(1) FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -1 SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS (ALPHA AND BETA),
CC THREE INTERMEDIATE CHAINS AND SEVERAL LIGHT CHAINS.
CC -1 SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X59603: G10710: -
DR PIR: S17653: S17653
KW MOTOR PROTEIN; MICROTUBULES; DYNEIN; ATP-BINDING; FLAGELLA;
KW HEPTAD REPEAT PATTERN.
FT FT NP_BIND 154 161 ATP (POTENTIAL).
FT FT NP_BIND 1852 1859 ATP (POTENTIAL).
FT FT NP_BIND 2133 2140 ATP (POTENTIAL).
FT FT NP_BIND 2460 2467 ATP (POTENTIAL).
FT FT NP_BIND 2805 2812 ATP (POTENTIAL).
FT FT VARIANT 611 615 MISSING.
FT FT VARIANT 3356 3358 LPPG -> LTNQFCCFWTAG.
SQ SEQUENCE 4466 AA; 511771 MW; 85541010 CRC32;
Query Match 30.9%; Score 73; DB 1; Length 4466;
Best Local Similarity 34.3%; Pred. No. 2; 69e+00;
Matches 12; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
Db 727 YNKRATVLEVEFPLIEGOLADIDRLKQAESELN 761
||| |||::: ||| ||| |||:
Qy 1 YNKRKATVQELDYNNKRRKATVQELDYNNKRRATYELD 35

RESULT 12
ID Y04M.BPT4 STANDARD: PRT: 130 AA.
AC P39252.
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 15.2 KD PROTEIN IN NRDC-MOBD INTERGENIC REGION.
DE Y04M OR NRDC.1.
OS BACTERIOPHAGE T4.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; MYOVIRIDAE;

```

```

CC T4-LIKE PHAGES.
RN [1]
RP SEQUENCE FROM N.A.
RA KUTTER E.M.;
RL SUBMITTED (NOV-1994) TO THE SWISS-PROT DATA BANK.
RN [2]
RP SEQUENCE OF 57-130 FROM N.A.
RC STRAIN=C;
RX MEDLINE; 87203398.
RA TOMASCHEWSKI J., RUEGER W.;
RT "Nucleotide sequence and primary structures of gene products coded
RL for by the T4 genome between map positions 48,266 kb and 39,166 kb."
NUCLEIC ACIDS RES. 15:3633-3633(1987).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y00122; NOT_ANNOTATED_CDS.
CC PIR: H30292; H30292.
CC HYPOTHEETICAL PROTEIN.
KW SEQUENCE 130 AA; 15181 MW; C9C24811 CRC32;
SQ
Query Match 30.5%; Score 72; DB 1; Length 130;
Best Local Similarity 34.6%; Pred. No. 3.65e+00;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Db 94 YKNMLSEVDIIYKHKEGTQGLDYPD 119
OY 1 YNKKATVQELDYNNKKKATVQELDYN 26
::: |:: | | | |
RESULT 13
ID Y443_METJA STANDARD; PRT; 227 AA.
AC Q57885;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHEETICAL PROTEIN M00443.
GN M0443.
OS METHANOCOCCUS JANNA SCHII.
SC ARCHAEA; EURARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
NC METHANOCOCCUS.
CC [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLATON R.A., GOCAYNE J.D.,
RA KERLANAGE A.R., DOUGHERTY B.A., TOM J.-F., ADAMS M.D., RETCH C.I.,
RA OVERBEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODER A.,
RA SCOTT J.L., GEOHAGSEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UPTON R.T., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BOROOVSKY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RN jannaschii."
RL SCIENCE 273:1058-1073(1996).
CC -----
CC -I- SIMILARITY: SOME, TO S.CREVISIAE YCL59C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U67495; G1591147; -.

```

DR TIGR: M00443: -
 DR PFAM: PF00013: KH-domain: 1.
 DR HSP: P02633: 2BCB
 KW HYPOTHETICAL PROTEIN
 SQ SEQUENCE 227 AA: 25839 MW: 669AE796 CRC32:

Query Match 30.5%; Score 72; DB 1; Length 227;
 Best Local Similarity 32.3%; Pred. No. 3.65e+00;
 Matches 10; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

Db 195 KKKSDVDEL-YEKMPNPEIEIEDEDEIE 224
 QY 3 KKKATVQELDYNKKATVQELDYNKKATVE 33

RESULT 14
 ID YABG_BACSU STANDARD; PRT; 290 AA.
 AC P37548;
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DE 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 GN HYPOTHETICAL 33.3 KD PROTEIN IN KSGA-VEG INTERGENIC REGION.
 GN YABG.
 OS BACILLUS SUBTILIS.
 OC BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP: BACILLACEAE:
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE: 96051385.
 RA OGASAWARA N., NAKAI S., YOSHIKAWA H.;
 RT "Systematic sequencing of the 180 kilobase region of the *Bacillus*
 subtilis chromosome containing the replication origin";
 RL DNA RES. 1:1-14(1994).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D26185; G467432; -
 DR EMBL: Z99104; E181976; -
 DR SUBTILIST; BG10106; YABG.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 290 AA: 33318 MW: EF47CB60 CRC32:

Query Match 30.5%; Score 72; DB 1; Length 290;
 Best Local Similarity 30.6%; Pred. No. 3.65e+00;
 Matches 11; Conservative 10; Mismatches 13; Indels 2; Gaps 2;

Db 169 YSKOKGIDDLNAYRSHKHVETVOTAKKIP-HLD 203
 QY 1 YNKKKATVQELD-YNKKKATVQELDYNKKATVELD 35

RESULT 15
 ID YH6-YEAST STANDARD; PRT; 340 AA.
 AC P38852;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 40.4 KD PROTEIN IN SPO16-REC104 INTERGENIC REGION.
 GN YHR156C.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOCYCETES: SACCAROMYCETALES;
 OC SACCAROMYCETACEAE: SACCAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RX MEDLINE: 94378003.

RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
 RA DU Z., FAVELLO A., FULTON L., GATUNG S., GEISEL C., KIRSTEN J.,
 RA KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
 RA LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENZES S., MOUSER L.,
 RA NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
 RA VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
 RA VAUDIN M.;
 RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
 VII";
 RL SCIENCE 265:2077-2082(1994).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U10397; G500664; -
 DR PIR: S46768; S46768.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 340 AA: 40368 MW: AAF26089 CRC32:

Query Match 30.5%; Score 72; DB 1; Length 340;
 Best Local Similarity 40.0%; Pred. No. 3.65e+00;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Db 84 KKKSKIQQLDIAEFKKENLADLDY 108
 QY 2 NKKKATVQELDYNK-KKATVQELDY 25

Search completed: Tue Aug 31 19:22:04 1999
 Job time : 12 secs.

THIS PAGE BLANK (USPTO)

MIRAGE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msrch_p protein - protein database search, using Smith-Waterman algorithm
kun on: Tue Aug 31 19:22:21 1999; Maspar time 6.56 Seconds
291.220 Million cell updates/sec
Tabular output not generated.

Title: >US-09-150-947-8
Description: (1-35) from US09150947.pep
Perfect Score: 236
Sequence: 1 INKKKATVQELDYNNKKKATVQELDYNNKKKATVELD 35

Scoring table:
PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl9
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 29.830; Variance 64.583; scale 0.462

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------|------------------------|-----------|
| 1 | 80 | 33.9 | 236 | 2 | P97163 | TYPE A EXOTOXIN PRECUR | 7.39e-01 |
| 2 | 80 | 33.9 | 236 | 2 | Q54779 | TYPE A EXOTOXIN PRECUR | 7.39e-01 |
| 3 | 80 | 33.9 | 236 | 2 | Q57453 | TYPE A EXOTOXIN PRECUR | 7.39e-01 |
| 4 | 79 | 33.5 | 342 | 2 | Q51104 | HYPOTHELICAL 41.0 KD P | 1.00e+00 |
| 5 | 79 | 33.5 | 1252 | 4 | Q75068 | KIAA0480 PROTEIN. | 1.00e+00 |
| 6 | 76 | 32.2 | 236 | 2 | Q54696 | TYPE A EXOTOXIN PRECUR | 2.49e+00 |
| 7 | 76 | 32.2 | 1501 | 5 | Q27720 | ATPASE 2 | 3.37e+00 |
| 8 | 75 | 31.8 | 1011 | 5 | Q61638 | DYNAMIN ASSOCIATED PRO | 3.37e+00 |
| 9 | 75 | 31.8 | 1094 | 5 | Q61618 | DYNAMIN ASSOCIATED PRO | 3.37e+00 |
| 10 | 74 | 31.4 | 239 | 2 | Q06532 | ENTEROTOXIN TYPE C-7 (| 4.53e+00 |
| 11 | 74 | 31.4 | 239 | 2 | Q06535 | ENTEROTOXIN TYPE C-3 (| 4.53e+00 |
| 12 | 74 | 31.4 | 239 | 2 | Q06531 | ENTEROTOXIN TYPE C-4 (| 4.53e+00 |
| 13 | 74 | 31.4 | 239 | 2 | Q03678 | ENTEROTOXIN (FRAGMENT) | 4.53e+00 |
| 14 | 74 | 31.4 | 239 | 2 | Q06533 | ENTEROTOXIN TYPE C (SE | 4.53e+00 |
| 15 | 74 | 31.4 | 239 | 2 | Q06534 | ENTEROTOXIN TYPE C (SE | 4.53e+00 |
| 16 | 74 | 31.4 | 255 | 2 | Q46176 | (CLONES PG14.(1,2)). | 4.53e+00 |
| 17 | 74 | 31.4 | 260 | 2 | Q54738 | SUPERANTIGEN SSA. | 4.53e+00 |
| 18 | 74 | 31.4 | 260 | 2 | Q54739 | SUPERANTIGEN SSA. | 4.53e+00 |
| 19 | 74 | 31.4 | 260 | 2 | Q54971 | SUPERANTIGEN | 4.53e+00 |
| 20 | 74 | 31.4 | 1743 | 5 | Q19004 | SIMILANTO GLUCAN 1. | 4.53e+00 |

| | | | | | | | |
|----|----|------|------|----|--------|------------------------|----------|
| 21 | 73 | 30.9 | 76 | 2 | P70850 | ORF11. | 6.09e+00 |
| 22 | 73 | 30.9 | 167 | 11 | Q35648 | CENTRIN. | 6.09e+00 |
| 23 | 73 | 30.9 | 239 | 2 | Q05157 | TYPE C ENTEROTOXIN (FR | 6.09e+00 |
| 24 | 73 | 30.9 | 422 | 2 | Q06829 | HYPOTHELICAL 46.9 KD P | 6.09e+00 |
| 25 | 73 | 30.9 | 2194 | 10 | Q40360 | NADH-DEPENDENT GLUTAMA | 6.09e+00 |
| 26 | 72 | 30.5 | 249 | 8 | Q20173 | ORF249. | 8.16e+00 |
| 27 | 72 | 30.5 | 460 | 3 | Q60095 | HYPOTHELICAL 52.7 KD P | 8.16e+00 |
| 28 | 72 | 30.5 | 594 | 10 | Q22723 | FLIP17.5 PROTEIN. | 8.16e+00 |
| 29 | 71 | 30.1 | 3394 | 5 | Q77384 | MA3P6.11 PROTEIN. | 1.46e+01 |
| 30 | 70 | 29.7 | 116 | 14 | Q70199 | NEP (FRAGMENT). | 1.46e+01 |
| 31 | 70 | 29.7 | 207 | 14 | Q41781 | HIY-1 ISOLATE 92RW009 | 1.46e+01 |
| 32 | 70 | 29.7 | 228 | 5 | Q01841 | COSMID F56F4. | 1.46e+01 |
| 33 | 70 | 29.7 | 660 | 2 | Q57443 | TRANSFERRIN BINDING PR | 1.46e+01 |
| 34 | 70 | 29.7 | 793 | 2 | Q24997 | HYPOTHELICAL 94.3 KD P | 1.46e+01 |
| 35 | 70 | 29.7 | 2098 | 5 | Q25757 | CRP. | 1.46e+01 |
| 36 | 69 | 29.2 | 202 | 14 | Q91022 | NEP PROTEIN (FRAGMENT) | 1.94e+01 |
| 37 | 69 | 29.2 | 204 | 14 | Q92654 | NEP PROTEIN. | 1.94e+01 |
| 38 | 69 | 29.2 | 205 | 14 | Q91032 | NEP PROTEIN (FRAGMENT) | 1.94e+01 |
| 39 | 69 | 29.2 | 207 | 14 | Q91024 | NEP PROTEIN (FRAGMENT) | 1.94e+01 |
| 40 | 69 | 29.2 | 207 | 14 | Q91020 | NEP PROTEIN (FRAGMENT) | 1.94e+01 |
| 41 | 69 | 29.2 | 348 | 2 | Q67350 | CATION EFFLUX SYSTEM (| 1.94e+01 |
| 42 | 69 | 29.2 | 455 | 3 | Q14039 | HYPOTHELICAL 51.3 KD P | 1.94e+01 |
| 43 | 69 | 29.2 | 663 | 3 | Q42832 | PMT2. | 1.94e+01 |
| 44 | 69 | 29.2 | 1028 | 5 | Q45247 | C13B4.1 PROTEIN. | 1.94e+01 |
| 45 | 69 | 29.2 | 1089 | 14 | Q37061 | RNA-DEPENDENT RNA POLY | 1.94e+01 |

ALIGNMENTS

| RESULT | ID | PRELIMINARY; | PRT; | 236 AA. |
|--|---|--------------|-----------|------------------|
| AC | P97163; | P97164; | | |
| DT | 01-MAY-1997 (TREMBLREL. 03, CREATED) | | | |
| DT | 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE) | | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) | | | |
| DE | TYPE A EXOTOXIN PRECURSOR (FRAGMENT). | | | |
| OS | SEPA. | | | |
| GN | STREPTOCOCCUS PYOGENES. | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; | | | |
| OC | STREPTOCOCCUS. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRATIN-MGAS156; AND MGAS500; | | | |
| RX | MEDLINE; 92044323. | | | |
| RA | NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.; | | | |
| RT | "characterization and clonal distribution of four alleles of the speA | | | |
| RT | gene encoding pyrogenic exotoxin A (scarlet fever toxin) in | | | |
| RT | Streptococcus pyogenes." | | | |
| RL | J. EXP. MED. 174:1271-1274(1991). | | | |
| DR | EMBL; X61556; G47292; - | | | |
| DR | EMBL; X61557; G47320; - | | | |
| DR | EMBL; X61560; G47288; - | | | |
| DR | EMBL; X61555; G47310; - | | | |
| DR | EMBL; X61558; G47322; - | | | |
| DR | EMBL; X61559; G47294; - | | | |
| DR | EMBL; X61554; G47328; - | | | |
| DR | PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1. | | | |
| DR | PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1. | | | |
| DR | PFAM: PF01123; Staph_strep_toxin; 1. | | | |
| KW | SIGNAL. | | | |
| FT | NON_TER | 1 | 1 | POTENTIAL. |
| FT | SIGNAL | <1 | 22 | TYPE A EXOTOXIN. |
| FT | CHAIN | 23 | >236 | |
| FT | NON_TER | 236 | 236 | |
| SO | SEQUENCE | 236 AA; | 27454 MW; | 81AOC2FE CXC32; |
| Query Match | | | | |
| Best Local Similarity 33.9%; Score 80; DB 2; Length 236; | | | | |
| Matches 10; Conservativity 50.0%; Pred. No. 7.39e-01; | | | | |
| Mismatches 4; Indels 0; Gaps 0; | | | | |
| Db | 154 DIENKKKATVQELDYNNKKK 173 | | | |
| Oy | 10 ELDYNNKKATVQELDYNNKKK 29 | | | |

```
RESULT 2
ID 054779; PRELIMINARY; PRT: 236 AA.
AC 054779; 054613; 054736; 054741;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes."
RT J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61562; G47300; -
DR EMBL; X61563; G47302; -
DR EMBL; X61567; G47326; -
DR EMBL; X61561; G47298; -
DR EMBL; X61564; G47306; -
DR EMBL; X61565; G47312; -
DR EMBL; X61566; G47318; -

Query Match
Best Local Similarity 50.0%; Score 80; DB 2; Length 236;
Pred. No. 7.39e-01;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 154 DIETNRKKNVTAQELDYKVRK 173
OY 10 ELDYNNKKATVQELDYNNKK 29

RESULT 3
ID 057453; PRELIMINARY; PRT: 236 AA.
AC 057453;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS496;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSEY J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes."
RT J. EXP. MED. 174:1271-1274(1991).
DR EMBL; X61562; G47300; -
DR EMBL; X61563; G47302; -
DR EMBL; X61567; G47326; -
DR EMBL; X61561; G47298; -
DR EMBL; X61564; G47306; -
DR EMBL; X61565; G47312; -
DR EMBL; X61566; G47318; -

Query Match
Best Local Similarity 50.0%; Score 80; DB 2; Length 236;
Pred. No. 7.39e-01;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 154 DIETNRKKNVTAQELDYKVRK 173
OY 10 ELDYNNKKATVQELDYNNKK 29
```

```
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_strep_toxin; 1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 22
FT CHAIN 23 >236
FT NON_TER 236 236
SO SEQUENCE 236 AA; 27484 MW; A5EB1ECD CRC32;

Query Match
Best Local Similarity 50.0%; Score 80; DB 2; Length 236;
Pred. No. 7.39e-01;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 154 DIETNRKKNVTAQELDYKVRK 173
OY 10 ELDYNNKKATVQELDYNNKK 29

RESULT 4
ID 051104; PRELIMINARY; PRT: 342 AA.
AC 051104;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 41.0 KD PROTEIN.
GN BB0077.
OS BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
OC BACTERIA: SPIROCHAETALES; SPIROCHAETACEAE; BORRELIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35210 / B31;
RX MEDLINE; 98065943.
RA FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
RA LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GINN M.,
RA DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
RA PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
RA VAN VIGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
RA UTERACK T., WATHEY L., McDONALD L., ARTIACH P., BOWMAN C.,
RA GALLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
RA SMITH H.O., VENTER J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
burgdorferi."
RT NATURE 380:580-586(1997).
RL EMBL; AE001120; G2687958; -
DR TIGR; BB0077; -
KW HYPOTHETICAL PROTEIN.
SO SEQUENCE 342 AA; 41049 MW; 6D17DF40 CRC32;

Query Match
Best Local Similarity 30.3%; Score 79; DB 2; Length 342;
Pred. No. 1.00e+00;
Matches 10; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Db 81 YDTRKTRKEIYDNLNKKIQLQIEYDSKLTLE 113
OY 1 YNNKKATVQELDYNNKKATVQELDYNNKKATVE 33

RESULT 5
ID 075068; PRELIMINARY; PRT: 1252 AA.
AC 075068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE KIA0480 PROTEIN.
GN KIA0480.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 98116662.
```



```

RESULT      7
ID           027720      PRELIMINARY;      PRT: 1501 AA.
AC           027720;
DT           01-NOV-1996 (TREMBLEL. 01, CREATED)
DT           01-NOV-1996 (TREMBLEL. 01, LAST SEQUENCE UPDATE)
DT           01-NOV-1998 (TREMBLEL. 08, LAST ANNOTATION UPDATE)
DE           ATPASE 2.
OS           PLASMODIUM FALCIPARUM.
OC           EUARYZOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM
RN           [1]
RP           SEQUENCE FROM N.A.
RX           MEDLINE: 95154293.
RA           TROTTEIN F., COMMAN A.F.;
RT           "Molecular cloning and sequence of two novel P-type
RL           adenosinetriphosphatases from Plasmodium falciparum.";
RL           EUR. J. BIOCHEM. 227:214-225(1995).

```

| | Query Match | 31.8% | Score 75; | DB 5; | Length 1094; |
|---------|-------------------------|--------------|---------------------|---------------|--------------|
| | Best Local Similarity | 40.0%; | Pred. No. 3.37e+00; | | |
| Matches | 8; | Conservative | 7; | Mismatches 5; | Indels 0; |
| Db | 607 EYDVQRTSVLELKNRKNET | 626 | | | |
| | : : :::: :: | | | | |
| Oy | 12 DYNNKATVQDELDDYNNKAT | 31 | | | |

```

RESULT 10 PRELIMINARY: PRT: 239 AA.
AC 006532:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-7 (SECT40N) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE: 94011313.
RA MARJ J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
SYNDROME.
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
PROGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13375; G295147; -
DR PFAM: P101123; Staph_Stp_toxin; 1.
KM ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON TER 1
SQ SEQUENCE 239 AA; 27642 MW; 81CAABC2 CRC32;

Query Match 31.4%; Score 74; DB 2; Length 239;
Best Local Similarity 44.0%; Pred. No. 4.53e+00;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1.

Db 136 YENKNTISFEVQDKSVTAQELD 160
QY 1 YNKKRAIVQ-ELDYNNKKRAIVQELD 24
1:::1:1:1:1:1111

RESULT 11 PRELIMINARY: PRT: 239 AA.
AC 006535:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 909;
RX MEDLINE: 94011313.
RA MARJ J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL INECT. IMMUN. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
SYNDROME.
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
PROGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13377; G295147; -
DR PFAM: P101123; Staph_Stp_toxin; 1.
KM ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON TER 1
SQ SEQUENCE 239 AA; 27648 MW; 1DC80C35 CRC32;

Query Match 31.4%; Score 74; DB 2; Length 239;
Best Local Similarity 44.0%; Pred. No. 4.53e+00;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1.

Db 136 YENKNTISFEVQDKSVTAQELD 160
QY 1 YNKKRAIVQ-ELDYNNKKRAIVQELD 24
1:::1:1:1:1:1111

```

| | | | | | | |
|----|--|----------------|-------------------------|-----------------|-------------|---------|
| | RESULT | 12 | | PRELIMINARY; | PRT; | 239 AA. |
| AC | 006531 | | | | | |
| DT | 01-NOV-1996 | (TREMBLREL_01, | CREATED) | | | |
| DT | 01-NOV-1996 | (TREMBLREL_01, | LAST SEQUENCE UPDATE) | | | |
| DT | 01-NOV-1998 | (TREMBLREL_08, | LAST ANNOTATION UPDATE) | | | |
| DE | ENTEROTOXIN TYPE C-4 | (SEC446) | (FRAGMENT). | | | |
| OC | STAPHYLOCOCCUS AUREUS. | | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | | |
| OC | STAPHYLOCOCCUS. | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | STRAIN=4446; | | | | | |
| RA | MEDLINE; 94011313. | | | | | |
| RA | MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.; | | | | | |
| RT | "Characterization of novel type C staphylococcal enterotoxins: | | | | | |
| RT | biological and evolutionary implications." | | | | | |
| RL | INECT. IMMUN. 61:4254-4262(1993). | | | | | |
| CC | -I DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION | | | | | |
| CC | STAPHYLOCOCCAL FOOD POISONING SYNDROME. | | | | | |
| CC | -I SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. | | | | | |
| CC | PROGENES PYROGENIC EXOTOXINS ARE ALL RELATED. | | | | | |
| DR | EMBL; L13374; G295141; . | | | | | |
| DR | PFAM; PF01123; Stap_Strp_toxin; 1. | | | | | |
| KW | ENTEROTOXIN; TOXIN; SUPERANTIGEN. | | | | | |
| FT | NON_TER | 1 | | | | |
| SQ | SEQUENCE | 239 AA; | 27612 MW; | 52B18853 CRC32; | | |
| | | | | | | |
| | Query Match | 31.4%; | Score 74; | DB 2; | Length 239; | |
| | Best Local Similarity | 44.0%; | Pred. No. 4.53e+00; | | | |
| | Matches | 11; | Conservative | 7; | Mismatches | 6; |
| | | | | | Indels | 1; |
| | | | | | Gaps | 1; |
| Db | 136 YENKRNITSEFVOTDKSKSVTAQEID | 160 | | | | |
| Oy | 1 YNKRRATVO-ELDYNNKKRATVEID | 24 | | | | |
| | | | | | | |
| | RESULT | 13 | | | | |
| ID | 053678 | | PRELIMINARY; | PRT; | 239 AA. | |
| AC | 053678; | | | | | |
| DT | 01-NOV-1996 | (TREMBLREL_01, | CREATED) | | | |
| DT | 01-NOV-1996 | (TREMBLREL_01, | LAST SEQUENCE UPDATE) | | | |
| DT | 01-NOV-1998 | (TREMBLREL_08, | LAST ANNOTATION UPDATE) | | | |
| DE | ENTEROTOXIN (FRAGMENT). | | | | | |
| OC | STAPHYLOCOCCUS AUREUS. | | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | | |
| OC | STAPHYLOCOCCUS. | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | MEDLINE; 94011313. | | | | | |
| RA | MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.; | | | | | |
| RT | "Characterization of novel type C staphylococcal enterotoxins: | | | | | |
| RT | biological and evolutionary implications." | | | | | |
| DL | INECT. IMMUN. 61:4254-4262(1993). | | | | | |
| DR | EMBL; L13376; G295145; . | | | | | |
| DR | PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1. | | | | | |
| DR | PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. | | | | | |
| KW | PFAM; PF01123; Stap_Strp_toxin; 1. | | | | | |
| KW | ENTEROTOXIN. | | | | | |
| FT | NON_TER | 1 | | | | |
| SQ | SEQUENCE | 239 AA; | 27618 MW; | 0810BB9D CRC32; | | |
| | | | | | | |
| | Query Match | 31.4%; | Score 74; | DB 2; | Length 239; | |
| | Best Local Similarity | 44.0%; | Pred. No. 4.53e+00; | | | |
| | Matches | 11; | Conservative | 7; | Mismatches | 6; |
| | | | | | Indels | 1; |
| | | | | | Caps | 1; |
| Db | 136 YENKRNITSEFVOTDKSKSVTAQEID | 160 | | | | |
| Oy | 1 YNKRRATVO-ELDYNNKKRATVEID | 24 | | | | |

Search completed: Tue Aug 31 19:23:13 1999
 Job time : 52 secs.

```

RESULT 14
ID 006533 PRELIMINARY: PRT: 239 AA.
AC 006533:
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MNCOPELAND:
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
  PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR PFAM: PF01123; Staph_Strep_toxin: 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA: 27651 MW; 7A5C4047 CRC32;

Query Match 31.4%; Score 74; DB 2; Length 239;
Best Local Similarity 44.0%; Pred. No. 4.53e+00;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

136 YENKRNITSEVYDVKSVTAQELD 160
1 YNKKRATVO-ELDYNNKKRATVOELD 24

RESULT 15
ID 006534 PRELIMINARY: PRT: 239 AA.
AC 006534:
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DE ENTEROTOXIN TYPE C (SECCOVINE) (FRAGMENT).
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
  biological and evolutionary implications.";
RL INFECT. IMMUN. 61:4254-4262(1993).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S.
  PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
DR PFAM: PF01123; Staph_Strep_toxin: 1.
KW ENTEROTOXIN; TOXIN; SUPERANTIGEN.
FT NON_TER 1
SQ SEQUENCE 239 AA: 27517 MW; 1293E9CA CRC32;

Query Match 31.4%; Score 74; DB 2; Length 239;
Best Local Similarity 44.0%; Pred. No. 4.53e+00;
Matches 11; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

136 YENKRNITSEVYDVKSVTAQELD 160
1 YNKKRATVO-ELDYNNKKRATVOELD 24
  
```

THIS PAGE BLANK (USPTO)

MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:27:10 1999; MasPar time 3.58 Seconds
Tabular output not generated.
Title: >US-09-150-947-9
Description: (1-14) from US09150947.pep
Perfect Score: 81
Sequence: 1 XYNKKATVQELDX 14
Scoring table: PAM 150
Gap 15
Searched: 170751 seqs, 21266608 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution Rights by Oxford Molecular Ltd

(7M)

MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:27:10 1999; MasPar time 3.58 Seconds
Tabular output not generated.
Title: >US-09-150-947-9
Description: (1-14) from US09150947.pep
Perfect Score: 81
Sequence: 1 XYNKKATVQELDX 14
Scoring table: PAM 150
Gap 15
Searched: 170751 seqs, 21266608 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.360; Variance 49.153; scale 0.353

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|---------------|-------|----------------|--------|--------|-----------------------|-----------|
| 1 | 81 | 100.0 | 12 34 | W64637 | Synthetic SEB peptide | 1.54e-02 |
| 2 | 81 | 100.0 | 13 34 | W64641 | Synthetic SEB peptide | 1.54e-02 |
| 3 | 81 | 100.0 | 13 34 | W64645 | Synthetic SEB peptide | 1.54e-02 |
| 4 | 81 | 100.0 | 14 34 | W64644 | Synthetic SEB peptide | 1.54e-02 |
| 5 | 81 | 100.0 | 14 34 | W64645 | Synthetic SEB peptide | 1.54e-02 |
| 6 | 81 | 100.0 | 24 34 | W64642 | Synthetic SEB peptide | 1.54e-02 |
| 7 | 81 | 100.0 | 35 34 | W64643 | Synthetic SEB peptide | 1.54e-02 |
| 8 | 64 | 79.0 | 10 34 | W64638 | Synthetic SEB peptide | 1.96e+00 |
| 9 | 59 | 72.8 | 28 19 | W04494 | Staphylococcal entero | 7.72e+00 |
| 10 | 59 | 72.8 | 36 36 | W72425 | Peptide #5 for reduci | 7.72e+00 |
| 11 | 59 | 72.8 | 38 36 | W72427 | Peptide #6 for reduci | 7.72e+00 |
| 12 | 59 | 72.8 | 91 27 | W24299 | Staphylococcus aureus | 7.72e+00 |
| 13 | 59 | 72.8 | 233 3 | R13203 | Staphylococcal entero | 7.72e+00 |
| 14 | 59 | 72.8 | 233 8 | R45011 | Staphylococcal entero | 7.72e+00 |
| 15 | 59 | 72.8 | 233 27 | W35373 | Staphylococcus entero | 7.72e+00 |
| 16 | 59 | 72.8 | 233 20 | W05738 | Staphylococcus entero | 7.72e+00 |

| | | | | | | |
|----|----|------|--------|--------|------------------------|----------|
| 17 | 58 | 71.6 | 12 34 | W64636 | Synthetic SEB peptide | 1.01e+01 |
| 18 | 58 | 71.6 | 13 34 | W64640 | Synthetic SEB peptide | 1.01e+01 |
| 19 | 58 | 71.6 | 239 34 | W64647 | Synthetic SEB peptide | 1.01e+01 |
| 20 | 58 | 71.6 | 239 8 | R45014 | Staphylococcal entero | 1.01e+01 |
| 21 | 58 | 71.6 | 239 3 | R13206 | Staphylococcal entero | 1.01e+01 |
| 22 | 58 | 71.6 | 255 20 | W06737 | Staphylococcus entero | 1.01e+01 |
| 23 | 57 | 70.4 | 228 3 | R13205 | Staphylococcal entero | 1.32e+01 |
| 24 | 57 | 70.4 | 228 8 | R45013 | Staphylococcal entero | 1.32e+01 |
| 25 | 54 | 66.7 | 24 36 | W72423 | Peptide #2 for reduci | 2.94e+01 |
| 26 | 54 | 66.7 | 28 36 | W72425 | Peptide #4 for reduci | 2.94e+01 |
| 27 | 53 | 65.4 | 10 34 | W64639 | Synthetic SEB peptide | 3.83e+01 |
| 28 | 53 | 65.4 | 230 3 | R13204 | Staphylococcal entero | 3.83e+01 |
| 29 | 53 | 65.4 | 230 8 | R45012 | Staphylococcal entero | 3.83e+01 |
| 30 | 53 | 65.4 | 245 27 | W35374 | Staphylococcus entero | 3.83e+01 |
| 31 | 53 | 65.4 | 245 27 | W35375 | Staphylococcus entero | 3.83e+01 |
| 32 | 52 | 64.2 | 221 8 | R45017 | Staphylococcal entero | 4.97e+01 |
| 33 | 52 | 64.2 | 250 24 | W12145 | Staphylococcus pyogene | 4.97e+01 |
| 34 | 52 | 64.2 | 251 24 | W12147 | Streptococcus pyogene | 4.97e+01 |
| 35 | 52 | 64.2 | 251 24 | W12147 | Streptococcus pyogene | 4.97e+01 |
| 36 | 52 | 64.2 | 251 24 | W12153 | Streptococcus pyogene | 4.97e+01 |
| 37 | 52 | 64.2 | 251 24 | W12057 | Streptococcus pyogene | 4.97e+01 |
| 38 | 52 | 64.2 | 251 33 | W59781 | Amino acid sequence o | 4.97e+01 |
| 39 | 52 | 64.2 | 251 33 | W59780 | Amino acid sequence o | 4.97e+01 |
| 40 | 52 | 64.2 | 251 24 | W12151 | Streptococcus pyogene | 4.97e+01 |
| 41 | 52 | 64.2 | 251 24 | W12150 | Streptococcus pyogene | 4.97e+01 |
| 42 | 52 | 64.2 | 251 24 | W12152 | Streptococcus pyogene | 4.97e+01 |
| 43 | 52 | 64.2 | 251 24 | W12146 | Streptococcus pyogene | 4.97e+01 |
| 44 | 52 | 64.2 | 251 24 | W12149 | Streptococcus pyogene | 4.97e+01 |
| 45 | 52 | 64.2 | 401 36 | W22779 | Human septin-2 protei | 4.97e+01 |

ALIGNMENTS

RESULT 1
ID W64637 standard; peptide; 12 AA.
AC W64637;
DE 23-OCV-1998 (first entry)
DE Synthetic SEB peptide p12(151-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W0982944-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-11938.
PA (YISS.) YISSUM RES. 6 DEV CO.
PI Fried G, Kaempfer R;
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 8: Page 41: 68pp: English.
CC W64636-W64637 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced
CC by PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 12 AA:
Query Match 100.0%; Score 81; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ynkktatvqeld 12

```

OY 2 YMKKATVQELD 13
|||||
RESULT 2
ID W64641 standard; peptide: 13 AA.
AC W64641;
DE 23-OCT-1998 (first entry)
KM Synthetic SEB peptide p12(150-161).
KM Enterotoxin B: SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
OS therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
FH Key
FH Modified_site 1 Location/Qualifiers
FT /note= "N-terminal Tyr modified by presence of
FT /note= "N-lauryl-cysteyl"
FT
FT W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS ) YISSUM RES & DEV CO.
PI Arad G. Kaempfer R;
PI WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 16; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA;

Query Match 100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvgeld 13
|||||
OY 2 YMKKATVQELD 13

RESULT 3
ID W64646 standard; peptide: 13 AA.
AC W64646;
DE 23-OCT-1998 (first entry)
KM Synthetic SEB peptide Ac-p12(150-161).
KM Enterotoxin B: SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
OS therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
FH Key
FH Modified_site 1 Location/Qualifiers
FT /note= "N-terminal Tyr modified by N-acetyl group"
FT /note= "D-form residue"
FT
FT Misc_difference 14
FT
FT W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS ) YISSUM RES & DEV CO.
PI Arad G. Kaempfer R;

```

```

DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 24; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 13 AA;

Query Match 100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkktatvgeld 12
|||||
OY 2 YMKKATVQELD 13

RESULT 4
ID W64644 standard; peptide: 14 AA.
AC W64644;
DE 23-OCT-1998 (first entry)
KM Synthetic SEB peptide Cys-p12(150-161).
KM Enterotoxin B: SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
OS therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
FH Key
FH Modified_site 1 Location/Qualifiers
FT /note= "N-terminal Cys modified by N-acetyl group"
FT /note= "D-form residue"
FT
FT Misc_difference 14
FT
FT W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS ) YISSUM RES & DEV CO.
PI Arad G. Kaempfer R;
PI WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 21; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvgeld 13
|||||
OY 2 YMKKATVQELD 13

RESULT 5

```

ID W64645 standard; peptide: 14 AA.
 AC W64645:
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide D-Ala.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 NW therapeutic; vaccine; food poisoning.
 OS Synthetic.
 ST Staphylococcus aureus.
 FT Key
 FT Misc_difference 1 Location/Qualifiers
 FT Misc_difference 14 /note="D-form residue"
 FT Misc_difference 14 /note="D-form residue"
 FT Misc_difference 14 /note="D-form residue"
 PN W09829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PS treatment of toxic shock caused by exotoxin(s)
 PS Claim 23; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SO Sequence 14 AA.
 Query Match 100.0%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 ynkktatvgeld 13
 QY 2 YNKKRATVOELD 13
 RESULT 6
 ID W64642 standard; peptide: 24 AA.
 AC W64642:
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide dimer.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 NW therapeutic; vaccine; food poisoning.
 OS Synthetic.
 ST Staphylococcus aureus.
 FT Key
 FT Misc_difference 1 Location/Qualifiers
 FT Misc_difference 14 /note="D-form residue"
 FT Misc_difference 14 /note="D-form residue"
 FT Misc_difference 14 /note="D-form residue"
 PN W09829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PS treatment of toxic shock caused by exotoxin(s)
 PS Claim 18; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SO Sequence 24 AA.
 Query Match 100.0%; Score 81; DB 34; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ynkktatvgeld 12
 QY 2 YNKKRATVOELD 13
 RESULT 7
 ID W64643 standard; peptide: 35 AA.
 AC W64643:
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide trimer.
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 NW therapeutic; vaccine; food poisoning.
 OS Synthetic.
 ST Staphylococcus aureus.
 FT Key
 FT Misc_difference 1 Location/Qualifiers
 FT Misc_difference 14 /note="D-form residue"
 FT Misc_difference 14 /note="D-form residue"
 FT Misc_difference 14 /note="D-form residue"
 PN W09829444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PS treatment of toxic shock caused by exotoxin(s)
 PS Claim 19; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SO Sequence 35 AA.
 Query Match 100.0%; Score 81; DB 34; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ynkktatvgeld 12
 QY 2 YNKKRATVOELD 13
 RESULT 8
 ID W64638 standard; peptide: 10 AA.
 AC W64638:
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide pSEB(152-161).
 KM Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 NW therapeutic; vaccine; food poisoning.
 OS Synthetic.
 ST Staphylococcus aureus.

PN W09829444-A1.
 PD 09-JUN-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI: 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antaggonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 10; Page 41; 68pp: English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET.
 SQ Sequence 10 AA;

Query Match 79.0%; Score 64; DB 34; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.96e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 kkkatvgeid 10
 |||:|||||
 QY 4 KKKATVGEID 13

RESULT 9
 ID W04494 standard; peptide: 28 AA.
 AC W04494;
 DT 10-DEC-1996 (first entry)
 DE Staphylococcal enterotoxin A residues 146-173, T-cell agonist.
 KW Staphylococcal enterotoxin A; agonist; T-cell proliferation;
 KW treatment: immunodeficiency; autoimmune disease; TNF-alpha;
 KW tumour necrosis factor alpha.
 OS Staphylococcus spp.
 PN US5545716-A.
 PD 13-AUG-1996.
 PF 08-SEP-1992; 941497.
 PR 08-SEP-1992; US-941497.
 PR 29-MAR-1994; US-220378.
 PA (UYFL) UNIV FLORIDA.
 PI Griggs ND, Johnson HM, Pontzer CH;
 DR WPI: 96-383718/38.
 PT Peptide fragments of Staphylococcal enterotoxin A (SEA) - useful as
 PT SEA agonists for stimulating T-cell proliferation, e.g. in treatment
 PT of immunodeficiency and autoimmune diseases
 PS Example 1: Columns 15-16: 17pp: English.
 CC The present peptide, comprising residues 146-173 of Staphylococcal
 CC enterotoxin A (SEA), is useful as an SEA agonist for stimulating
 CC T-cell proliferation, e.g. in the treatment of immunodeficiency and
 CC autoimmune diseases. Supernatant from PBMC stimulated with
 CC 100 microm of the peptide for 18 hrs., was collected and assayed
 CC for TNF-alpha activity by cytotoxicity on L-929 cells. The result
 CC given as units/ml of TNF-alpha activity was 1.85, compared to 24.1
 CC for the most effective agonist, comprising SEA residues 121-149.
 SQ Sequence 28 AA;

Query Match 72.8%; Score 59; DB 19; Length 28;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 nkkntvgeid 11
 |||:|||||
 QY 3 NKKATVGEID 13

RESULT 10
 ID W72426 standard; peptide: 36 AA.
 AC W72426;
 DT 22-DEC-1998 (first entry)
 DE Peptide #5 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW Staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PF 01-APR-1998; 006663.
 PR 07-APR-1997; US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabitskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp: English.
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kd.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1YX2X3X4X5N #1,
 CC K6X7X8X9X10X11X12X13X14X15X16RX17X18X27X19X20X21X22X3X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SPE or SEA, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 SQ Sequence 36 AA;

Query Match 72.8%; Score 59; DB 36; Length 36;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkkntvgeid 22
 |||:|||||
 QY 3 NKKATVGEID 13

RESULT 11
 ID W72427 standard; peptide: 38 AA.
 AC W72427;
 DT 22-DEC-1998 (first entry)
 DE Peptide #6 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW Staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PF 01-APR-1998; 006663.
 PR 07-APR-1997; US-838413.
 PA (UYRO) UNIV ROCKEFELLER.
 PI Bannan JD, Zabitskie JB;
 DR WPI: 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp: English.
 CC The present invention describes peptides having consensus sequences #1

or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1YX23X4X5N #1,
 CC KX6X7X8X9X10X11X12X13X14X15X16X17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SPSA or SFA, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 SQ Sequence 38 AA;

Query Match 72.8%; Score 59; DB 36; Length 38;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvtygeid 22
 |||:|||||
 QY 3 NKKKATVOEID 13

RESULT 12
 ID W24299 standard; Protein; 91 AA.
 AC W24299;
 DT 14-APR-1998 (first entry)
 DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
 KW Staphylococcus aureus MCH 29; antagonist; antibacterial; immunogen;
 OS vaccine; disease; protection; isolation.
 FH Staphylococcus aureus.
 FT Key Location/Qualifiers
 FT Misc_difference 29
 FT W09731114-A2.
 FT W09731114-A2.
 PD 28-AUG-1997.
 PR 25-FEB-1997; G00524.
 PR 26-FEB-1996; GB-004045.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Burnham MKR, Hodgson JE;
 DR WPI: 97-435166/40.
 DR N-PSDB; V01865.
 PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for
 PT isolating antagonist of the polypeptide(s) useful as anti-bacterials
 PS Claim 11; Page 33; 117pp; English.
 CC The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from Staphylococcus aureus. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds
 CC that bind and inhibit the activity of the polypeptide. Such compounds
 CC can be used as anti-bacterial compounds. The polypeptide may also be
 CC used as an immunogen to vaccinate an animal for protection against
 CC Staphylococcus aureus caused disease.
 SQ Sequence 91 AA;

Query Match 72.8%; Score 59; DB 27; Length 91;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 40 nkknvtygeid 50
 |||:|||||
 QY 3 NKKKATVOEID 13

RESULT 13
 ID R13203 standard; Protein; 233 AA.
 AC R13203;
 DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin A.
 KW SEA; Cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.
 PN W09110680-A.
 PD 25-JUL-1991.
 PR 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure; Fig 1; 74pp; English.
 CC SEA was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEA. Synthetic
 CC polypeptides having structural homology to staphylococcal exotoxins
 CC are claimed. Provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydropathy profiles.
 CC See also R13204-R13211.
 SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 3; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtygeid 156
 |||:|||||
 QY 3 NKKKATVOEID 13

RESULT 14
 ID R45011 standard; Protein; 233 AA.
 AC R45011;
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SEA.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Misc_difference 49
 FT /note="Given in the specification as O, no further
 FT details given"
 FT FT
 FT W09324136-A.
 PD 09-DEC-1993.
 PR 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS Disclosure; Fig 1; 90pp; English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 8; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtygeid 156
 |||:|||||
 QY 3 NKKKATVOEID 13

RESULT 15
 ID W35373 standard: peptide; 233 AA.
 AC W35373;
 DT 20-APR-1998 (first entry)
 DE Staphylococcus enterotoxin SEA wild-type superantigen.
 KM SEA: Staphylococcus enterotoxin; superantigen; conjugate;
 KW treatment; cancer; infection; autoimmune disease; antibody.
 OS Staphylococcus sp.
 PN W09736932-A1.
 PD 09-OCT-1997.
 PE 26-MAR-1997; SE0537.
 PR 12-AUG-1996; US-695692.
 PR 29-MAR-1996; SE-001245.
 PA (PHAA) PHARMACIA & UPJOHN AB.
 PI Abrahamson L, Antonsson P, Björk P, Dohlsten M,
 PI Forsberg G, Hansson J, Kalland T;
 DR WPI: 97-503052/46.
 PT Conjugate of target seeking moiety and modified superantigen -
 PT useful for activating the immune system to treat cancer, viral
 PT infections, parasitic infestations and autoimmune diseases
 PS Claim 8; Pages 36-37; 58pp; English.
 CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
 CC SEA superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to
 CC T cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in beta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 27; Length 233;

Best Local Similarity 81.8%; Pred. No. 7.72e+00;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtygeld 156

QY 3 NKKRTVOELD 13

Search completed: Tue Aug 31 19:27:27 1999
 Job time : 17 secs.

MUSENET
(TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mparch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:26:37 1999; Maspar time 3.74 Seconds
Tabular output not generated. 149.878 Million cell updates/sec

Title: >US-09-150-947-9
Description: (1-14) from US09150947.pep
Perfect Score: 81
Sequence: 1 XYNKKKATVQELDX 14

Scoring table:
PAM 150
Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 24.268; Variance 31.113; scale 0.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------|-----------------------|-----------|
| 1 | 59 | 72.8 | 233 | 2 | A29566 | enterotoxin A - Staph | 2.55e+01 |
| 2 | 59 | 72.8 | 257 | 2 | A28664 | enterotoxin A precurs | 2.55e+01 |
| 3 | 59 | 72.8 | 362 | 2 | S27530 | sporulation protein - | 2.55e+01 |
| 4 | 58 | 71.6 | 266 | 1 | ENSAB6 | enterotoxin B precurs | 4.14e+01 |
| 5 | 57 | 70.4 | 258 | 2 | A33953 | enterotoxin D precurs | 6.68e+01 |
| 6 | 53 | 65.4 | 257 | 2 | A28179 | enterotoxin E precurs | 4.30e+00 |
| 7 | 53 | 65.4 | 671 | 2 | A40692 | signal recognition pa | 4.30e+00 |
| 8 | 53 | 65.4 | 880 | 2 | S51473 | probable membrane pro | 4.30e+00 |
| 9 | 53 | 65.4 | 1233 | 2 | I54383 | gene SBI.8/DXS423E pr | 4.30e+00 |
| 10 | 52 | 64.2 | 127 | 2 | B69767 | conserved hypochetica | 6.76e+00 |
| 11 | 52 | 64.2 | 146 | 2 | A49746 | probable membrane pro | 6.76e+00 |
| 12 | 52 | 64.2 | 236 | 2 | S18786 | exotoxin type A precu | 6.76e+00 |
| 13 | 52 | 64.2 | 235 | 2 | S18783 | exotoxin type A precu | 6.76e+00 |
| 14 | 52 | 64.2 | 251 | 2 | S29659 | exotoxin type A precu | 6.76e+00 |
| 15 | 51 | 63.0 | 224 | 2 | S58590 | ribosomal protein S3 | 1.05e+01 |
| 16 | 51 | 63.0 | 239 | 1 | R3R23 | ribosomal protein S3 | 1.05e+01 |
| 17 | 51 | 63.0 | 262 | 2 | C70372 | flagellar hook basal | 1.05e+01 |
| 18 | 51 | 63.0 | 412 | 2 | S48861 | rRNA (guanosine-2'-O- | 1.05e+01 |
| 19 | 51 | 63.0 | 3418 | 1 | G02334 | breast cancer tumor s | 1.05e+01 |
| 20 | 50 | 61.7 | 274 | 2 | B64087 | outer membrane protei | 1.64e+01 |
| 21 | 50 | 61.7 | 391 | 2 | S18666 | KIN17 protein - mouse | 1.64e+01 |
| 22 | 50 | 61.7 | 1075 | 1 | OYRXH | heat-stable enterotox | 1.64e+01 |
| 23 | 50 | 61.7 | 1223 | 2 | I38111 | phosphorylase kinase | 1.64e+01 |

| | | | | | | | |
|----|----|------|------|---|--------|------------------------|----------|
| 24 | 50 | 61.7 | 3685 | 1 | A27605 | dystrophin, muscle - | 1.64e+01 |
| 25 | 49 | 60.5 | 280 | 2 | S66072 | hypothetical protein | 2.52e+01 |
| 26 | 49 | 60.5 | 384 | 2 | S46523 | transcription factor | 2.52e+01 |
| 27 | 49 | 60.5 | 452 | 2 | T01694 | calcium-dependent pro | 2.52e+01 |
| 28 | 49 | 60.5 | 455 | 2 | S55019 | MAD polypeptide - fru | 2.52e+01 |
| 29 | 49 | 60.5 | 465 | 2 | S68987 | transcription activat | 2.52e+01 |
| 30 | 49 | 60.5 | 599 | 2 | T02994 | CDPK-related protein | 2.52e+01 |
| 31 | 49 | 60.5 | 607 | 2 | T03023 | calcium-dependent pro | 2.52e+01 |
| 32 | 49 | 60.5 | 625 | 2 | T02033 | calcium/calmodulin-de | 2.52e+01 |
| 33 | 49 | 60.5 | 803 | 2 | I68600 | dipeptidyl aminopepti | 2.52e+01 |
| 34 | 49 | 60.5 | 803 | 2 | A41793 | dipeptidyl aminopepti | 2.52e+01 |
| 35 | 49 | 60.5 | 831 | 2 | B64528 | conserved hypothetical | 2.52e+01 |
| 36 | 49 | 60.5 | 865 | 2 | I54331 | dipeptidyl aminopepti | 2.52e+01 |
| 37 | 49 | 60.5 | 1134 | 2 | A60234 | Iga Fc receptor precu | 2.52e+01 |
| 38 | 49 | 60.5 | 1164 | 1 | JC4860 | Iga Fc receptor precu | 2.52e+01 |
| 39 | 49 | 60.5 | 1369 | 2 | S28916 | protein-tyrosine kina | 2.52e+01 |
| 40 | 49 | 60.5 | 3678 | 2 | S28916 | dystrophin - mouse | 2.52e+01 |
| 41 | 48 | 59.3 | 303 | 2 | E69164 | conserved hypothetical | 3.86e+01 |
| 42 | 48 | 59.3 | 324 | 2 | S48122 | transcription factor | 3.86e+01 |
| 43 | 48 | 59.3 | 332 | 2 | S15347 | transcription factor | 3.86e+01 |
| 44 | 48 | 59.3 | 844 | 2 | T00529 | bZIP-like protein - A | 3.86e+01 |
| 45 | 48 | 59.3 | 1381 | 2 | S60004 | hypothetical protein | 3.86e+01 |

ALIGNMENTS

| | | | |
|-----------------------|---|---|----------------|
| RESULT | 1 | A29566 | #type complete |
| ENTRY | | enterotoxin A - Staphylococcus aureus | |
| TITLE | | #formal_name Staphylococcus aureus | |
| ORGANISM | | 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change | |
| DATE | | 18-Jun-1993 | |
| ACCESSIONS | | A29566 | |
| REFERENCE | | A29566 | |
| #authors | | Huang, I. Y.; Hughes, J. L.; Bergdoll, M. S.; Schantz, E. J. | |
| #journal | | J. Biol. Chem. (1987) 262:7006-7013 | |
| #title | | Complete amino acid sequence of staphylococcal enterotoxin A. | |
| #cross-references | | WID:87222293 | |
| #accession | | A29566 | |
| #molecule_type | | protein | |
| #residues | | 1-233 | #label HUA |
| GENETICS | | | |
| #gene | | entA | |
| #map_position | | 6 | |
| SUMMARY | | #length 233 #molecular-weight 27079 #checksum 9580 | |
| Query Match | | 72.8% Score 59; DB 2; Length 233; | |
| Best Local Similarity | | 81.8% Pred. No. 2.55e+01; | |
| Matches | | 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |
| DB | | 146 NKKKATVQELDX 156 | |
| QY | | 3 NKKKATVQELDX 13 | |
| RESULT | 2 | A28664 | #type complete |
| ENTRY | | enterotoxin A precursor - Staphylococcus aureus (strain | |
| TITLE | | FR1337) | |
| ORGANISM | | #formal_name Staphylococcus aureus | |
| DATE | | 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change | |
| ACCESSIONS | | A28664 | |
| REFERENCE | | A28664 | |
| #authors | | Betley, M. J.; Mekalanos, J. J. | |
| #journal | | J. Bacteriol. (1988) 170:34-41 | |
| #title | | Nucleotide sequence of the type A staphylococcal enterotoxin | |
| #cross-references | | WID:88086892 | |
| #accession | | A28664 | |
| #molecule_type | | DNA | |
| #residues | | 1-257 | #label BET |
| #cross-references | | GB:M18970; NID:g153120; PID:g153121 | |

```
##experimental_source strain FR1337
SUMMARY      #length 257 #molecular_weight 29669 #checksum 2543
Query Match  72.8% Score 59; DB 2; Length 257;
Best Local Similarity 81.8% Pred. No. 2,35e-01;
Matches      9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 170 NKKRATVOELD 180
|||:|||||
|||:|||||
3 NKKRATVOELD 13

RESULT 3
ENTRY   S27530 #type complete
TITLE   sporulation protein - Clostridium acetobutylicum
ORGANISM #formal_name Clostridium acetobutylicum
DATE     06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
09-Sep-1997

ACCESSIONS
REFERENCE S27530
#authors Reid, S.J.; Hancock, K.; Santangelo, J.D.; Woods, D.R.
#submission Submitted to the EMBL Data Library, March 1992
#description Cloning and sequencing of a spoIID gene from Clostridium acetobutylicum.
#accession S27530
#status preliminary
#molecule_type DNA
#residues 1-362 #label REI
##cross-references EMBL:M87835; NID:g144914; PID:g144915
SUMMARY #length 362 #molecular_weight 40998 #checksum 3634

Query Match 72.8% Score 59; DB 2; Length 362;
Best Local Similarity 58.3% Pred. No. 2,55e-01;
Matches      7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKRNSYEELD 78
|||:|||||
|||:|||||
2 YHKRATVOELD 13

RESULT 4
ENTRY   ENSAB6 #type complete
TITLE   enterotoxin B precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE     24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change
11-Sep-1998

ACCESSIONS
REFERENCE S27360; A92065; S27240; A01815
#authors Jones, C.L.; Khan, S.A.
#journal J. Bacteriol. (1986) 166:29-33
#title Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
#cross-references MUD:86168029
#accession S27360
#molecule_type DNA
#residues 1-266 #label JON
##cross-references EMBL:M1118; NID:g152999; PID:g153000
##experimental_source strain S6
REFERENCE A92065
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3518-3525
#title The primary structure of staphylococcal enterotoxin B. II. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.
#cross-references MUD:71007902
#accession A92065
#molecule_type protein
#residues 28-55, 'NND', '59-68', 'NE', '71', 'FDPIIV', '78-117', '119-127', 'N', '129', 'D', '131-132', 'ENT', '136-148', 'GN', '151-156', 'Y', '157-184', 'EO', '187-232', 'N', '234-245', 'ND', '248-266' #label HUA
##experimental_source strain S-6
REFERENCE A92064
```

```
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3511-3517
#title The primary structure of staphylococcal enterotoxin B. II. Isolation, composition, and sequence of chymotryptic peptides.
#cross-references MUD:71007901
#contents annotation; chymotryptic peptides
REFERENCE A92063
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3493-3510
#title The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, and sequence of tryptic peptides from oxidized entero-toxin B.
#cross-references MUD:71007900
#contents annotation; tryptic peptides
REFERENCE A90348
#authors Schantz, E.J.; Roessler, W.G.; Magman, J.; Spero, L.; Dunnehy, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin B.
#cross-references MUD:66035792
#contents annotation; biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.; Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of staphylococcal enterotoxin B.
#accession S27240
#molecule_type protein
#residues 28-42;128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin; extracellular protein; toxin
FEATURE 1-27 #domain signal sequence #status predicted #label SIG\
28-266 #product enterotoxin B #status experimental #label MAT\
120-140 #disulfide bonds #status experimental
SUMMARY #length 266 #molecular_weight 31436 #checksum 4249

Query Match 71.6% Score 58; DB 1; Length 266;
Best Local Similarity 81.8% Pred. No. 4,14e-01;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 178 NKKRATVOELD 188
|||:|||||
|||:|||||
3 NKKRATVOELD 13

RESULT 5
ENTRY   A33953 #type complete
TITLE   enterotoxin D precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE     09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
09-Sep-1997

ACCESSIONS
REFERENCE A33953
#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.
#cross-references MUD:89359112
#accession A33953
#status preliminary
#molecule_type DNA
#residues 1-258 #label BAY
##cross-references GB:M28521; NID:g1492109; PID:g758691
SUMMARY #length 258 #molecular_weight 29746 #checksum 39

Query Match 70.4% Score 57; DB 2; Length 258;
Best Local Similarity 72.7% Pred. No. 6,68e-01;
Matches      8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Db      171 DKKNVTQELD 181
      :||:'.|||||
Qy      3  NKKKATVQELD 13
```

| RESULT | ENTRY | 6 |
|-------------------------|-------------------------|-------------|
| TITLE | | |
| ORGANISM | | |
| DATE | | |
| A28179 | #type complete | |
| enterotoxin E precursor | - Staphylococcus aureus | |
| #formal_name | Staphylococcus aureus | |
| 30-Jun-1989 | #sequence_revision | 30-Jun-1989 |
| 09-Sep-1997 | #text_change | |

```

#residues      1-257  ##label COU
#cross-references GB:M2I319; NID:g153001; PID:g153002
SUMMARY      #length 257  #molecular-weight 29358  #checksum 2562

```

| | |
|----------|---|
| RESULT | 7 |
| ENTRY | A40692 |
| TITLE | #type complete |
| ORGANISM | signal_recognition_particle_72k_chain - dog |
| DATE | #formal_name Canis lupus familiaris #common_name dog |
| | 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change |

| | | | | |
|-----------------------|--------|---------------------|-------|---------------|
| Query Match | 65.4%; | Score 53; | DB 2; | Length 671; |
| Best Local Similarity | 33.3%; | Pred. No. 4.30e+00; | | |
| Matches | 4; | Conservative | 5; | Mismatches 3; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

| | | |
|-----------------|--|--------------------------------|
| RESULT | 8 | |
| ENTRY | S51473 | #type complete |
| TITLE | probable membrane protein YJR368w - yeast (Saccharomyces cerevisiae) | |
| ALTERNATE_NAMES | hypothetical protein L3502.1 | |
| ORGANISM | #formal_name Saccharomyces cerevisiae | |
| DATE | 23-Feb-1995 | #sequence_revision 12-May-1995 |
| | 21-Nov-1997 | #text_change |
| ACCESSIONS | S51473 | |

| | |
|--------------|---|
| REFERENCE | S51466 |
| #authors | Du, Z. |
| #submission | submitted to the EMBL Data Library, December 1996 |
| #description | The sequence of <i>S. cerevisiae</i> cosmid U502. |
| #accession | S51473 |

| | |
|---------------|--|
| GENELICS | |
| #map_position | 12R |
| KEYWORDS | transmembrane protein |
| FEATURE | |
| 426-442 | #domain transmembrane #status predicted #label TMM |
| SUMMARY | #length 80 #molecular-weight 99771 #checksum 5546 |

| | | | | |
|-----------------------|-------|--------------|----------|---------------------------------|
| Query Match | 63.4% | Score 53 | DB 2 | Length 880 |
| Best Local Similarity | 50.0% | Pred. No. | 4.30e+00 | |
| Matches | 6 | Conservative | 4 | Mismatches 2; Indels 0; Gaps 0; |

| | | |
|------------|---------------------------|--|
| RESULT | 9 | |
| ENTRY | | |
| TITLE | I54383 | #type complete |
| ORGANISM | gene SB1.8/DXS43E protein | # human |
| DATE | 01-Nov-1996 | #formal_name Homo sapiens #common_name man |
| | 28-Feb-1997 | #sequence_revision 01-Nov-1996 |
| ACCESSIONS | I54383 | |
| | I54383 | |
| REFERENCE | | |

| | | | | |
|-----------------------|------------------|------------------|--------|--------------|
| Query Match | 65.4% | Score 35 | DB 2 | Length 1233 |
| Best Local Similarity | 41.7% | Pred. 0.4.30e+00 | | |
| Matches | 5 | Conservative | 6 | Mismatches 1 |
| | | | Indels | 0 |
| | | | Gaps | 0 |
| Db | 326 YKKRRGDMDELE | 337 | | |
| | : : : : : : | | | |
| Oy | 2 YKKKATVQELD | 13 | | |

| ENTRY | RESULT | 10 |
|-------------|---|----------------|
| TITLE | B69767 | #type complete |
| ORGANISM | conserved hypothetical protein yzcC - <i>Bacillus subtilis</i> | |
| DATE | #formal_name Bacillus subtilis | |
| 05-Dec-1997 | #sequence_revision | 05-Dec-1997 |
| | #text_change | 24-Sep-1998 |
| ACCESSIONS | B69767 | |
| REFERENCE | A69580 | |
| #authors | Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortero, M.G.; Bessieres, P.; Bolojin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codan, J.J.; Conerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Diestelhorst, A.; | |

Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Galleron, N.; Gilm, S.Y.; Glaser, P.; Goffeau, A.; Gollighly, E.J.; Grandi, G.; Guisepi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Konungstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, N.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Potwolk, S.; Prescott, A.M.; Prescan, E.; Pujic, P.; Purrelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanton, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Tanahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpeira, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambolt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
#cross-references M01D:98044033
#accession B69767
#status preliminary; nucleic acid sequence not shown;
#gene translation not shown

##molecule-type DNA
##residues 1-127 ##label KUN
##cross-references GB:299105; GB:AL009126; NID:92632457; PID:e1182223;
#experimental_source strain 168

GENETICS

SUMMARY

#gene yzcZ
#length 127 #molecular-weight 13950 #checksum 9937

Query Match 64.2%; Score 52; DB 2; Length 127;
Best Local Similarity 45.5%; Pred. No. 6.76e+00;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 107 FTKKOTVHDM 117
: 111 111:::
QY 2 YNKKATVOEL 12

RESULT 11
ENTRY S49746
TITLE #type complete
#probable membrane protein YML033w - yeast (*Saccharomyces cerevisiae*)
ORGANISM #formal_name *Saccharomyces cerevisiae*
DATE 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 21-Nov-1997

ACCESSIONS
REFERENCE S49746
S49741
#authors Badcock, K.; Churcher, C.
#submission submitted to the EMBL Data Library, November 1994
#accession S49746
#molecule-type DNA
##residues 1-146 ##label BAD
##cross-references EMBL:Z46659; NID:9575680; PID:9575686; MIPS:YML033w

GENETICS
#map_position 13L
KEYWORDS #map_position 13L
FEATURE #domain transmembrane protein
19-35 #domain transmembrane #status predicted #label TM

SUMMARY

#length 146 #molecular-weight 17729 #checksum 5607

Query Match 64.2%; Score 52; DB 2; Length 146;
Best Local Similarity 54.5%; Pred. No. 6.76e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 40 YNKKATVOEL 50
: 111 111:::
QY 2 YNKKATVOEL 12

RESULT 12
ENTRY S18786
TITLE #type fragment
#exotoxin type A precursor (allele 2) - *Streptococcus pyogenes* (phage strain MGAS250 isolate California and others)
ALTERNATE_NAMES scarlet fever toxin
#formal_name *Streptococcus pyogenes* phage strain MGAS250 isolate California; strain MGAS251 isolate California; strain MGAS256 isolate California; strain MGAS285 isolate Colorado; strain MGAS480 isolate Yugoslavia; strain MGAS492 isolate United Kingdom; strain MGAS496 isolate Germany
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998
ACCESSIONS S18786; S18787; S18788; S18790; S18792; S18795; S18799
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the *speA* gene encoding pyrogenic exotoxin A (scarlet fever toxin) in *Streptococcus pyogenes*.
#cross-references M01D:92044323
#accession S18786
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEL
##cross-references EMBL:X61561; NID:947297; PID:947298
#experimental_source strain MGAS250 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18787
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61562; NID:947299; PID:947300
#experimental_source strain MGAS251 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18788
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEZ
##cross-references EMBL:X61563; NID:947301; PID:947302
#experimental_source strain MGAS256 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18790
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61564; NID:947305; PID:947306
#experimental_source strain MGAS285 isolate Colorado unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18792
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61565; NID:947311; PID:947312
#experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

##accession S18795
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61566; NID:q47317; PID:q47318
##experimental_source strain MGAS492 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

##accession S18799
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NES
##cross-references EMBL:X61567; NID:q47325; PID:q47326
##experimental_source strain MGAS496 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
#note domain signal sequence (fragment) #status predicted
#label sig
#product exotoxin type A (fragment) #status predicted
#label MAT

23-236 #length 236 #checksum 1685

SUMMARY
Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATQVELD 168
|||: 1 1111
QY 3 NKKKATQVELD 13

RESULT 13
ENTRY S18783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isolate Nebraska and others) (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage
#strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS624 isolate Germany; strain MGAS495 isolate Germany 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998
DATE S18783; S18793; S18794; S18801; S18798
S18782
REFERENCE Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#authors J. Exp. Med. (1991) 174:1271-1274
#journal Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M01D:92044323
#accession S18783
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61568; NID:q47289; PID:q47290
##experimental_source strain MGAS158 isolate Nebraska unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

##accession S18793
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61569; NID:q47313; PID:q47314
##experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

##accession S18794
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NE2
##cross-references EMBL:X61570; NID:q47315; PID:q47316
##experimental_source strain MGAS491 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

##accession S18801
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61572; NID:q47333; PID:q47334
##experimental_source strain MGAS624 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

##accession S18798
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61571; NID:q47323; PID:q47324
##experimental_source strain MGAS495 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
#note domain signal sequence (fragment) #status predicted
#label sig
#product exotoxin type A (fragment) #status predicted
#label MAT

23-236 #length 236 #checksum 612

SUMMARY
Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATQVELD 168
|||: 1 1111
QY 3 NKKKATQVELD 13

RESULT 14
ENTRY S29659 #type complete
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change 25-Mar-1998
ACCESSION S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
REFERENCE S29659
#authors Weeks, C.R.; Ferrerli, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references GB:U0453; EMBL:M19350; NID:q1877426; PID:q1877430
#accession S29659
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-251 ##label WEE
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M01D:92044323

```
#accession  S18782
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-244 ##label NEI
##cross-references EMBL:X61560; NID:947287; PID:947288
##experimental_source Streptococcus pyogenes strain MGAS156 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18784
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-244 ##label NEA
##cross-references EMBL:X61556; NID:947291; PID:947292
##experimental_source Streptococcus pyogenes strain MGAS165 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18785
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-244 ##label NEZ
##cross-references EMBL:X61559; NID:947293; PID:947294
##experimental_source Streptococcus pyogenes strain MGAS167 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18791
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-244 ##label NEY
##cross-references EMBL:X61555; NID:947309; PID:947310
##experimental_source Streptococcus pyogenes strain MGAS327 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18796
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-244 ##label NEO
##cross-references EMBL:X61557; NID:947319; PID:947320
##experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18797
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-244 ##label NEH
##cross-references EMBL:X61558; NID:947321; PID:947322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

#accession  S18800
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 9-228 ##label NES
##cross-references EMBL:X61554; NID:947327; PID:947328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
              Zealand unassigned phage
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

GENETICS
#gene        speA, speA1
CLASSIFICATION #superfamily enterotoxin B
FEATURES
1-30          #domain signal sequence #status predicted #label SIG\
31-251        #product exotoxin type A #status predicted #label MAT
SUMMARY
length 251 #molecular-weight 29246 #checksum 1475

Query Match 64.2%; Score 52; DB 2; Length 251;
```

```
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 166 NKKMVTAGELD 176
OY 3 NKKKATVGELD 13

RESULT 15
ENTRY 558590 #type complete
TITLE ribosomal protein S3 - maize chloroplast
ORGANISM #formal_name chloroplast Zea mays #common_name maize
DATE 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change
17-Mar-1999
ACCESSIONS 558590
REFERENCE 558531
#authors Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
#journal J. Mol. Biol. (1995) 251:614-628
#title Complete sequence of the maize chloroplast genome: gene
content, hotspots of divergence and fine tuning of genetic
information by transcript editing.
#cross-references MUID:95395841
#accession 558590
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 1-224 ##label MAI
##cross-references EMBL:X86563; NID:902200; PID:902260
#note        the nucleotide sequence was submitted to the EMBL Data
              Library, April 1995

GENETICS
#gene        rps3
#genome      chloroplast
CLASSIFICATION #superfamily Escherichia coli ribosomal protein S3
KEYWORDS      chloroplast; protein biosynthesis; ribosome
SUMMARY       #length 224 #molecular-weight 25916 #checksum 3426

Query Match 63.0%; Score 51; DB 2; Length 224;
Best Local Similarity 50.0%; Pred. No. 1.05e+01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKGAIIELE 102
OY 4 KKKATVGELD 13

Search completed: Tue Aug 31 19:26:51 1999
Job time : 14 secs.
```


RL NAT. STRUCT. BIOL. 2:680-686(1995).
 RN [6]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE: 97334373.
 RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity".
 RL J. MOL. BIOL. 269:270-280(1997).
 CC -1- SUBUNIT: MONOMER.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M18970: G153121: -.
 CC PIR: A28664: A28664.
 CC PIR: A29566: A29566.
 CC PDB: 1SEF: 11-JUL-96.
 CC PDB: 1SEA: 15-OCT-95.
 CC PDB: 1SXT: 19-NOV-97.
 CC PROSITE: PS00277: STAPH_STREP_TOXIN_1; 1.
 CC PROSITE: PS00278: STAPH_STREP_TOXIN_2; 1.
 CC PRAM: PF01123: Staph-Strep_toxin; 1.
 CC DR ENTEROTOXIN: TOXIN; SIGNAL; SUPEROXIDANT; ZINC; 3D-STRUCTURE.
 CC KM STGNAL: 1 24
 CC FT CHAIN 25 257 ENTEROTOXIN A.
 CC FT DISULFID 120 130
 CC FT METAL 25 25 ZINC.
 CC FT METAL 211 211 ZINC.
 CC FT METAL 249 249 ZINC.
 CC FT METAL 251 251 ZINC.
 CC FT CONFLICT 242 242 T -> S (IN REF. 2).
 CC SQ SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;
 CC -----
 CC Query Match 72.8%; Score 59; DB 1; Length 257;
 CC Best Local Similarity 81.8%; Pred. No. 4.80e-02;
 CC Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC Dh 170 NKKRVQVQLD 180
 CC |||:|||||
 CC Qy 3 NKKRVQVQLD 13
 CC -----
 CC RESULT 2
 CC ID ETXB_STAUV STANDARD; PRT: 266 AA.
 CC AC P01552;
 CC DT 21-JUL-1986 (REL. 01, CREATED)
 CC DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 CC DT 13-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 CC DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
 CC GN ENTB.
 CC OS STAPHYLOCOCCUS AUREUS.
 CC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC STAPHYLOCOCCUS.
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE: 86168029.
 CC RA JONES C.L., KHAN S.A.;
 CC "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
 CC aureus".
 CC RT J. BACTERIOL. 166:29-33(1986).
 CC [2]
 CC RP SEQUENCE OF 40-91 FROM N.A.

RX MEDLINE: 85298255.
 RA RANELLI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in
 RT Escherichia coli and Staphylococcus aureus".
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985).
 RN [3]
 RP SEQUENCE OF 28-266 (S-6).
 RX MEDLINE: 71007902.
 RA HUANG I.-Y., BERGDOL M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The
 RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
 RT B, and the complete amino acid sequence".
 RL J. BIOL. CHEM. 245:3518-3525(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE: 93063291.
 RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen".
 RL NATURE 359:801-806(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RX MEDLINE: 94203282.
 RA JARDEZKY T.S., BROWN J.H., GORCA J.C., STERN L.J., URBAN R.G.,
 RA CHI Y.I., STAUFFACHER C., STROMINGER J.L., WILEY D.C.;
 RT "three-dimensional structure of a human class II histocompatibility
 RT molecule complexed with superantigen".
 RL NATURE 368:711-718(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE: 98181012.
 RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal
 RT enterotoxin B at 1.5-A resolution: implications for superantigen
 RT recognition by MHC class II molecules and T-cell receptors".
 RL J. MOL. BIOL. 277:61-79(1998).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M1118: G153000: -.
 CC PIR: A01815: ENSAB6.
 CC PIR: S27360: S27360.
 CC PDB: 1SEB: 20-JUN-96.
 CC PDB: 2SEB: 28-JAN-98.
 CC PDB: 3SEB: 27-MAY-98.
 CC PDB: 1SE4: 16-JUN-97.
 CC PDB: 1SE4: 15-OCT-97.
 CC PROSITE: PS00277: STAPH_STREP_TOXIN_1; 1.
 CC PROSITE: PS00278: STAPH_STREP_TOXIN_2; 1.
 CC PRAM: PF01123: Staph-Strep_toxin; 1.
 CC DR ENTEROTOXIN: TOXIN; SIGNAL; SUPEROXIDANT; 3D-STRUCTURE.
 CC KM STGNAL: 1 27
 CC FT CHAIN 28 266 ENTEROTOXIN B.
 CC FT DISULFID 120 140
 CC FT CONFLICT 56 58
 CC FT CONFLICT 69 77 DQLYFDLI -> NEFFDIYLI (IN REF. 3).
 CC FT CONFLICT 118 118 MISSING (IN REF. 3).
 CC FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
 CC FT CONFLICT 133 135 QTD -> GN (IN REF. 3).
 CC FT CONFLICT 149 150 NG -> GN (IN REF. 3).
 CC FT CONFLICT 156 156 Y -> YY (IN REF. 3).
 CC FT CONFLICT 185 186 OE -> EQ (IN REF. 3).
 CC FT CONFLICT 233 233 D -> N (IN REF. 3).
 CC FT CONFLICT 246 247 DN -> ND (IN REF. 3).

50 SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;

Query Match 71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 8.32e-02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 178 NKKKATVOELD 188
1111111111
3 NKKKATVOELD 13

```

RESULT 3
ID ETRD_STAU STANDARD: PRT: 258 AA.
AC P20723;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE D PRECURSOR (SED).
ENTD.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89359112.
RA BAYLES K.W., IANDOLO J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
enterotoxin D."
RL J. BACTERIOL. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX STRAIN-ATCC 23225;
RX MEDLINE: 97157473.
RA SUNDSROM M., ABRAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,
DOHLSTEN M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals
Zn2+-mediated homodimerization."
RL EMBO J. 15:6832-6840(1996).
CC -1- SUBUNIT: HOMODIMER. ZINC-DEPENDENT.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M28521; G758691; -
DR PIR: A33953; A33953.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph-Strep-Toxin; 1.
DR HSP: P13163; ISXT.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23225).
SQ SEQUENCE 258 AA; 29746 MW; 2D1AA120 CRC32;

Query Match 70.4%; Score 57; DB 1; Length 258;
Best Local Similarity 72.7%; Pred. No. 1.43e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 171 DKNVTOELD 181
1111111111

```

```

Oy 3 NKKKATVOELD 13

RESULT 4
ID ETRD_STAU STANDARD: PRT: 257 AA.
AC P12993;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
ENTE.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RX STRAIN-MJ265;
RX MEDLINE: 88257005.
RA COUCH J.L., SOLTIS M.T., BETLEY M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal
enterotoxin gene."
RL J. BACTERIOL. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE: 96022987.
RA SNAMINATHAN S., FUREY M.F., BLECHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
enterotoxins."
RL NAT. STRUCT. BIOL. 2:680-686(1995).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21319; G153002; -
DR PIR: A28179; A28179.
DR PDB: 1SEE; 15-OCT-95.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PRAM: PF01123; Staph-Strep-Toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 28 257 ENTEROTOXIN E.
SQ SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;

Query Match 65.4%; Score 53; DB 1; Length 257;
Best Local Similarity 72.7%; Pred. No. 1.18e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 170 SKKEVTOELD 180
1111111111
Oy 3 NKKKATVOELD 13

RESULT 5
ID SR72_CANFA STANDARD: PRT: 670 AA.
AC P33731;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).
SN SRP72.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.

```



```

FT CONFLICT 40 40 H -> Q (IN REF. 2).
FT CONFLICT 43 43 S -> N (IN REF. 2).
FT CONFLICT 47 59 NLONRYFLYEGDP -> TFKIYIFMRVTL (IN
FT CONFLICT 129 129 REF. 2).
FT CONFLICT 165 178 I -> L (IN REF. 2).
FT CONFLICT 165 178 TNNKMTAQLDYK -> QIRNGNCSRIYST (IN
FT REF. 2).
SQ SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;

Query Match
Best Local Similarity 64.2%; Score 52; DB 1; Length 251;
Pred. No. 1.97e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 166 NKKMTAQLDYK 176
|||:||||
Qy 3 NKKMTAQLDYK 13

RESULT 8
ID YCF4.CYAPA STANDARD: PRT: 187 AA.
AC P48192:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 21.2 KD PROTEIN YCF4.
GN YCF4.
OS CYANOPHORA PARADOXA.
OC CYANELLE.
OC EURAROTIA: GLAUCOCYSTOPHYCEAE: CYANOPHORACEAE: CYANOPHORA.
RN [1]
RP SEQUENCE FROM N.A.
PC STRAIN-LB555 / PRINGSHEIM;
RA STREHM V.L., MICHALOWSKI C.B., LUFFELHARDT W., BOHNERT H.J.,
RA BRYANT D.A.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: BELONGS TO THE YCF4 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U30821; GI016091; -
DR MENDEL; 7950; CYAPA:YCF4;1.
KW CYANELLE: HYPOTHETICAL PROTEIN.
SQ SEQUENCE 187 AA; 21207 MW; B5D7E756 CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 187;
Pred. No. 3.26e+00;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 97 YNKKKGTV 104
||||:|
Qy 2 YNKKKATV 9

RESULT 9
ID R3.MAIZE STANDARD: PRT: 224 AA.
AC P06586:
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ZEA MAIZE (MAIZE).
OC CHLOROPLAST.
OC EURAROTIA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; LILIPSIDA: POALES;
OC POACEAE; ZEA.
CC [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 87231045.
RA MCLAUGHLIN W.E., LARRINDA I.M.;
RT "The sequence of the maize plastid encoded rps3 locus.";
RL NUCLEIC ACIDS RES. 15:4689-4689(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95395841.
RA MATER R.M., NECKERMAN K., IGLOI G.L., KOESSEL H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. MOL. BIOL. 251:614-628(1995).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y00340; G12469; -
DR EMBL: M31336; G552741; -
DR EMBL: X86563; G902260; -
DR MAIZEDB: 66303; -
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
DR PFAM: PF00189; S3_C; 1.
DR PFAM: PF00417; S3_N; 1.
DR MENDEL; 13473; ZEMA:RPS3;1.
KW RIBOSOMAL PROTEIN; CHLOROPLAST.
SQ SEQUENCE 224 AA; 25916 MW; 3ED95CFF CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 224;
Pred. No. 3.26e+00;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKGAIIELE 102
||||:|
Qy 4 KKKATQELD 13

RESULT 10
ID R3-ORYZA STANDARD: PRT: 239 AA.
AC P12146:
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ORYZA SATIVA (RICE).
OC CHLOROPLAST.
OC EURAROTIA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; LILIPSIDA: POALES;
OC POACEAE; ORYZA.
RN [1]
RP SEQUENCE FROM N.A.
PC STRAIN-CV. NIPONBARE;
RA SUGIURA M.;
RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP COMPLETE GENOME.
RX MEDLINE: 89364698.
RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,
RA MORI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-Q.,
RA KANNO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct tRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL MOL. GEN. GENET. 217:185-194(1989).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----

```

```

DR EMBL; L19947; G431760; -.
DR EMBL; X03245; G3779; -.
DR EMBL; Z75107; E252073; -.
DR PIR; S07682; S07682.
DR SCD; L0001392; P0756.
DR PFM; PF00588; Spol_methylase; 1.
DR KW MITOCHONDRION; TRANSFERASE; METHYLTRANSFERASE.
SO SEQUENCE 412 AA; 46387 MW; B3436655 CRC32.

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 412;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 79 YKKKAYEKL 89
|||||1:1
Oy 2 YNKKATVOEL 12

RESULT 12
ID LIGAMOUSE STANDARD; PRT; 566 AA.
AC 061211;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE LIGATIN (FRAGMENT).
GN LGTN.
OS MUS MUSCULUS (MOUSE).
OC EUMETAZOA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIURIGNATHI; MORIDAE; MORINAE; MUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 97224508.
RA MAINAR-DRAGOJEVIC D., TRACHTULEC Z., VINCEK V.;
RT "Assignment of the mouse ligatin gene (Lgtn) to chromosome 1f by in
RT situ hybridization."
RL GENOMICS 40:192-193(1997).
CC -I- FUNCTION: TRAFFICKING RECEPTOR FOR PHOSPHOLYCOPROTEINS. LOCALIZES
CC PHOSPHOLYCOPROTEINS WITHIN ENDOSOMES AND AT THE CELL PERIPHERY
CC WHERE THEY PARTICIPATE IN SPECIFIC METABOLIC PROCESSES AS WELL AS
CC INTERCELLULAR ADHESION (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D58337; G1377880; -.
DR MGD; MGI:109342; LGTN.
KW MEMBRANE.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 566 AA; 62239 MW; AAB58F4B CRC32;

Query Match
Best Local Similarity 50.0%; Score 51; DB 1; Length 566;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 503 YNKKATVOEL 13
|||||1:1
Oy 2 YNKKATVOEL 13

RESULT 13
ID BRC2_HUMAN STANDARD; PRT; 3418 AA.
AC P51587;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN.

```


FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 268 EARLY NODULIN 20.
 FT DOMAIN 23 ? PLASTOCYANIN-LIKE.
 FT DOMAIN 136 145 POLY-PRO.
 SQ SEQUENCE 268 AA; 28668 MW; 29EAFD8F CRC32;
 Query Match 61.7%; Score 50; DB 1; Length 268;
 Best Local Similarity 41.7%; Pred. No. 5.36e+00;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

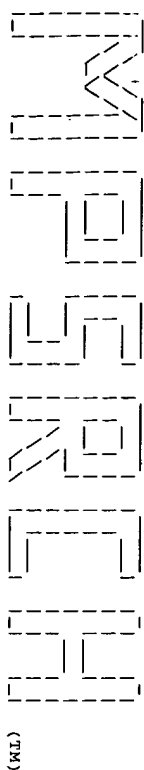
Db 65 YNKTESVHEVE 76
 ||| :|| :
 QY 2 YNKKATVOELD 13

RESULT 15
 ID HEL_HAEIN STANDARD; PRT: 274 AA.
 AC P26093;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LIPOPROTEIN E PRECURSOR (OUTER MEMBRANE PROTEIN P4) (OMP P4).
 GN HEL OR OMP4 OR H10693.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURILLACEAE;
 OC HAEMOPHILUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 263-274.
 SC STRAIN-RD / KW20B;
 RX MEDLINE; 91348867.
 RA GREEN B.A., FARLEY J.E., QUINN-DEY T., DEICH R.A., ZLOTNICK G.W.;
 RT "The e (p4) outer membrane protein of Haemophilus influenzae: the
 RT biologic activity of anti-e serum and cloning and sequencing of the
 RT structural gene.";
 RL INECT. IMUN. 59:3191-3198(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 SC STRAIN-RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BOLT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., CORTON M.D.,
 RA UETTERACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL SCIENCE 269:496-512(1995).
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
 CC ANCHOR.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M68502; G148896; -;
 DR EMBL; U32752; G1573696; -;
 DR PIR; A43604; A43604.
 DR TIGR; H10693; -;
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW OUTER MEMBRANE; LIPOPROTEIN; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 274 LIPOPROTEIN E.
 FT LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
 FT CONFLICT 30 30 G -> E (IN REF. 1).
 SQ SEQUENCE 274 AA; 30431 MW; 55289338 CRC32;

Query Match 61.7%; Score 50; DB 1; Length 274;
 Best Local Similarity 70.0%; Pred. No. 5.36e+00;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 77 KKAIVADLD 86
 ||| | :||
 QY 4 KKAIVADLD 13

Search completed: Tue Aug 31 19:25:14 1999
 Job time : 8 secs.


 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Aug 31 19:25:32 1999; Maspar time 5.43 Seconds
 140.712 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-150-947-9
 Description: (1-14) from US09150947.pep
 Perfect Score: 81
 Sequence: 1 XYNKKKATVQELDX 14

Scoring table:
 PAM 150
 Gap 15

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

sptrembl9
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mmc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 23.956; Variance 28.794; scale 0.832

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|--------|------------------------|-----------|
| 1 | 63 | 77.8 | 268 | 2 | 085217 | ENTEROTOXIN J. | 1.71e-02 |
| 2 | 60 | 74.1 | 460 | 3 | 060095 | HYPOTHETICAL 52.7 KD P | 8.45e-02 |
| 3 | 59 | 72.8 | 362 | 2 | 045833 | SPOULIATION PROTEIN. | 1.43e-01 |
| 4 | 58 | 71.6 | 260 | 2 | 054971 | SUPERANTIGEN. | 2.39e-01 |
| 5 | 58 | 71.6 | 260 | 2 | 054738 | SUPERANTIGEN SSA. | 2.39e-01 |
| 6 | 58 | 71.6 | 260 | 2 | 054739 | SUPERANTIGEN SSA. | 2.39e-01 |
| 7 | 58 | 71.6 | 3394 | 5 | 077384 | MAL3P6.11 PROTEIN. | 2.39e-01 |
| 8 | 56 | 69.1 | 464 | 13 | 091683 | MOTHERS AGAINST DPP. | 6.64e-01 |
| 9 | 56 | 69.1 | 760 | 3 | P91308 | COSMID F46F11. | 6.64e-01 |
| 10 | 56 | 69.1 | 1232 | 13 | 093308 | 14S COHESIN SMC1 SUBUN | 6.64e-01 |
| 11 | 55 | 67.9 | 811 | 3 | P87145 | HYPOTHETICAL 92.5 KD P | 1.10e+00 |
| 12 | 54 | 66.7 | 490 | 2 | 007382 | HISTIDINE KINASE LKIN | 1.80e+00 |
| 13 | 54 | 66.7 | 1233 | 13 | 073686 | MITOSIS-SPECIFIC CHROM | 1.80e+00 |
| 14 | 53 | 65.4 | 241 | 2 | 053585 | ENTEROTOXIN H PRECURSO | 2.94e+00 |
| 15 | 53 | 65.4 | 271 | 10 | 063075 | HYPOTHETICAL 30.9 KD P | 2.94e+00 |
| 16 | 53 | 65.4 | 325 | 5 | 061207 | H04J21.1 PROTEIN (FRAG | 2.94e+00 |
| 17 | 53 | 65.4 | 393 | 4 | 060870 | KIN17 PROTEIN. | 2.94e+00 |
| 18 | 53 | 65.4 | 725 | 4 | 014995 | KINA0178 (FRAGMENT). | 2.94e+00 |
| 19 | 53 | 65.4 | 880 | 3 | 006708 | CHROMOSOME XII COSMID | 2.94e+00 |
| 20 | 53 | 65.4 | 1225 | 4 | 014683 | KINA0178 PROTEIN (FRAG | 2.94e+00 |

| 21 | 53 | 65.4 | 1233 | 4 | 016351 | SB1.8/DXS423P-MITOSIS- | 2.94e+00 |
|----|----|------|------|----|--------|------------------------|----------|
| 22 | 52 | 64.2 | 127 | 2 | 031469 | YC6C PROTEIN. | 4.78e+00 |
| 23 | 52 | 64.2 | 236 | 2 | P97163 | TYPE A EXOTOXIN PRECUR | 4.78e+00 |
| 24 | 52 | 64.2 | 226 | 2 | 054779 | TYPE A EXOTOXIN PRECUR | 4.78e+00 |
| 25 | 52 | 64.2 | 236 | 2 | 057453 | TYPE A EXOTOXIN PRECUR | 4.78e+00 |
| 26 | 52 | 64.2 | 508 | 4 | 092599 | MYELOBLAST KINA0202 (F | 4.78e+00 |
| 27 | 51 | 63.0 | 109 | 5 | 044441 | B0546.1 PROTEIN | 7.71e+00 |
| 28 | 51 | 63.0 | 258 | 2 | 085382 | EXTRACELLULAR ENTEROTO | 7.71e+00 |
| 29 | 51 | 63.0 | 262 | 2 | 067006 | FLAGELLAR HOOK BASAL-B | 7.71e+00 |
| 30 | 51 | 63.0 | 319 | 14 | 065408 | POLYPROTEIN (FRAGMENTS | 7.71e+00 |
| 31 | 51 | 63.0 | 319 | 14 | 065409 | POLYPROTEIN (FRAGMENTS | 7.71e+00 |
| 32 | 51 | 63.0 | 319 | 14 | 065407 | POLYPROTEIN (FRAGMENTS | 7.71e+00 |
| 33 | 51 | 63.0 | 334 | 4 | 015008 | BCA2 (FRAGMENT) | 7.71e+00 |
| 34 | 51 | 63.0 | 336 | 5 | 021645 | SIMILAR TO ACETICOLIN | 7.71e+00 |
| 35 | 51 | 63.0 | 674 | 11 | 035920 | CALPAIN LARGE SUBUNIT | 7.71e+00 |
| 36 | 51 | 63.0 | 713 | 11 | 088666 | CALPAIN I LARGE SUBUNI | 7.71e+00 |
| 37 | 51 | 63.0 | 713 | 11 | P97571 | MO-CALPAIN LARGE SUBUN | 7.71e+00 |
| 38 | 51 | 63.0 | 713 | 11 | 035350 | CALPAIN 1 | 7.71e+00 |
| 39 | 51 | 63.0 | 791 | 5 | 019148 | COSMID F07C3 | 7.71e+00 |
| 40 | 51 | 63.0 | 804 | 5 | 044896 | ZK484.4 PROTEIN. | 7.71e+00 |
| 41 | 51 | 63.0 | 3418 | 4 | 013879 | BRCA2 GENE EXON 2 (AND | 7.71e+00 |
| 42 | 50 | 61.7 | 288 | 13 | 091491 | DYSTROPHIN (FRAGMENT) | 1.23e+01 |
| 43 | 50 | 61.7 | 367 | 14 | 089736 | POLYPROTEIN (FRAGMENT) | 1.23e+01 |
| 44 | 50 | 61.7 | 367 | 14 | 089735 | POLYPROTEIN (FRAGMENT) | 1.23e+01 |
| 45 | 50 | 61.7 | 3685 | 4 | 014205 | DYSTROPHIN (DMD). | 1.23e+01 |

ALIGNMENTS

| RESULT | ID | 085217 | PRELIMINARY: | PRT: | 268 AA. |
|--|--|--------------|--------------|-----------------|---------|
| AC | 085217 | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, CREATED) | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN J. | | | | |
| GN | SEJ. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OG | PLASMID P18A85. | | | | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | |
| OC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-KS11410. | | | | |
| RA | ZHANG S., IANLOLO J.J., STEWART G.C.; | | | | |
| RT | "The enterotoxin D plasmid of Staphylococcus aureus encodes a second | | | | |
| RT | enterotoxin determinant (sej)"; | | | | |
| RL | SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS. | | | | |
| DR | EMBL: AF053140; G3372542; -. | | | | |
| DR | PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1. | | | | |
| DR | PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1. | | | | |
| KW | PLASMID. | | | | |
| SO | SEQUENCE | 268 AA; | 31230 MW; | 52EB1B06 CRC32; | |
| Query Match | | | | | |
| Best local similarity 81.8%; Pred. No. 1.71e-02; | | | | | |
| Matches %; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | | | | | |
| DB | 170 NKKKATVQELDX 180 | | | | |
| OY | 3 NKKKATVQELDX 13 | | | | |
| RESULT | | | | | |
| ID | 060095 | PRELIMINARY: | PRT: | 460 AA. | |
| AC | 060095 | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 07, CREATED) | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE) | | | | |
| DT | 01-NOV-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE) | | | | |
| DE | HYPOTHETICAL 52.7 KD PROTEIN. | | | | |
| GN | SPB14C8.15 | | | | |
| OS | SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). | | | | |
| OC | EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHTASCOMYCETES; | | | | |

OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 OC SCHIZOSACCHAROMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.;
 RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AL022305; E1285407; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 460 AA; 52670 MW; 835D7303 CRC32;

Query Match 74.1%; Score 60; DB 3; Length 460;
 Best Local Similarity 50.0%; Pred. No. 8,45e-02;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 105 YKKKKGKTEELN 116
 1:111:111:
 QY 2 YNKKKATVOEELD 13

RESULT 3
 ID 045833; PRELIMINARY; PRT; 362 AA.
 AC 045833;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE SPOULATION PROTEIN.
 GN SPOID.
 OS CLOSTRIDIUM ACETOBUTYLICUM.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
 OC CLOSTRIDIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA REID S.J., HANCOCK K., SANTANGELO J.D., WOODS D.R.;
 RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: M87835; G144915; -
 KW SPOULATION.
 SQ SEQUENCE 362 AA; 40998 MW; 75E3556E CRC32;

Query Match 72.8%; Score 59; DB 2; Length 362;
 Best Local Similarity 58.3%; Pred. No. 1,43e-01;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKKDSVEELD 78
 1:11:111:
 QY 2 YNKKKATVOEELD 13

RESULT 4
 ID 054971; PRELIMINARY; PRT; 260 AA.
 AC 054971;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SUPERANTIGEN.
 GN SSA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WELLER;
 RX MEDLINE: 94222556.
 RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
 RA RICH R.R.;
 RT "Molecular characterization and phylogenetic distribution of the
 streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
 RT INECT. IMMUN. 62:1867-1874(1994).
 DR EMBL: L28565; G476764; -
 DR PFAM: PF01123; Strep_Stp_toxin; 1.
 RN SUPERANTIGEN.
 SQ SEQUENCE 260 AA; 29797 MW; FE391C2B CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;
 Best Local Similarity 81.8%; Pred. No. 2,39e-01;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKKQTVQOELD 183
 111111111
 QY 3 NKKKATVOEELD 13

RESULT 5
 ID 054738; PRELIMINARY; PRT; 260 AA.
 AC 054738;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SUPERANTIGEN SSA.
 GN SSA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MGAS 1842;
 RX MEDLINE: 94222556.
 RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
 RA RICH R.R.;
 RT "Molecular characterization and phylogenetic distribution of the
 streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
 RT INECT. IMMUN. 62:1867-1874(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MGAS 1842;
 RX MEDLINE: 96178602.
 RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
 RT "Phylogenetic distribution of streptococcal superantigen ssa allelic
 variants provides evidence for horizontal transfer of ssa within
 streptococcus pyogenes.";
 RT INECT. IMMUN. 64:1161-1165(1996).
 DR EMBL: U48793; G1245174; -
 DR PFAM: PF01123; Strep_Stp_toxin; 1.
 SQ SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;
 Best Local Similarity 81.8%; Pred. No. 2,39e-01;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKKQTVQOELD 183
 111111111
 QY 3 NKKKATVOEELD 13

RESULT 6
 ID 054739; PRELIMINARY; PRT; 260 AA.
 AC 054739; 054737;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SUPERANTIGEN SSA.
 GN SSA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 94222556.
 RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
 RA RICH R.R.;
 RT "Molecular characterization and phylogenetic distribution of the
 streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
 RT INECT. IMMUN. 62:1867-1874(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96178602.

RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL INFECT. IMMUN. 64:1161-1165(1996).

DR EMBL: U48794; G1245176; -;
DR EMBL: U48792; G1245172; -;
DR PFAM: PF01123; Strep-Stp toxin. 1.
SQ SEQUENCE 260 AA; 29767 MW; C81446C1 CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;

Best Local Similarity 81.8%; Pred. No. 2.39e-01;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKKQTVQELD 183
||| |||||
3 NKKQTVQELD 13

RESULT 7
ID 077384 PRELIMINARY; PRT; 3394 AA.

AC 077384;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE MAL3P6.11 PROTEIN.

OS PLASMODIUM FALCIPARUM.

OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-3D7;

RA MURPHY L., LAMSON D., BARRELL B.;

RL SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: 298551; E1331922; -;

SQ SEQUENCE 3394 AA; 402947 MW; 4C3F2778 CRC32;

Query Match 71.6%; Score 58; DB 5; Length 3394;

Best Local Similarity 50.0%; Pred. No. 2.39e-01;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 373 YNKSNTIOQLN 384
||| |::|:
2 YNKSNTIOQLN 13

RESULT 8
ID 091693 PRELIMINARY; PRT; 464 AA.

AC 091693;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE MOTHERS AGAINST DPP.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENODIDINE; XENOPUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96312915.

RA THOMSEN G.H.;

RT "Xenopus mothers against decapentaplegic is an embryonic ventralizing
RT agent that acts downstream of the BMP-2/4 receptor.";

RL DEVELOPMENT 122:2359-2366(1996).

DR EMBL: U58834; G1381671; -;

DR PFAM: PF00968; Dwarf1n. 1.

SQ SEQUENCE 464 AA; 52346 MW; 4017799F CRC32;

Query Match 69.1%; Score 56; DB 13; Length 464;
Best Local Similarity 54.5%; Pred. No. 6.64e-01;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 42 KKKKAIOELE 52

QY :|||||: 3 NKKKATVQELD 13

RESULT 9
ID P91308 PRELIMINARY; PRT; 760 AA.

AC P91308;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE COSMID F46F11.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECRETINTEA; RHABDITIDA; RHABDITIDA;

OC RHABDITINA; RHABDITIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,

RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LATSTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL NATURE 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA PAULEY A., GATTUNG S.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA WATERSTON R.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U88173; G1825648; -;

SQ SEQUENCE 760 AA; 88595 MW; D1020BBA CRC32;

Query Match 69.1%; Score 56; DB 5; Length 760;

Best Local Similarity 33.3%; Pred. No. 6.64e-01;

Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 569 YDSKNSIDLE 580
|:|::|:
2 YNKSNTIOQLN 13

RESULT 10
ID 093308 PRELIMINARY; PRT; 1232 AA.

AC 093308;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE 14S COHESIN SMC1 SUBUNIT.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENODIDINE; XENOPUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96315077.

RA LOSADA A., HIRANO M., HIRANO T.;

RT "Identification of Xenopus SMC protein complexes required for sister
RT chromatid cohesion.";

RL GENES DEV. 12:1966-1997(1998).

DR EMBL: AF051784; G3328231; -;

SQ SEQUENCE 1232 AA; 142627 MW; FDE05B84 CRC32;

Query Match 69.1%; Score 56; DB 13; Length 1232;
 Best Local Similarity 50.0%; Pred. No. 6.64e+01;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRADMDEL 337

QY 2 YNKKATVQELD 13

RESULT 11
 ID P87145 PRELIMINARY; PRT: 811 AA.
 AC P87145;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DE HYPOTHETICAL 92.5 KD PROTEIN C25H2.03 IN CHROMOSOME II.
 GN SPBC35H2.03.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA: FUNGI: ASCOMYCOTA: ARCHIASCOMYCETES:
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 OC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-9712;
 RA RAJANDREAN M.A., CONNOR R.E.,
 RA DURSO G., IYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 DR EMBL: 295397; E316120; -.
 KW HYPOTHETICAL PROTEIN: TRANSMEMBRANE.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT TRANSMEM 362 382 POTENTIAL.
 FT TRANSMEM 602 622 POTENTIAL.
 FT TRANSMEM 630 650 POTENTIAL.
 SQ SEQUENCE 811 AA; 92452 MW; E1E2B77 CRC32;

Query Match 67.9%; Score 55; DB 3; Length 811;
 Best Local Similarity 58.3%; Pred. No. 1.10e+00;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 14 YDKRKATVELE 25

QY 2 YNKKATVQELD 13

RESULT 12
 ID 007382 PRELIMINARY; PRT: 490 AA.
 AC 007382;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HISTIDINE KINASE LTKINA.
 GN LTKINA.
 OS LACTOCOCCUS LACTIS CREAMORIS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC LACTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MG1363;
 RX MEDLINE: 97316457.
 RA O'CONNELL-WOTHERWAY M., FITZGERALD G.F., VAN SINDEREN D.;
 RT "Cloning and sequence analysis of putative histidine protein kinases
 isolated from *Lactococcus lactis* MG1363."
 RL APPL. ENVIRON. MICROBIOL. 63:2454-2459(1997).
 DR EMBL: U81166; G2182835; -.
 DR PRAM: PF00512; signal1.1.
 SQ SEQUENCE 490 AA; 55884 MW; 05197910 CRC32;

Query Match 66.7%; Score 54; DB 2; Length 490;
 Best Local Similarity 70.0%; Pred. No. 1.80e+00;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 7 FNKKETVEE 16

QY 2 YNKKATVQELD 11

RESULT 13
 ID 073696 PRELIMINARY; PRT: 1233 AA.
 AC 073696;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DE MITOSIS-SPECIFIC CHROMOSOME SEGREGATION PROTEIN SWC1 HOMOLOG.
 GN SWC1.
 OS FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: ACTINOPTERYGII; NEOPTERYGII;
 OC TELEOSTEI: EUTELEOSTEI: ACANTHOPTERYGII; PERCOMORPHA;
 OC TETRAODONTIFORMES; TETRAODONTIFORMES; TETRAODONTIDAE; FUGU.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RIBOLDI TUNNICLIFFE G.R., PLATZER M., NYAKATURA G., ELGAR G.S.,
 RA BRENNER S., ROSENTHAL A.;
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF026198; G3098266; -.
 SQ SEQUENCE 1233 AA; 143100 MW; FBD2F859 CRC32;

Query Match 66.7%; Score 54; DB 13; Length 1233;
 Best Local Similarity 50.0%; Pred. No. 1.80e+00;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRADMDEL 337

QY 2 YNKKATVQELD 13

RESULT 14
 ID Q53585 PRELIMINARY; PRT: 241 AA.
 AC Q53585;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN H PRECURSOR.
 GN SEH.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D4508;
 RA REN K., BANNAN J.D., PANCHOLI V., CHEUNG A.L., ROBBINS J.C.,
 RA FISCHETTI V.A., ZABRISKIE J.B.;
 RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U11702; G510692; -.
 DR PRAM: PF01123; Staph_Strep-toxin; 1.
 KW SIGNAL.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 241 ENTEROTOXIN H.
 SQ SEQUENCE 241 AA; 27858 MW; AE5AB04A CRC32;

Query Match 65.4%; Score 53; DB 2; Length 241;
 Best Local Similarity 72.7%; Pred. No. 2.94e+00;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 153 NKKVTLQELD 163

QY 3 NKKATVQELD 13

RESULT 15
 ID 065075 PRELIMINARY; PRT: 271 AA.
 AC 065075;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 30.9 KD PROTEIN (FRAGMENT).
GN S850.
OS PICEA MARIANA.
OC EUDARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC PICEA.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.;
RL GENETICS 0:0-0(1998).
DR EMBL; AF051236; G2982303; -.
KW HYPOTHETICAL PROTEIN.
FT NON_TER
SQ SEQUENCE 271 AA; 30897 MW; 1DEA85B1 CRC32;

Query Match 65.4%; Score 53; DB 10; Length 271;
Best Local Similarity 54.5%; Pred. No. 2,94e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 115 YSKTKAWEDL 125
QY 2 YNKKKATVOEL 12

Search completed: Tue Aug 31 19:26:19 1999
Job time : 47 secs.

THIS PAGE BLANK (USPTO)

M P S R C H
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:29:42 1999; Maspar time 3.60 Seconds
Tabular output not generated. 82.681 Million cell updates/sec

Title: >US-09-150-947-10
Description: (1-14) from US09150947.pep
Perfect Score: 81
Sequence: 1 YNKKKATVQELDX 14
Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.360; Variance 49.153; scale 0.353

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 81 | 100.0 | 12 34 | W64637 | Synthetic SEB peptide | 1.54e-02 |
| 2 | 81 | 100.0 | 13 34 | W64641 | Synthetic SEB peptide | 1.54e-02 |
| 3 | 81 | 100.0 | 13 34 | W64645 | Synthetic SEB peptide | 1.54e-02 |
| 4 | 81 | 100.0 | 14 34 | W64644 | Synthetic SEB peptide | 1.54e-02 |
| 5 | 81 | 100.0 | 14 34 | W64645 | Synthetic SEB peptide | 1.54e-02 |
| 6 | 81 | 100.0 | 24 34 | W64642 | Synthetic SEB peptide | 1.54e-02 |
| 7 | 81 | 100.0 | 35 34 | W64643 | Synthetic SEB peptide | 1.54e-02 |
| 8 | 64 | 79.0 | 10 34 | W64638 | Synthetic SEB peptide | 1.96e+00 |
| 9 | 59 | 72.8 | 28 19 | W04494 | Staphylococcal entero | 7.72e+00 |
| 10 | 59 | 72.8 | 36 36 | W72425 | Peptide #5 for reduci | 7.72e+00 |
| 11 | 59 | 72.8 | 38 36 | W72427 | Peptide #6 for reduci | 7.72e+00 |
| 12 | 59 | 72.8 | 91 27 | W24299 | Staphylococcus aureus | 7.72e+00 |
| 13 | 59 | 72.8 | 233 3 | R13203 | Staphylococcal entero | 7.72e+00 |
| 14 | 59 | 72.8 | 233 8 | R45011 | Staphylococcal entero | 7.72e+00 |
| 15 | 59 | 72.8 | 233 27 | W35373 | Staphylococcus entero | 7.72e+00 |
| 16 | 59 | 72.8 | 233 20 | W06738 | Staphylococcus entero | 7.72e+00 |

| | | | | | | |
|----|----|------|--------|--------|------------------------|----------|
| 17 | 58 | 71.6 | 12 34 | W64636 | Synthetic SEB peptide | 1.01e+01 |
| 18 | 58 | 71.6 | 13 34 | W64640 | Synthetic SEB peptide | 1.01e+01 |
| 19 | 58 | 71.6 | 239 34 | W64647 | Synthetic SEB protein | 1.01e+01 |
| 20 | 58 | 71.6 | 239 8 | R45014 | Staphylococcal entero | 1.01e+01 |
| 21 | 58 | 71.6 | 239 3 | R13206 | Staphylococcal entero | 1.01e+01 |
| 22 | 58 | 71.6 | 255 20 | W06737 | Staphylococcus entero | 1.01e+01 |
| 23 | 57 | 70.4 | 228 3 | R13205 | Staphylococcal entero | 1.32e+01 |
| 24 | 57 | 70.4 | 228 8 | R45013 | Staphylococcal entero | 1.32e+01 |
| 25 | 54 | 66.7 | 24 36 | W72423 | Peptide #2 for reduci | 2.94e+01 |
| 26 | 54 | 66.7 | 28 36 | W72425 | Peptide #4 for reduci | 2.94e+01 |
| 27 | 53 | 65.4 | 10 34 | W64639 | Synthetic SEB peptide | 3.83e+01 |
| 28 | 53 | 65.4 | 230 3 | R13204 | Staphylococcal entero | 3.83e+01 |
| 29 | 53 | 65.4 | 230 8 | R45012 | Staphylococcal entero | 3.83e+01 |
| 30 | 53 | 65.4 | 245 27 | W35374 | Staphylococcus entero | 3.83e+01 |
| 31 | 53 | 65.4 | 252 27 | W35375 | Staphylococcus entero | 3.83e+01 |
| 32 | 52 | 64.2 | 221 3 | R13209 | Streptococcus pyogenes | 4.97e+01 |
| 33 | 52 | 64.2 | 221 8 | R45017 | Streptococcus pyogenes | 4.97e+01 |
| 34 | 52 | 64.2 | 250 24 | W12145 | Streptococcus pyogenes | 4.97e+01 |
| 35 | 52 | 64.2 | 251 24 | W12147 | Streptococcus pyogenes | 4.97e+01 |
| 36 | 52 | 64.2 | 251 24 | W12153 | Streptococcus pyogenes | 4.97e+01 |
| 37 | 52 | 64.2 | 251 24 | W12097 | Streptococcus pyogenes | 4.97e+01 |
| 38 | 52 | 64.2 | 251 33 | W59781 | Amino acid sequence o | 4.97e+01 |
| 39 | 52 | 64.2 | 251 33 | W59780 | Amino acid sequence o | 4.97e+01 |
| 40 | 52 | 64.2 | 251 24 | W12151 | Streptococcus pyogenes | 4.97e+01 |
| 41 | 52 | 64.2 | 251 24 | W12150 | Streptococcus pyogenes | 4.97e+01 |
| 42 | 52 | 64.2 | 251 24 | W12152 | Streptococcus pyogenes | 4.97e+01 |
| 43 | 52 | 64.2 | 251 24 | W12146 | Streptococcus pyogenes | 4.97e+01 |
| 44 | 52 | 64.2 | 251 24 | W12149 | Streptococcus pyogenes | 4.97e+01 |
| 45 | 52 | 64.2 | 401 36 | W22779 | Human sepiin-2 protel | 4.97e+01 |

ALIGNMENTS

RESULT 1
ID W64637 standard; peptide; 12 AA.
AC W64637;
DE 23-DEC-1998 (first entry)
DE Synthetic SEB peptide p12(151-161).
KW Enterotoxin B; SEB; Pyrogenic exotoxin; PERT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W0882944 A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-11938.
PA (YISS) YISSUM RES 6 DEV CO.
PI Arad G, Kaempfer R.
DR WPI: 98-38042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 8, Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PERT or by a mixture of PERTs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PERTs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PERT.
SQ Sequence 12 AA:
Query Match 100.0%; Score 81; DB 34; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ynkktatvqeld 12

```

OY      2 YNKKRATVOELD 13
      |||||||
RESULT  2
ID      W64641 standard; peptide; 13 AA.
AC      W64641;
DR      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide p121c(150-161).
KM      Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
FH      Staphylococcus aureus.
FT      Key
        Modified_site 1 location/Qualifiers
        /note= "N-terminal Tyr modified by presence of
        N-lauryl-cysteyl"
PN      WO9829444-A1.
PD      09-JUL-1998.
PE      30-DEC-1997; IL0438.
PR      30-DEC-1996; IL-119938.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
        WPI; 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PR      Claim 16; Page 41; 68pp; English.
PS      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PERT or by a mixture of PERTs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PERTs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PERT. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PERT.
        Sequence 13 AA.
SQ
Query Match      100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 ynkkratvgeid 13
      |||||||
OY      2 YNKKRATVOELD 13
      |||||||
RESULT  3
ID      W64646 standard; peptide; 13 AA.
AC      W64646;
DR      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide AC-p12(150-161).
KM      Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
FH      Staphylococcus aureus.
FT      Key
        Modified_site 1 location/Qualifiers
        /note= "N-terminal Tyr modified by N-acetyl group"
        Misc_difference 14 /note= "D-form residue"
PN      WO9829444-A1.
PD      09-JUL-1998.
PE      30-DEC-1997; IL0438.
PR      30-DEC-1996; IL-119938.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;

```

```

DR      WPI; 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 24; Page 41; 68pp; English.
PR      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PERT or by a mixture of PERTs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PERTs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PERT. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PERT.
        Sequence 13 AA.
SQ
Query Match      100.0%; Score 81; DB 34; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 ynkkratvgeid 12
      |||||||
OY      2 YNKKRATVOELD 13
      |||||||
RESULT  4
ID      W64644 standard; peptide; 14 AA.
AC      W64644;
DR      23-OCT-1998 (first entry)
DE      Synthetic SEB peptide Cys-p12(150-161).
KM      Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
        toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
        therapeutic; vaccine; food poisoning.
OS      Synthetic.
FH      Staphylococcus aureus.
FT      Key
        Modified_site 1 location/Qualifiers
        /note= "N-terminal Cys modified by presence of
        N-lauryl-cysteyl"
PN      WO9829444-A1.
PD      09-JUL-1998.
PE      30-DEC-1997; IL0438.
PR      30-DEC-1996; IL-119938.
PA      (YISS ) YISSUM RES & DEV CO.
PI      Arad G, Kaempfer R;
        WPI; 98-388042/33.
PT      New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
        antagonising toxin-mediated activation of T cells and prevention or
        treatment of toxic shock caused by exotoxin(s)
PS      Claim 21; Page 41; 68pp; English.
PR      W64636-W64657 are peptides homologous to the amino acid sequence of a
        fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
        capable of eliciting protective immunity against toxic shock induced by
        PERT or by a mixture of PERTs. Such peptides are also capable of
        antagonising toxin-mediated activation of T-cells, inhibiting expression
        of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
        TNF-beta genes. The peptides may be used to prepare therapeutics or
        vaccines for the treatment of prophylaxis of toxin-mediated activation
        of T cells and eliciting protective immunity against toxic shock induced
        by PERTs. They can also be used for the treatment of harmful effects
        (especially food poisoning) and toxic shock caused by PERT. Antiserum to
        the peptides can also be used for alleviating toxic shock induced by PERT.
        Sequence 14 AA.
SQ
Query Match      100.0%; Score 81; DB 34; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 ynkkratvgeid 13
      |||||||
OY      2 YNKKRATVOELD 13
      |||||||
RESULT  5

```


| | | |
|-----------------------|--|------------------------------------|
| ID | W64645 | standard; peptide: 14 AA. |
| DT | 23-OCT-1998 | (first entry) |
| DE | Synthetic SEB peptide D-Ala. | |
| KW | Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity; | |
| KW | toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor; | |
| OS | therapeutic; vaccine; food poisoning. | |
| OS | Synthetic. | |
| OS | Staphylococcus aureus. | |
| FT | Key | Location/Qualifiers |
| FT | Misc_difference 1 | /note- "D-form residue" |
| FT | Misc_difference 14 | /note- "D-form residue" |
| FN | W09829444-A1. | |
| PD | 09-JUL-1998. | |
| PF | 30-DEC-1997. | IL0438. |
| PR | 30-DEC-1996. | IL-119938. |
| PA | (YISS) YISSUM RES & DEV CO. | |
| PI | Arad G, Kaempfer R. | |
| DR | WPI: 98-388042/33. | |
| PT | New peptide(s) derived from pyrogenic exotoxin - useful for, e.g. | |
| PT | antagonising toxin-mediated activation of T cells and prevention or | |
| PT | treatment of toxic shock caused by exotoxin(s) | |
| PS | Claim 23: Page 41: 68pp: English. | |
| CC | W64638-W64657 are peptides homologous to the amino acid sequence of a | |
| CC | fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide | |
| CC | capable of eliciting protective immunity against toxic shock induced by | |
| CC | PET or by a mixture of PETs. Such peptides are also capable of | |
| CC | antagonising toxin-mediated activation of T-cells, inhibiting expression | |
| CC | of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or | |
| CC | TN-beta genes. The peptides may be used to prepare therapeutics or | |
| CC | vaccines for the treatment of prophylaxis of toxin-mediated activation | |
| CC | of T cells and eliciting protective immunity against toxic shock induced | |
| CC | by PETs. They can also be used for the treatment of harmful effects | |
| CC | (especially food poisoning) and toxic shock caused by PET. Antiserum to | |
| CC | the peptides can also be used for alleviating toxic shock induced by PET | |
| SQ | Sequence 14 AA; | |
| Query Match | 100.0%; | Score 81; DB 34; Length 14; |
| Best Local Similarity | 100.0%; | Pred. No. 1,54e-02; |
| Matches | 12; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| Db | 2 ynrkkatvgeid 13 | |
| QY | 2 ynrkkatvgeid 13 | |
| RESULT | 6 | |
| ID | W64642 | standard; peptide: 24 AA. |
| AC | W64642; | |
| DT | 23-OCT-1998 | (first entry) |
| DE | Synthetic SEB peptide dimer. | |
| KW | Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity; | |
| KW | toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor; | |
| KW | therapeutic; vaccine; food poisoning. | |
| OS | Synthetic. | |
| OS | Staphylococcus aureus. | |
| PN | W09829444-A1. | |
| PD | 09-JUL-1998. | |
| PF | 30-DEC-1997. | IL0438. |
| PR | 30-DEC-1996. | IL-119938. |
| PA | (YISS) YISSUM RES & DEV CO. | |
| PI | Arad G, Kaempfer R. | |
| DR | WPI: 98-388042/33 | |
| PT | New peptide(s) derived from pyrogenic exotoxin - useful for, e.g. | |
| PT | antagonising toxin-mediated activation of T cells and prevention or | |
| PT | treatment of toxic shock caused by exotoxin(s) | |
| PS | Claim 18: Page 41: 68pp: English. | |
| CC | W64638-W64657 are peptides homologous to the amino acid sequence of a | |
| CC | fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide | |
| CC | capable of eliciting protective immunity against toxic shock induced by | |
| CC | PET or by a mixture of PETs. Such peptides are also capable of | |

CC antagonising toxin-mediated activation of T-cells, inhibiting expression of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-beta genes. The peptides may be used to prepare therapeutics or vaccines for the treatment of prophylaxis of toxin-mediated activation of T cells and eliciting protective immunity against toxic shock induced by PEs. They can also be used for the treatment of harmful effects (especially food poisoning) and toxic shock caused by PET. Antiserum to the peptides can also be used for alleviating toxic shock induced by PET.

Sequence 24 AA;

Query Match 100.0%; Score 81; DB 34; Length 24;
Best Local Similarity 100.0%; Pred. No. 1,54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkktatvgeld 12
|||||
2 YNKKKATVQELD 13

RESULT 7
ID W64643 standard; peptide; 35 AA.
AC W64643;
DT 23-OCF-1998 (first entry)
DE Synthetic SEB peptide trimer.
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
RN therapeutic; vaccine; food poisoning.
OS Synthetic.
PS Staphylococcus aureus.
PN M09J829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R:
MPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 19; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETS. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETS. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.

Sequence 35 AA;

Query Match 100.0%; Score 81; DB 34; Length 35;
Best Local Similarity 100.0%; Pred. No. 1,54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkktatvgeld 12
|||||
2 YNKKKATVQELD 13

RESULT 8
ID W64638 standard; peptide; 10 AA.
AC W64638;
DT 23-OCF-1998 (first entry)
DE Synthetic SEB peptide pSEB(152-161).
KM Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
RN toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
RN therapeutic; vaccine; food poisoning.
OS Synthetic.
PS Staphylococcus aureus.

PN W09829444-A1.
 PD 09-JUL-1998.
 PE 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI; 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonsing toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Claim 10; Page 41; 68pp; English.
 CC W04636-W04637 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 10 AA;

Query Match 79.08; Score 64; DB 34; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.96e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 kkkatvgeid 10
 |||||
 QY 4 NKKRATVQELD 13

RESULT 9
 ID W04494 standard; peptide: 28 AA.
 AC W04494;
 DE 10-DEC-1996 (first entry)
 DE Staphylococcal enterotoxin A residues 146-173. T-cell agonist.
 KW Staphylococcal enterotoxin A; agonist; T-cell proliferation;
 KW treatment; immunodeficiency; autoimmune disease; TNF-alpha;
 KW tumour necrosis factor alpha.
 KM Staphylococcus spp.
 OS US545716-A.
 PD 13-AUG-1996.
 PE 08-SEP-1992; 941497.
 PR 08-SEP-1992; US-941497.
 PR 29-MAR-1994; US-220378.
 PA (UYFL) UNIV FLORIDA.
 PI Griegs ND, Johnson HM, Pontzer CH;
 DR WPI; 96-383718/38.
 PT Peptide fragments of Staphylococcal enterotoxin A (SEA) - useful as
 PT SEA agonists for stimulating T-cell proliferation, e.g. in treatment
 PT of immunodeficiency and autoimmune diseases
 PS Example 1; Columns 15-16; 17pp; English.
 CC The present peptide, comprising residues 146-173 of Staphylococcal
 CC enterotoxin A (SEA), is useful as an SEA agonist for stimulating
 CC T-cell proliferation, e.g. in the treatment of immunodeficiency and
 CC autoimmune diseases. Supernatant from PBMC stimulated with
 CC 100 microm of the peptide for 18 hrs., was collected and assayed
 CC for TNF-alpha activity by cytotoxicity on L-929 cells. The result
 CC given as units/ml of TNF-alpha activity was 1.85, compared to 24.1
 CC for the most effective agonist, comprising SEA residues 121-149.
 SQ Sequence 28 AA;

Query Match 72.88; Score 59; DB 19; Length 28;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 nkknvtygeid 11
 |||||
 QY 3 NKKRATVQELD 13

RESULT 10
 ID W72426 standard; peptide: 36 AA.
 AC W72426;
 DE 22-DEC-1998 (first entry)
 DE Peptide #5 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 KM Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PE 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UYRQ) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI; 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1TX23X4X5N #1,
 CC KX6X7X8X9X10X11X12X13X14X15X16X17X18X21X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SPD, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 SQ Sequence 36 AA;

Query Match 72.88; Score 59; DB 36; Length 36;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvtygeid 22
 |||||
 QY 3 NKKRATVQELD 13

RESULT 11
 ID W72427 standard; peptide: 38 AA.
 AC W72427;
 DE 22-DEC-1998 (first entry)
 DE Peptide #6 for reducing symptoms of toxic shock syndrome.
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 KM Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 PN W09845325-A1.
 PD 15-OCT-1998.
 PE 01-APR-1998; U06663.
 PR 07-APR-1997; US-838413.
 PA (UYRQ) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 DR WPI; 98-568335/48.
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 PS Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGX1TX23X4X5N #1,
CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
CC are used: (i) for diagnostic detection of SPE or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit biotransgenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
SQ Sequence 38 AA;

Query Match 72.8%; Score 59; DB 36; Length 38;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvtvgeld 22
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 12
ID W24299 standard; Protein: 91 AA.

AC W24299;
DT 14-APR-1998 (first entry)
DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
KW Staphylococcus aureus MCHU 29; antagonist; antibacterial; immunogen;
KM vaccine; disease; protection; isolation.
OS Staphylococcus aureus.
FH Key Location/Qualifiers
FT MISC_difference 29
FT MISC_difference 29 /note="Unspecified amino acid"
PN WO9731114-A2.
PD 28-AUG-1997.
PE 25-FEB-1997; G00524.
PK 26-FEB-1996; GB-004045.
PA (SMK) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Hodgson JE;
DR WPI: 97-435166/40.
DR N-PSDB: V01865.
PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for
PT isolating antagonist of the polypeptide(s) useful as anti-bacterials
PS Claim 11; Page 33; 117pp; English.
CC The present sequence represents a novel polypeptide, which is optionally
CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
CC it, are derived from Staphylococcus aureus. Cells expressing ligands
CC binding the polypeptide can be used to isolated candidate compounds
CC that bind and inhibit the activity of the polypeptide. Such compounds
CC can be used as anti-bacterial compounds. The polypeptide may also be
CC used as an immunogen to vaccinate an animal for protection against
CC Staphylococcus aureus caused disease.
SQ Sequence 91 AA;

Query Match 72.8%; Score 59; DB 27; Length 91;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 40 nkknvtvgeld 50
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 13
ID R13203 standard; protein: 233 AA.
AC R13203;
DT 15-OCT-1991 (first entry)
DE Staphylococcal enterotoxin A.
KW SEA; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.
PN WO9110680-A.
PD 25-JUL-1991.
PE 17-JAN-1991; U00342.
PK 17-JAN-1990; US-466577.
PA (TERM/) TERMAN D S.
PI Terman DS;
DR WPI: 91-237984/32.
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
PS Disclosure: Fig 1; 74pp; English.
CC SEA was isolated and purified from S. aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC ibuprofen to attenuate toxic reaction to SEA. Synthetic
CC polypeptides having structural homology to Staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydrophobic profiles.
CC See also R13204-R13211.
SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 3; Length 233;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtvgeld 156
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 14
ID R45011 standard; protein: 233 AA.
AC R45011;
DT 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SEA.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KM autoimmune disease; toxicity; Protein A; perfusion system.
OS Staphylococcus aureus.
FH Key Location/Qualifiers
FT MISC_difference 49
FT MISC_difference 49 /note="Given in the specification as O, no further
FT details given"
PN WO9324136-A.
PD 09-DEC-1993.
PE 01-JUN-1993; U05213.
PK 01-JUN-1992; US-891718.
PA (STON/) STONE J L.
PA (TERM/) TERMAN D S.
PI Stone JL, Terman DS;
DR WPI: 93-405418/50.
PT Use of staphylococcal enterotoxin(s) and homologues - for
PT treating cancer in a patient or for the treatment of auto-immune
PT diseases

PS Disclosure: Fig 1; 90pp; English.
CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the Protein A perfusion system. They may be administered
CC by i.v. injection.
SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 8; Length 233;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtvgeld 156
|||: |||||
QY 3 NKKKATVQELD 13

RESULT 15
 ID W35373 standard; peptide: 233 AA.
 AC W35373;
 DT 20-APR-1998 (first entry)
 DE Staphylococcus enterotoxin SEA wild-type superantigen.
 KW SEA; Staphylococcus enterotoxin; superantigen; conjugate;
 OS Staphylococcus sp.
 PN W09736932-A1.
 PD 09-OCT-1997.
 PE 26-MAR-1997; SE0537.
 PR 12-AUG-1996; US-695692.
 PR 29-MAR-1996; SE-001245.
 PA (PHAA) PHARMACIA & UPJOHN AB.
 PI Ahrhansen L, Antonsson P, Bjoerk P, Dohlsten M,
 PI Forsberg G, Hansson J, Kalland T;
 DR WPI; 97-503052/46.
 PT Conjugate of target seeking moiety and modified superantigen -
 PT useful for activating the immune system to treat cancer. Viral
 PT infections, parasitic infestations and autoimmune diseases
 PS Claim 8; Pages 36-37; 58pp; English.
 CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
 CC SEA superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to
 CC T cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 SU Sequence 233 AA;

Query Match 72.8%; Score 59; DB 27; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 146 nkknvtvgeld 156
 |||:|||||
 QY 3 NKKKATVQELD 13

Search completed: Tue Aug 31 19:29:59 1999
 Job time : 17 secs.

[W] [O] [R] [E] [I] [T] (TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:29:09 1999; MasPar time 3.56 Seconds

Tabular output not generated. 157.775 Million cell updates/sec

Title: >US-09-150-947-10

Description: (1-14) from US09150947.pap

Perfect Score: 81

Sequence: 1 XNKKKATVQELDX 14

Scoring table: PAM 150

Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: p1r60

1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 24.268; Variance 31.113; scale 0.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|------------------------------|-----------|
| 1 | 59 | 72.8 | 233 | 2 | A29566 enterotoxin A - Staph | 2.55e-01 |
| 2 | 59 | 72.8 | 257 | 2 | A28664 enterotoxin A precurs | 2.55e-01 |
| 3 | 59 | 72.8 | 362 | 2 | S27530 sporulation protein - | 2.55e-01 |
| 4 | 58 | 71.6 | 266 | 1 | ENSAB6 enterotoxin B precurs | 4.14e-01 |
| 5 | 57 | 70.4 | 258 | 2 | A33953 enterotoxin D precurs | 6.68e-01 |
| 6 | 53 | 65.4 | 257 | 2 | A28179 enterotoxin E precurs | 4.30e+00 |
| 7 | 53 | 65.4 | 671 | 2 | A40692 signal recognition pa | 4.30e+00 |
| 8 | 53 | 65.4 | 880 | 2 | S51473 probable membrane pro | 4.30e+00 |
| 9 | 53 | 65.4 | 1233 | 2 | S51483 gene Sbl.8/DXS423E pr | 4.30e+00 |
| 10 | 52 | 64.2 | 127 | 2 | B69767 conserved hypotetica | 6.76e+00 |
| 11 | 52 | 64.2 | 146 | 2 | A49746 probable membrane pro | 6.76e+00 |
| 12 | 52 | 64.2 | 236 | 2 | S18786 exotoxin type A precu | 6.76e+00 |
| 13 | 52 | 64.2 | 236 | 2 | S18783 exotoxin type A precu | 6.76e+00 |
| 14 | 52 | 64.2 | 251 | 2 | S29659 exotoxin type A precu | 6.76e+00 |
| 15 | 51 | 63.0 | 224 | 1 | S58590 ribosomal protein S3 | 1.05e+01 |
| 16 | 51 | 63.0 | 239 | 1 | R3R23 ribosomal protein S3 | 1.05e+01 |
| 17 | 51 | 63.0 | 262 | 2 | C70372 flagellar hook basal | 1.05e+01 |
| 18 | 51 | 63.0 | 412 | 2 | A48881 rRNA (guanosine-2'-O- | 1.05e+01 |
| 19 | 51 | 63.0 | 3418 | 1 | G02334 breast cancer tumor s | 1.05e+01 |
| 20 | 50 | 61.7 | 274 | 2 | B64087 outer membrane protei | 1.64e+01 |
| 21 | 50 | 61.7 | 391 | 2 | S18666 KIN17 protein - mouse | 1.64e+01 |
| 22 | 50 | 61.7 | 1075 | 1 | OYRTHX heat-stable enterotox | 1.64e+01 |
| 23 | 50 | 61.7 | 1223 | 2 | I38111 phosphorylase kinase | 1.64e+01 |

| | | | | | | |
|----|----|------|------|---|------------------------------|----------|
| 24 | 50 | 61.7 | 3685 | 1 | A27605 dystrophin, muscle - | 1.64e+01 |
| 25 | 49 | 60.5 | 290 | 2 | S66072 hypothetical protein | 2.52e+01 |
| 26 | 49 | 60.5 | 384 | 2 | S46523 transcription factor | 2.52e+01 |
| 27 | 49 | 60.5 | 452 | 2 | T01694 calcium-dependent pro | 2.52e+01 |
| 28 | 49 | 60.5 | 455 | 2 | S55019 MAD polypeptide - fru | 2.52e+01 |
| 29 | 49 | 60.5 | 465 | 2 | S68987 transcription activat | 2.52e+01 |
| 30 | 49 | 60.5 | 599 | 2 | T02994 CDPK-related protein | 2.52e+01 |
| 31 | 49 | 60.5 | 607 | 2 | T03023 calcium-dependent pro | 2.52e+01 |
| 32 | 49 | 60.5 | 625 | 2 | T02033 calcium/calmodulin-de | 2.52e+01 |
| 33 | 49 | 60.5 | 803 | 2 | I68600 dipeptidyl aminopepti | 2.52e+01 |
| 34 | 49 | 60.5 | 831 | 2 | A41793 conserved hypotetica | 2.52e+01 |
| 35 | 49 | 60.5 | 831 | 2 | B64528 conserved hypotetica | 2.52e+01 |
| 36 | 49 | 60.5 | 865 | 2 | I54331 dipeptidyl aminopepti | 2.52e+01 |
| 37 | 49 | 60.5 | 1134 | 2 | A60234 Iga Fc receptor precu | 2.52e+01 |
| 38 | 49 | 60.5 | 1164 | 1 | FC50AG Iga Fc receptor precu | 2.52e+01 |
| 39 | 49 | 60.5 | 1369 | 2 | JC4860 protein-tyrosine kina | 2.52e+01 |
| 40 | 49 | 60.5 | 3678 | 2 | S28916 conserved hypotetica | 3.86e+01 |
| 41 | 48 | 59.3 | 303 | 2 | E69164 transcription factor | 3.86e+01 |
| 42 | 48 | 59.3 | 324 | 2 | S48122 transcription factor | 3.86e+01 |
| 43 | 48 | 59.3 | 332 | 2 | S15347 bZIP-like protein - A | 3.86e+01 |
| 44 | 48 | 59.3 | 844 | 2 | T00529 hypothetical protein | 3.86e+01 |
| 45 | 48 | 59.3 | 1381 | 2 | S60004 | |

ALIGNMENTS

| | | |
|-----------------------|---|-------------------------|
| RESULT | 1 | |
| ENTRY | A29566 | #type complete |
| TITLE | enterotoxin A - Staphylococcus aureus | |
| ORGANISM | Staphylococcus aureus | |
| DATE | 05-Jun-1988 | #sequence_1 |
| DATE | 18-Jun-1993 | #revision_1 |
| ACCESSIONS | A29566 | |
| REFERENCE | A29566 | |
| #authors | Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J. | |
| #journal | J. Biol. Chem. (1987) 262:7006-7013 | |
| #title | Complete amino acid sequence of staphylococcal enterotoxin A. | |
| #cross-references | MUID:87222293 | |
| #accession | A29566 | |
| #molecule-type | protein | |
| #residues | 1-233 | #label HVA |
| GENETICS | | |
| #gene | enta | |
| #map-position | 6 | |
| SUMMARY | #length 233 | #molecular-weight 27079 |
| SUMMARY | #checks 9580 | |
| Query Match | 72.8%; Score 59; DB 2; Length 233; | |
| Best local similarity | 81.8%; Pred. No. 2.55e-01; | |
| Matches | 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |
| Db | 146 NKKKATVQELD 156 | |
| Oy | 3 NKKKATVQELD 13 | |
| RESULT | 2 | |
| ENTRY | A28664 | #type complete |
| TITLE | enterotoxin A precursor - Staphylococcus aureus (strain | |
| ORGANISM | Staphylococcus aureus | |
| DATE | 30-Jun-1989 | #sequence_1 |
| DATE | 20-Mar-1998 | #text_change |
| ACCESSIONS | A28664 | |
| REFERENCE | A28664 | |
| #authors | Betley, M.J.; Mekalanos, J.J. | |
| #journal | J. Bacteriol. (1988) 170:34-41 | |
| #title | Nucleotide sequence of the type A staphylococcal enterotoxin | |
| #cross-references | MUID:88086892 | |
| #accession | A28664 | |
| #molecule-type | DNA | |
| #residues | 1-257 | #label BFM |
| #cross-references | GB:M18970; NID:g153120; PID:g153121 | |

##experimental_source strain FR1337
SUMMARY #length 257 #molecular-weight 29669 #checksum 2543

Query Match 72.8%; Score 59; DB 2; Length 257;
Best Local Similarity 81.8%; Pred. No. 2,55e-01;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 170 NKKKVTQVELD 180
|||:|||||
QY 3 NKKKATVQVELD 13

RESULT 3
ENTRY S27530 #type complete
TITLE sporulation protein - Clostridium acetobutylicum
ORGANISM #formal_name Clostridium acetobutylicum
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997

ACCESSIONS S27530
REFERENCE S27530
#authors Reid, S.J.; Hancock, K.; Santangelo, J.D.; Woods, D.R.
#description Submitted to the EMBL Data Library, March 1992
#accession S27530
#status preliminary
#molecule_type DNA
#residues 1-362 #label RE1
SUMMARY ##cross-references EMBL:M87835; NID:g144914; PID:g144915
#length 362 #molecular-weight 40998 #checksum 3634

Query Match 72.8%; Score 59; DB 2; Length 362;
Best Local Similarity 58.3%; Pred. No. 2,55e-01;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 67 YHKKNSVEELD 78
1:11:1:111
QY 2 YNKKKATVQVELD 13

RESULT 4
ENTRY ENSAB6 #type complete
TITLE enterotoxin B precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 11-Sep-1998

ACCESSIONS S27360; A92065; S27240; A01815
REFERENCE S27360
#authors Jones, C.L.; Khan, S.A.
#journal J. Bacteriol. (1986) 166:29-33
#title Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
#accession S27360
##cross-references MUID:86168029
#molecule_type DNA
#residues 1-266 #label JON
SUMMARY ##cross-references EMBL:M1118; NID:g152999; PID:g153000
#experimental_source strain S6

REFERENCE A92065
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3518-3525
#title The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.
#cross-references MUID:71007902
#accession A92065
#molecule_type protein
#residues 28-55; 'NND',59-68; 'NE',71; 'FDLIVY',78-117,119-127, 'N',129; 'D',131-132; 'ENT',136-148; 'GN',151-156; 'Y',157-184; 'EO',187-232; 'N',234-245; 'ND',248-266 ##label HVA
SUMMARY ##experimental_source strain S-6
REFERENCE A92064

#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3511-3517
#title The primary structure of staphylococcal enterotoxin B. II. Isolation, composition, and sequence of chymotryptic peptides.
#cross-references MUID:71007901
#contents annotation; chymotryptic peptides
REFERENCE A92063
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3493-3510
#title The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, and sequence of tryptic peptides from oxidized entero-toxin B.
#cross-references MUID:71007900
#contents annotation; tryptic peptides
REFERENCE A90548
#authors Schantz, E.J.; Roesler, W.G.; Wagman, J.; Spero, L.; Dunnehy, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin B.
#cross-references MUID:66035792
#contents annotation; biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinisky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskalova, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.; Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of staphylococcal enterotoxin B.
#accession S27240
##molecule_type protein
#residues 28-42;128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin; extracellular protein; toxin
FEATURE 1-27
28-266
120-140
SUMMARY #length 266 #molecular-weight 31436 #checksum 4249

Query Match 71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 4,14e-01;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 178 NKKKVTQVELD 188
|||||:|||||
QY 3 NKKKATVQVELD 13

RESULT 5
ENTRY A33953 #type complete
TITLE enterotoxin D precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Sep-1997

ACCESSIONS A33953
REFERENCE A33953
#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.
#cross-references MUID:89359112
#accession A33953
#status preliminary
#molecule_type DNA
#residues 1-258 #label BAY
SUMMARY ##cross-references GB:M28521; NID:g1492109; PID:g738691
#length 258 #molecular-weight 29746 #checksum 39

Query Match 70.4%; Score 57; DB 2; Length 258;
Best Local Similarity 72.7%; Pred. No. 6,68e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 171 DRKNVTOELD 181
:|||||
QY 3 NKKKATVOELD 13

RESULT 6
ENTRY A28179 #type complete
TITLE enterotoxin E precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Sep-1997

ACCESSIONS A28179
REFERENCE A28179
#authors Couch, J.L.; Solitis, M.T.; Betley, M.J.
#journal J. Bacteriol. (1988) 170:2954-2960
#title Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
#cross-references MUID:88257005
#accession A28179
#molecule_type DNA
#residues 1-257 #label COU
#cross-references GB:M21319; NID:g153001; PID:g153002
SUMMARY #length 257 #molecular_weight 29358 #checksum 2562

Query Match 65.4%; Score 53; DB 2; Length 257;
Best Local Similarity 72.7%; Pred. No. 4.30e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 170 SKREVTQELD 180
:|||||
QY 3 NKKKATVOELD 13

RESULT 7
ENTRY A40692 #type complete
TITLE signal recognition particle 72k chain - dog
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997

ACCESSIONS A40692; S32167
REFERENCE A40692
#authors Lutcke, H.; Prehn, S.; Ashford, A.J.; Remus, M.; Frank, R.;
#journal Dobberstein, B.
#title J. Cell Biol. (1993) 121:977-985
#cross-references MUID:93273803
#accession A40692
#status preliminary
#molecule_type mRNA; protein
#residues 1-671 #label LUT
#cross-references EMBL:X67813; NID:g297767; PID:g297768
#note Sequence extracted from NCBI backbone (NCBIP:132901)
SUMMARY #length 671 #molecular_weight 74493 #checksum 6822

Query Match 65.4%; Score 53; DB 2; Length 671;
Best Local Similarity 33.3%; Pred. No. 4.30e+00;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 450 YGRKKAISDL 471
:|||||
QY 2 YNKKATVOELD 13

RESULT 8
ENTRY S51473 #type complete
TITLE probable membrane protein YLR386w - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein IJ502.1
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Nov-1997
ACCESSIONS S51473

REFERENCE S51466
#authors Du, Z.
#submission submitted to the EMBL Data Library, December 1994
#description The sequence of S. cerevisiae cosmid IJ502.
#accession S51473
#molecule_type DNA
#residues 1-880 #label DUZ
#cross-references EMBL:U19104; NID:g609423; PID:g609424; MIPS:YLR386w

GENETICS
#map_position 12R
KEYWORDS transmembrane protein
FEATURE 436-442
SUMMARY #domain transmembrane #status predicted #label TM
#length 880 #molecular_weight 99771 #checksum 5546

Query Match 65.4%; Score 53; DB 2; Length 880;
Best Local Similarity 50.0%; Pred. No. 4.30e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 14 YEKRRKAULE 25
:|||||
QY 2 YNKKATVOELD 13

RESULT 9
ENTRY I54383 #type complete
TITLE gene SBI.8/DXS423E protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 28-Feb-1997

ACCESSIONS I54383
REFERENCE I54383
#authors Rocques, P.J.; Clark, J.; Ball, S.; Crew, J.; Gill, S.;
#journal Christodoulou, Z.; Borts, R.H.; Louis, E.J.; Davies, K.E.;
#title Hum. Mol. Genet. (1995) 4:243-249
#cross-references MUID:95276737
#accession I54383
#status preliminary; translated from GB/EMBL/DBD
#molecule_type mRNA
#residues 1-1233 #label RES
#cross-references GB:S78271; NID:g999379; PID:g999380

GENETICS
SUMMARY SBI.8/DXS423E
#length 1233 #molecular_weight 143204 #checksum 7067

Query Match 65.4%; Score 53; DB 2; Length 1233;
Best Local Similarity 41.7%; Pred. No. 4.30e+00;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRKGDMDELE 337
:|||||
QY 2 YNKKATVOELD 13

RESULT 10
ENTRY B69767 #type complete
TITLE conserved hypothetical protein yzc - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998

ACCESSIONS B69767
REFERENCE B69767
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
#journal Allonl, G.; Azevedo, V.; Bertero, M.G.; Bessières, P.;
#title Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
#journal A.; Brum, M.; Bridgell, S.C.; Bron, S.; Brouillet, S.;
#title Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;
#journal Choi, S.K.; Codani, J.J.; Comercon, I.F.; Cummings, N.J.;
#journal Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;

#accession S18795
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEH
##cross-references EMBL:X61566; NID:947317; PID:947318
##experimental_source strain MGAS492 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18799
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NES
##cross-references EMBL:X61567; NID:947325; PID:947326
##experimental_source strain MGAS496 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
#domain signal sequence (fragment) #status predicted
#label sig
#product exotoxin type A (fragment) #status predicted
#label MAT
23-236 #length 236 #checksum 1685

SUMMARY
Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATVOELD 168
|||:| ||||
v 3 NKKKATVOELD 13

RESULT 13
ENTRY S18783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS624 isolate Germany; strain MGAS495 isolate Germany 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998
DATE S18783; S18793; S18794; S18801; S18798
S18782
REFERENCE Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#authors J. Exp. Med. (1991) 174:1271-1274
#journal Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M01D:92044323
#accession S18783
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEU
##cross-references EMBL:X61568; NID:947289; PID:947290
##experimental_source strain MGAS158 isolate Nebraska unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18793
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61569; NID:947313; PID:947314
##experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18794
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEZ
##cross-references EMBL:X61570; NID:947316; PID:947316
##experimental_source strain MGAS491 isolate United Kingdom unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18801
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEY
##cross-references EMBL:X61572; NID:947333; PID:947334
##experimental_source strain MGAS624 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18798
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEO
##cross-references EMBL:X61571; NID:947323; PID:947324
##experimental_source strain MGAS495 isolate Germany unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
#domain signal sequence (fragment) #status predicted
#label sig
#product exotoxin type A (fragment) #status predicted
#label MAT
23-236 #length 236 #checksum 612

SUMMARY
Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKKATVOELD 168
|||:| ||||
v 3 NKKKATVOELD 13

RESULT 14
ENTRY S29659 #type complete
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes (fragment)
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change 25-Mar-1998
S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
REFERENCE S29659
#authors Weeks, C.R.; Ferrerelli, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references M01D:86166804
#accession S29659
##molecule_type DNA
##residues 1-251 ##label WEE
##cross-references GB:U04053; EMBL:M19350; NID:91877426; PID:91877430
REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M01D:92044323

```

#accession      S18782
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-244 ##label NEZ
##cross-references EMBL:X61560; NID:q47287; PID:q47288
##experimental_source Streptococcus pyogenes strain MGAS156 isolate
#note           the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

#accession      S18784
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-244 ##label NEA
##cross-references EMBL:X61556; NID:q47291; PID:q47292
##experimental_source Streptococcus pyogenes strain MGAS165 isolate
#note           the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

#accession      S18785
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-244 ##label NEZ
##cross-references EMBL:X61559; NID:q47293; PID:q47294
##experimental_source Streptococcus pyogenes strain MGAS167 isolate
#note           the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

#accession      S18791
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-244 ##label NEY
##cross-references EMBL:X61555; NID:q47309; PID:q47310
##experimental_source Streptococcus pyogenes strain MGAS327 isolate
#note           the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

#accession      S18796
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-244 ##label NEO
##cross-references EMBL:X61557; NID:q47319; PID:q47320
##experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note           the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

#accession      S18797
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-244 ##label NEH
##cross-references EMBL:X61558; NID:q47321; PID:q47322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note           the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

#accession      S18800
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues      9-228 ##label NES
##cross-references EMBL:X61554; NID:q47327; PID:q47328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
#note           Zealand unassigned phage
#               the nucleotide sequence was submitted to the EMBL Data
#               Library, September 1991

GENETICS
#gene           speA1
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS        exotoxin
FEATURE
1-30            #domain signal sequence #status predicted #label SIG\
31-251          #product exotoxin type A #status predicted #label MAT
SUMMARY
length 251 #molecular-weight 29246 #checksum 1475

Query Match      64.2%; Score 52; DB 2; length 251;

```

```

Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Db      166 NKKKATVQELD 176
      |||: | |||
Qy      3 NKKKATVQELD 13

RESULT      15
ENTRY
TITLE      S58590 #type complete
ORGANISM   ribosomal protein S3 - maize chloroplast
DATE       #formal_name chloroplast Zea mays #common_name maize
           29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change
           17-Mar-1999

ACCESSIONS
REFERENCE   S58590
AUTHORS     Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
J. Mol. Biol. (1995) 251:614-628
#title      Complete sequence of the maize chloroplast genome: gene
           content, hotspots of divergence and fine tuning of genetic
           information by transcript editing.

#cross-references MUID:95395841
#accession   S58590
#status      nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues   1-724 ##label MAI
##cross-references EMBL:X86563; NID:9902200; PID:9902260
#note        the nucleotide sequence was submitted to the EMBL Data
           Library, April 1995

GENETICS
#gene        rps3
CLASSIFICATION #superfamily Escherichia coli ribosomal protein S3
KEYWORDS     chloroplast; protein biosynthesis; ribosome
SUMMARY      #length 224 #molecular-weight 25916 #checksum 3426

Query Match      63.0%; Score 51; DB 2; length 224;
Best Local Similarity 50.0%; Pred. No. 1,05e+01;
Matches      5; Conservative      5; Mismatches      0; Indels      0; Gaps      0;

Db      93 KKKGAIEELE 102
      |||::: |||
Qy      4 KKKATVQELD 13

Search completed: Tue Aug 31 19:29:25 1999
Job time : 16 secs.

```

 W P E R E H
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Aug 31 19:27:45 1999; Mspar time 2.64 Seconds
 Tubular output not generated. 150.063 Million cell updates/sec

Title: >US-09-150-947-10
 Description: (1-14) from US09150947.pep
 Perfect Score: 81
 Sequence: 1 XYNKKRATVQELDX 14

Scoring table: PAM 150
 Gap 15

Searched: 77977 segs, 28268293 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 24.929; Variance 27.412; scale 0.909

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 59 | 72.8 | 257 | 1 | ETXA_STAAU ENTEROTOXIN TYPE A PRE | 4.80e+02 |
| 2 | 58 | 71.6 | 266 | 1 | ETXB_STAAU ENTEROTOXIN TYPE B PRE | 8.32e+02 |
| 3 | 57 | 70.4 | 258 | 1 | ETXD_STAAU ENTEROTOXIN TYPE D PRE | 1.43e+01 |
| 4 | 53 | 65.4 | 257 | 1 | ETXE_STAAU ENTEROTOXIN TYPE E PRE | 1.18e+00 |
| 5 | 53 | 65.4 | 670 | 1 | SR72_CANFA SIGNAL RECOGNITION PAR | 1.18e+00 |
| 6 | 52 | 64.2 | 146 | 1 | YMD3_YENST HYPOHETICAL 17.7 KD P | 1.97e+00 |
| 7 | 52 | 64.2 | 251 | 1 | SPEA_STRPY EXOTOXIN TYPE A PRECUR | 1.97e+00 |
| 8 | 51 | 63.0 | 187 | 1 | YCF4_CYAPA HYPOHETICAL 21.2 KD P | 3.26e+00 |
| 9 | 51 | 63.0 | 224 | 1 | RR3_ORYSA CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 10 | 51 | 63.0 | 432 | 1 | RR3_ORYSA CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 11 | 51 | 63.0 | 412 | 1 | PT56_YEAST RIBOSE METHYLTRANSFERA | 3.26e+00 |
| 12 | 51 | 63.0 | 556 | 1 | LIGA_MOUSE LIGATIN (FRAGMENT) | 3.26e+00 |
| 13 | 51 | 63.0 | 3418 | 1 | BRC2_HUMAN BREAST CANCER TYPE 2 S | 5.36e+00 |
| 14 | 50 | 61.7 | 268 | 1 | NO20_HUMAN EARLY MODULIN 20 PRECU | 5.36e+00 |
| 15 | 50 | 61.7 | 274 | 1 | HEL_HAELN LIPOPROTEIN E PRECURSO | 5.36e+00 |
| 16 | 50 | 61.7 | 386 | 1 | YAMH_SCHPO HYPOHETICAL 44.5 KD P | 5.36e+00 |
| 17 | 50 | 61.7 | 1072 | 1 | HSEB_RAT HEAT-STABLE ENTEROTOXI | 5.36e+00 |
| 18 | 50 | 61.7 | 1223 | 1 | KPB1_HUMAN PHOSPHORILASE B KINASE | 5.36e+00 |
| 19 | 50 | 61.7 | 3685 | 1 | DMD_HUMAN DYSTROPHIN | 5.36e+00 |
| 20 | 49 | 60.5 | 290 | 1 | YABG_BACSU HYPOHETICAL 33.3 KD P | 8.72e+00 |
| 21 | 49 | 60.5 | 455 | 1 | MAD_DROME MOTHERS AGAINST DPP PR | 8.72e+00 |
| 22 | 49 | 60.5 | 559 | 1 | KIF2_XENLA KINESIN-LIKE PROTEIN K | 8.72e+00 |
| 23 | 49 | 60.5 | 670 | 1 | SR72_HUMAN SIGNAL RECOGNITION PAR | 8.72e+00 |

ALIGNMENTS

| RESULT ID | 1 | ETXA_STAAU | STANDARD: | PRT: | 257 AA. |
|-----------|--|------------|-----------|------|---------|
| AC | P13163: | | | | |
| DT | 01-JAN-1990 (REL. 13, CREATED) | | | | |
| DT | 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) | | | | |
| DT | 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN TYPE A PRECURSOR (SEA). | | | | |
| GN | ENTX. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | |
| CC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-FRI337. | | | | |
| RX | MEDLINE: 88086892. | | | | |
| RA | BETLEY M.J., MEKALANOS J.J.: | | | | |
| RT | "Nucleotide sequence of the type A staphylococcal enterotoxin gene." | | | | |
| RL | J. BACTERIOL. 170:34-41(1988). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 25-257. | | | | |
| RX | MEDLINE: 87222293. | | | | |
| RA | HUANG I.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J.: | | | | |
| RT | "Complete amino acid sequence of staphylococcal enterotoxin A." | | | | |
| RL | J. BIOL. CHEM. 262:7006-7013(1987). | | | | |
| RN | [3] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). | | | | |
| RX | MEDLINE: 95354648. | | | | |
| RA | SCHAD E.M., ZAITSEVA I., ZAITSEV V.N., DOHLSTEN M., KALLAND T., | | | | |
| RT | SCHLIEVERT P.M., OHLENDORF D.H., SVENSSON L.A.: | | | | |
| RL | "Crystal structure of the superantigen staphylococcal enterotoxin | | | | |
| RT | type A." | | | | |
| RL | EMBO J. 14:3292-3301(1995). | | | | |
| RN | [4] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). | | | | |
| RX | MEDLINE: 97113025. | | | | |
| RA | SUNDSTROM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEN M., | | | | |
| RA | ABRAHAMSEN L.: | | | | |
| RT | "The co-crystal structure of staphylococcal enterotoxin type A with | | | | |
| RT | zn2+ at 2.7-A resolution. Implications for major histocompatibility | | | | |
| RT | complex class II binding." | | | | |
| RL | J. BIOL. CHEM. 271:32212-32216(1996). | | | | |
| RN | [5] | | | | |
| RP | 3D-STRUCTURE MODELLING. | | | | |
| RX | MEDLINE: 96022987. | | | | |
| RA | SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.: | | | | |
| RT | "Residues defining V beta specificity in staphylococcal | | | | |
| RT | enterotoxins." | | | | |

SQ SEQUENCE 266 AA: 31436 MW: E2C09D63 CRC32;

Query Match 71.6%; Score 58; DB 1; Length 266;

Best Local Similarity 81.8%; Pred. No. 8.32e-02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 178 NKKKATVQELD 188

QY 3 NKKKATVQELD 13

RESULT 3

ID ETXD-STPAU STANDARD: PRT: 258 AA.

AC P20723;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE ENTEROTOXIN TYPE D PRECURSOR (SED).

GN ENTD.

OS STAPHYLOCOCCUS AUREUS.

OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;

OC STAPHYLOCOCCUS.

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 89359112.

RA BAYLES K.W., IANDOLO J.J.;

"Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";

RT J. BACTERIOL. 171:4799-4806(1989).

RL [2]

RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RC STRAIN-ATCC 23235;

RX MEDLINE: 97157473.

RA SUNDSTROM M., ABRAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,

DOHJSTIN M.;

"The crystal structure of staphylococcal enterotoxin type D reveals

zn²⁺-mediated homodimerization.";

RL EMBO J. 15:6832-6840(1996).

CC -1- SUBUNIT: HOMODIMER: ZINC-DEPENDENT.

CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.

CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES

CC PYROGENIC EXOTOXINS ARE ALL RELATED.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

CC -----

CC EMBL: M28521; G578691; -

DR PIR: A33953; A33953.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

DR PFAM: PF01123; Staph_Strep_toxin; 1.

DR HSRP: P13163; 1SXT.

KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.

FT SIGNAL 1 25

FT CHAIN 26 258 ENTEROTOXIN D.

FT METAL 212 212 ZINC.

FT METAL 250 250 ZINC.

FT METAL 252 252 ZINC.

FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).

SQ SEQUENCE 258 AA: 29746 MW: 2D1AA120 CRC32;

Query Match 70.4%; Score 57; DB 1; Length 258;

Best Local Similarity 72.7%; Pred. No. 1.43e-01;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 171 DKKNTVQELD 181

:||:|||||

QY 3 NKKKATVQELD 13

RESULT 4

ID ETXE-STPAU STANDARD: PRT: 257 AA.

AC P12993;

DT 01-JAN-1990 (REL. 13, CREATED)

DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE ENTEROTOXIN TYPE E PRECURSOR (SEE).

GN ENTE.

OS STAPHYLOCOCCUS AUREUS.

OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;

OC STAPHYLOCOCCUS.

RM [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.

RC STRAIN-MJB265;

RX MEDLINE: 88257005.

RA COUCH J.L., SOLTIS M.T., BETLEY M.J.;

"Cloning and nucleotide sequence of the type E staphylococcal

enterotoxin gene.";

RT J. BACTERIOL. 170:2954-2960(1988).

RL [2]

RP 3D-STRUCTURE MODELLING.

RX MEDLINE: 96022987.

RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;

"Residues defining v beta specificity in staphylococcal

enterotoxins.";

RT NAT. STRUCT. BIOL. 2:680-686(1995).

CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.

CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES

CC PYROGENIC EXOTOXINS ARE ALL RELATED.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

CC -----

CC EMBL: M21319; G153002; -

DR PIR: A28179; A28179.

DR PDB: 1SEB; 15-OCT-95.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

DR PFAM: PF01123; Staph_Strep_toxin; 1.

KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.

FT SIGNAL 1 27

FT CHAIN 28 257 ENTEROTOXIN E.

SQ SEQUENCE 257 AA: 29358 MW: 88BA67C3 CRC32;

Query Match 65.4%; Score 53; DB 1; Length 257;

Best Local Similarity 72.7%; Pred. No. 1.18e+00;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 170 SKREYTVQELD 180

QY 3 NKKKATVQELD 13

RESULT 5

ID SR72-CANFA STANDARD: PRT: 670 AA.

AC P33731;

DT 01-FEB-1994 (REL. 28, CREATED)

DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).

GN SRP72.

OS CANIS FAMILIARIS (DOG).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

OC CARNIVORA: FISSIPEDIA: CANIDAE: CANIS.

[1]
 CC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE: 93273803.
 RA LUETCKE H., PREHN S., ASHFORD A.J., REMUS M., FRANK R.,
 RT DOBERBERSTEIN B.:
 "Assembly of the 68- and 72-kD proteins of signal recognition
 particle with 7S RNA."
 RL J. CELL BIOL. 121:977-985(1993).
 CC -1- FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE
 IN TARGETING SECRETORY PROTEINS TO THE ROUGH ENDOPLASMIC
 RETICULUM MEMBRANE. SRP72 BINDS THE 7S RNA ONLY IN PRESENCE OF
 SRP68. THIS RIBONUCLEOPROTEIN COMPLEX MIGHT INTERACT DIRECTLY WITH
 IN THE ELONGATION ARREST FUNCTION.
 CC -1- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE
 OF 300 NUCLEOTIDES AND SIX PROTEIN SUBUNITS: SRP72, SRP68, SRP54,
 SRP19, SRP14 AND SRP9.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- DOMAIN: THE C-TERMINAL IS ESSENTIAL FOR THE INTERACTION WITH THE
 SRP68/7S RNA COMPLEX.
 CC -1- SIMILARITY: BELONGS TO THE SRP72 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X67813; G297768; -
 DR PIR: S32167; S32167.
 DR PIR: A40692; A40692.
 KW SIGNAL RECOGNITION PARTICLE; RIBONUCLEOPROTEIN.
 FT INIT MET 0 0 PROBABLE.
 FT MOD_RES 1 1 BLOCKED.
 FT DOMAIN 551 560 POLY-LYS.
 FT DOMAIN 661 664 POLY-LYS.
 SQ SEQUENCE 670 AA; 74362 MW; 9CB38962 CRC32;
 Db 459 YGRKKAISDLE 470
 1:11::1:
 2 YNKKATVQELD 13
 Oy
 RESULT 6
 ID YMD3 YEAST STANDARD; PRT; 146 AA.
 AC 003712;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOHETICAL 1.7 KD PROTEIN IN AMD1-RAD52 INTERGENIC REGION.
 GN YML033W.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCAROMYCETALES;
 OC SACCAROMYCETACEAE; SACCAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA BADCOCK K., CHURCHER C., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST YDR458C.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----

CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z46659; G575686; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 146 AA; 17729 MW; 9A378D91 CRC32;
 Db 40 YGRKRIEEL 50
 1:11::1:
 2 YNKKATVQEL 12
 Oy
 RESULT 7
 ID SPEA-STREP STANDARD; PRT; 251 AA.
 AC P08095;
 DT 01-AUG-1988 (REL. 08, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
 DE (SPE A).
 GN SPEA.
 OS STREPTOCOCCUS PYOGENES.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86166804.
 RA WEEKS C.R., FERRETTI J.J.;
 RT "Nucleotide sequence of the type A streptococcal exotoxin
 (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 T12."
 RL INFECT. IMMUN. 52:144-150(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86284313.
 RA JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 related to Staphylococcus aureus enterotoxin B."
 RL MOL. GEN. GENET. 203:354-356(1986).
 CC -1- DISEASE: THE STREPTOCOCCAL PYOGENIC TOXINS A, B, AND C ARE
 THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 FEVER.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 PYOGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U40453; G1877430; -
 DR EMBL: X03929; G47442; -
 DR PIR: A26152; A26152.
 DR PIR: S29659; S29659.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph-Strep-toxin; 1.
 DR HSSP: P01552; ISEB.
 KW TOXIN; SIGNAL.
 FT SIGNAL 1 30
 FT CHAIN 31 251
 FT CONFLICT 6 6
 FT CONFLICT 17 18
 FT CONFLICT 25 35
 EXOTOXIN TYPE A.
 K -> E (IN REF. 2).
 VT -> MK (IN REF. 2).
 SQEVAQDDPD -> LPKICSTRPK (IN REF. 2).

```

FT CONFLICT 40 40 H -> Q (IN REF. 2).
FT CONFLICT 43 43 S -> N (IN REF. 2).
FT CONFLICT 47 59 NUCLEOTIDE -> TFKIIFPMRYTL (IN
FT CONFLICT 129 129 REF. 2).
FT CONFLICT 165 178 I -> L (IN REF. 2).
FT CONFLICT 165 178 INKMTAQLDLYK -> QIKNGCSRISYT (IN
FT SEQUENCE 251 AA: 29246 MM; 535FE465 CRC32;
REF. 2).

Query Match
Best Local Similarity 64.2%; Score 52; DB 1; Length 251;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Dh 166 NKMTAQLD 176
|||:||||
Qy 3 NKMTAQLD 13

RESULT 8
ID YCF4_CYAPA STANDARD; PRT; 187 AA.
AC P48192;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 21.2 KD PROTEIN YCF4.
GN YCF4.
OS CYANOPHORA PARADOXA.
OC CYANELLE.
OC EURKARYOTA: GLAUCOCYSTOPHYCEAE; CYANOPHORACEAE; CYANOPHORA.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-LB555 / PRINGSHEIM;
RA STREMBALT V.L., MICHALOWSKI C.B., LUFFELHARDT W., BOHNET H.J.,
RA BRYANT D.A.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: BELONGS TO THE YCF4 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U30821; G1016091; -;
DR MENDEL; 7950; CYAPA; ycf4.1.
KW CYANELLE; HYPOTHETICAL PROTEIN.
SQ SEQUENCE 187 AA: 21207 MM; B5D7E756 CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 187;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dh 97 YNKKKGTV 104
||||:|
Qy 2 YNKKKATV 9

RESULT 9
ID R3_MAIZE STANDARD; PRT; 224 AA.
AC P06586;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ZEA MAYS (MAIZE).
OC CHLOROPLAST.
OC EURKARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 87231045.
RA MCLAUGHLIN W.E., LARRINDA I.M.;
RT "The sequence of the maize plastid encoded rps3 locus.";
RL NUCLEIC ACIDS RES. 15:4689-4689(1987).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE: 95395841.
RA MAIER R.M., NECKERMANN K., IGLOI G.L., KOESSEL H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. MOL. BIOL. 251:614-628(1995).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y00340; G12469; -;
DR EMBL: M31336; G552741; -;
DR EMBL: X86563; G902260; -;
DR MAIZEDB: 66303; -;
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
DR PFAM: PF00189; S3_C; 1.
DR PFAM: PF00417; S3_N; 1.
DR MENDEL; 13473; ZEAMA; rps3.1.
KW RIBOSOMAL PROTEIN; CHLOROPLAST.
SQ SEQUENCE 224 AA: 25916 MM; 3ED95CFF CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 224;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Dh 93 KKGAIIELE 102
||||:|
Qy 4 KKKATVQELD 13

RESULT 10
ID R3_ORYZA STANDARD; PRT; 239 AA.
AC P12146;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ORYZA SATIVA (RICE).
OC CHLOROPLAST.
OC EURKARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ORYZA.
RN [1]
RX SEQUENCE FROM N.A.
RX STRAIN-CV. NIPPONBARE;
RA SUGIURA M.;
RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RX COMPLETE GENOME.
RX MEDLINE: 89364698.
RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,
RA MORI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-O.,
RA KANNO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;
RT "The complete sequence of the rice (oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct trna genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL MOL. GEN. GENET. 217:185-194(1989).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X15901; G12025; -
 DR PIR: J00255; R3R23; -
 DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
 DR PFAM: PF00189; S3_C; 1.
 DR PFAM: PF00417; S3_N; 1.
 DR MENDEL: 13258; ORSsa:rp33;1.
 DR RIBOSOMAL PROTEIN: CHLOROPLAST.
 SW SEQUENCE 239 AA: 27518 MW: 385916EE CRC32:
 Query Match 63.0%; Score 51; DB 1; Length 239;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 DB 108 KKKGAEELE 117
 QY 4 KKKATVQELD 13
 RESULT 11
 ID PT56 YEAST STANDARD; PRT; 412 AA.
 AC P25270.
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE RIBOSE METHYLTRANSFERASE PT56 (EC 2.1.1.-) (MITOCHONDRIAL LARGE
 DE RIBOSOMAL RNA RIBOSE METHYLASE) (21S RNA [Gm2251] 2'-O-
 DE METHYLTRANSFERASE).
 GN PETS6 OR YOR201C.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94090319.
 RA SIRM-CONNOLLY K., MASON T.L.;
 RT "Functional requirement of a site-specific ribose methylation in
 RT ribosomal RNA.";
 RL SCIENCE 262:1886-1889(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA HUGHES B., POHL T.M.;
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE OF 1-95 FROM N.A.
 RX MEDLINE: 86093663.
 RA STRUHL K.;
 RT "Nucleotide sequence and transcriptional mapping of the yeast
 RT pet56-his3-de1 gene region.";
 RL NUCLEIC ACIDS RES. 13:8587-8601(1985).
 CC -i- FUNCTION: ENCODES AN ESSENTIAL RIBOSE METHYLTRANSFERASE THAT
 CC SPECIFICALLY MODIFIES TO 2'-O-METHYLGUANOSINE A UNIVERSALLY
 CC CONSERVED NUCLEOTIDE, G-2270, IN THE PEPTIDYL TRANSFERASE CENTER
 CC OF THE MITOCHONDRIAL LARGE RIBOSOMAL RNA (21S). THIS MODIFICATION
 CC SEEMS TO BE IMPORTANT FOR THE NORMAL ACCUMULATION OF THIS LATTER
 CC 21S SUBUNIT.
 CC -i- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: L19947; G431760; -
 DR EMBL: X03245; G3779; -
 DR EMBL: 275107; E252073; -
 DR PIR: S07682; S07682.
 DR SGD: L0001392; PET56.
 DR PFAM: PF00588; Spou methylase; 1.
 KW MITOCHONDRION; TRANSFERASE; METHYLTRANSFERASE.
 SW SEQUENCE 412 AA: 46387 MW: B3436655 CRC32:
 Query Match 63.0%; Score 51; DB 1; Length 412;
 Best Local Similarity 63.6%; Pred. No. 3.26e+00;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 DB 79 YGKKAHVEKL 89
 QY 2 YNKKRATVQELD 12
 RESULT 12
 ID LIGA_MOUSE STANDARD; PRT; 566 AA.
 AC Q61211.
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE LIGATIN (FRAGMENT).
 GN LGTN.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97224508.
 RA MALVAR-DRAGOJEVIC D., TRACHTUEC Z., VINCEK V.;
 RT "Assignment of the mouse ligatin gene (lgtn) to chromosome 1F by in
 RT situ hybridization.";
 RL GENOMICS 40:192-193(1997).
 CC -i- FUNCTION: TRAFFICKING RECEPTOR FOR PHOSPHOLYCOPROTEINS. LOCALIZES
 CC PHOSPHOLYCOPROTEINS WITHIN ENDOSOMES AND AT THE CELL PERIPHERY
 CC WHERE THEY PARTICIPATE IN SPECIFIC METABOLIC PROCESSES AS WELL AS
 CC INTERCELLULAR ADHESION (BY SIMILARITY).
 CC -i- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U58337; G1377880; -
 DR MGD: MGI:109342; LGTN.
 KW MEMBRANE.
 FT NON TER 1 1
 FT 566 566
 SW SEQUENCE 566 AA: 62239 MW: AAB58F4B CRC32:
 Query Match 63.0%; Score 51; DB 1; Length 566;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 DB 503 YNKKATVVRNLE 514
 QY 2 YNKKRATVQELD 13
 RESULT 13
 ID BRC2_HUMAN STANDARD; PRT; 3418 AA.
 AC P51587.
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN.

GN BRCA2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96172838.
RA TAVTIGIAN S.V., ROMMENS J.M., COUCH F.J., NEUHAUSEN S., BELL R.,
BERRY S., BOGDEN R., CHEN Q., DAVIS T., FRYE C., HATTIER T.,
JAMMULAPATI S., JANECKI T., JIANG P., KEHRER R., SCHROEDER M.,
SNYDER S., STINGELLOW M., STROUP C., SWEDLUND B., TENG D.,
THOMAS A., TRAN T., WEAVER-FELDAUS J., WONG A., LEBLANC J.-F.,
BELANGER C., TRANCHANT M., SAMSON C., DUMONT M.,
MCARTHUR-MORRISON J., MCSWENEY D., PENG Y., SHIZUYA H.,
SLEPAK T., SIMON M.I., LABRIE F., SHATTUCK-EIDENS D., SKOLNICK M.,
GOLDFAR D., WEBER B.L., SIMARD J., KAMB A.,
RT "The complete BRCA2 gene and mutations in chromosome 13q-linked
RT kindreds." [2]
RN NAT. GENET. 12:333-337(1996).
RP VARIANTS ASN-372; ASP-991; SER-1147; MET-1915 AND CYS-2034.
RX MEDLINE: 96241588.
RA COUCH F.J., FARID L.M., DESHANO M.L., TAVTIGIAN S.V., CALZONE K.,
RA CAMPEAU L., PENG Y., BOGDEN B., CHEN Q., NEUHAUSEN S.,
RA SHATTUCK-EIDENS D., GODWIN A.K., DALY M., RADFORD D.M., SEDLACEK S.,
RA ROMMENS J., SIMARD J., GARBER J., MERADVER S., WEBER B.L.,
RT "BRCA2 germline mutations in male breast cancer cases and breast
RT cancer families." [3]
RN NAT. GENET. 13:123-125(1996).
RP VARIANTS GLD-3095.
RX MEDLINE: 96225455.
RA LANCASTER J.M., WOOSTER R., MANGION J., PHELAN C.M., COCHRAN C.,
RA GUMBS C., SEAL S., BARFOOT R., COLLINS N., BIGGELL G., PAHEL S.,
RA HAMOUDI R., LARSSON C., WISEMAN R.W., BERCHUCK A., IGLEHART J.D.,
RA MARKS J.R., ASHWORTH A., STRATTON M.R., FUTREAL P.A.,
RT "BRCA2 mutations in primary breast and ovarian cancers." [4]
RN NAT. GENET. 13:238-240(1996).
RP VARIANTS.
RX MEDLINE: 96225457.
RA TENG D.H.-F., BOGDEN R., MITCHELL J., BAUMGARD M., BELL R., BERRY S.,
RA DAVIS T., HA P.C., KEHRER R., JAMMULAPATI S., CHEN Q., OFERT K.,
RA SKOLNICK M.H., TAVTIGIAN S.V., JHANWAR S., SWEDLUND B., WONG A.K.C.,
RA KAMB A.,
RT "Low incidence of BRCA2 mutations in breast carcinoma and other
RT cancers." [5]
RN NAT. GENET. 13:241-244(1996).
RP VARIANTS ASN-2415.
RX MEDLINE: 96225458.
RA MIKI Y., KATAGIRI T., KASUMI F., YOSHIMOTO T., NAKAMURA Y.,
RT "Mutation analysis in the BRCA2 gene in primary breast cancers." [6]
RN NAT. GENET. 13:245-247(1996).
RP TISSUE SPECIFICITY: HIGHEST LEVELS OF EXPRESSION IN BREAST AND
-1- THYROID, WITH SLIGHTLY LOWER LEVELS IN LUNG, OVARY, AND SPLEEN,
-1- AFFECTING ONE IN EIGHT WOMEN DURING THEIR LIFETIME. A POSITIVE
-1- FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OF
-1- DEVELOPMENT OF THE DISEASE. AND THIS LINK IS STRIKING FOR EARLY-
-1- ONSET BREAST CANCER. MUTATIONS IN BRCA2 ARE THOUGHT TO BE
-1- RESPONSIBLE FOR SOME INHERITED BREAST CANCER. IT IS LINKED WITH
-1- MALE BREAST CANCER.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL, U43746; G1161384; -

DR MIM: 600185; -
DR PFAM: PF00634; BRCA2 repeat; 8
KW DISEASE MUTATION: POLYMORPHISM, REPEAT.
FT NP_BIND 262 269
FT DOMAIN 1009 2082
FT REPEAT 1009 1033
FT REPEAT 1219 1243
FT REPEAT 1428 1452
FT REPEAT 1524 1548
FT REPEAT 1671 1695
FT REPEAT 1844 1868
FT REPEAT 1978 2002
FT REPEAT 2058 2082
FT VARIANT 75 75
FT VARIANT 289 289
FT VARIANT 355 355
FT VARIANT 372 372
FT VARIANT 630 630
FT VARIANT 728 728
FT VARIANT 991 991
FT VARIANT 1147 1147
FT VARIANT 1302 1302
FT VARIANT 1529 1529
FT VARIANT 1880 1880
FT VARIANT 1915 1915
FT VARIANT 2034 2034
FT VARIANT 2274 2274
FT VARIANT 2415 2415
FT VARIANT 2421 2421
FT VARIANT 3095 3095
FT VARIANT 3103 3103
FT VARIANT 3357 3357
FT VARIANT 3412 3412
SQ SEQUENCE 3418 AA; 384280 MW; F5785BCB CRC32;
Query Match Best Local Similarity 50.0%; Score 51; DB 1; Length 3418;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
DB 3159 FNKKNTEVEND 3170
QY 2 YNKKKATVOELD 13
ID NO20 MEDTR STANDARD; PRT; 268 AA.
AC P93329;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE EARLY NODULIN 20 PRECURSOR (N-20).
GN ENOD20.
OS MEDICAGO TRUNCATULA (BARREL MEDIC).
OC EUPHYLLOPHYTES: SPERMATOPHYTES: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
OC FABACEAE: FABACEAE: PAPILIONOIDEAE: MEDICAGO.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, JEMALONG;
RL GREENE E.A., ERARD M., DEDIEU A., BARKER D.G.;
RT SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL, X99467; E258656; -
KW MODULATION: SIGNAL.

FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 268 EARLY NODULIN 20.
 FT DOMAIN 23 ? PLASTOCYANIN-LIKE.
 FT DOMAIN 136 145 POLY-PRO.
 SQ SEQUENCE 268 AA; 28668 MW; 29EAFD8F CRC32;

Query Match
 Best Local Similarity 41.7%; Score 50; DB 1; Length 268;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 65 YNKTESVEYE 76
 ||| :||:
 QY 2 YNKKRATVQELD 13

Query Match
 Best Local Similarity 70.0%; Score 50; DB 1; Length 274;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 77 KKKAVADLD 86
 ||||| :||:
 QY 4 KKKRATVQELD 13

Search completed: Tue Aug 31 19:27:52 1999
 Job time : 7 secs.

RESULT 15
 ID HEL_HAEIN STANDARD; PRT; 274 AA.
 AC P26093;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LIPOPROTEIN E PRECURSOR (OUTER MEMBRANE PROTEIN P4) (OMP P4).
 GN HEL OR OMP4 OR H10693.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURRELLACEAE;
 OC HAEMOPHILUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 263-274.
 RC STRAIN-RD / KW20B;
 RX MEDLINE; 91348867.
 RA GREEN B.A., FARLEY J.E., QUINN-DEY T., DEICH R.A., ZLOTNICK G.W.;
 RT "The e (P4) outer membrane protein of Haemophilus influenzae:
 RT biologic activity of anti-e serum and cloning and sequencing of the
 RT structural gene.";
 RL INFECT. IMMUN. 59:3191-3198(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLANAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., CORTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA ETNE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEORHAGEN N.S.M.,
 RA GUEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL SCIENCE 269:496-512(1995).
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
 CC ANCHOR.
 CC
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL: M68502; G148896; -;
 DR EMBL: U32752; G1573696; -;
 DR PIR: A43604; A43604.
 DR TIGR: H10693; -;
 DR PROSITE: PS00013; PROKAR.LIPOPROTEIN; 1.
 DR KM OUTER MEMBRANE: LIPOPROTEIN; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 274 LIPOPROTEIN E.
 FT LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
 FT CONFLICT 30 30 G -> E (IN REF. 1).
 SQ SEQUENCE 274 AA; 30431 MW; 55289338 CRC32;

MIPS RELEASE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:28:10 1999; MasPar time 5.43 Seconds
140.736 Million cell updates/sec
Tabular output not generated.

Title: >US-09-150-947-10
Description: (1-14) from US09150947.pep
Perfect Score: 81
Sequence: 1 XTNRKATVQELDX 14

Scoring table:
PAM 150
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl9
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp-organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 23.956; Variance 28.794; scale 0.832

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|-------------------------------|-----------|
| 1 | 63 | 77.8 | 268 | 2 | 085217 ENTEROTOXIN J | 1.71e-02 |
| 2 | 60 | 74.1 | 460 | 3 | 060095 HYPOTHETICAL 52.7 KD P | 8.45e-02 |
| 3 | 59 | 72.8 | 362 | 2 | 045833 SPOULATON PROTEIN. | 1.43e-01 |
| 4 | 58 | 71.6 | 260 | 2 | 054971 SUPERANTIGEN. | 2.39e-01 |
| 5 | 58 | 71.6 | 260 | 2 | 054738 SUPERANTIGEN SSA. | 2.39e-01 |
| 6 | 58 | 71.6 | 260 | 2 | 054739 SUPERANTIGEN SSA. | 2.39e-01 |
| 7 | 58 | 71.6 | 3394 | 5 | 077384 MAL3P6.11 PROTEIN | 2.39e-01 |
| 8 | 56 | 69.1 | 464 | 13 | 091693 MOTHERS AGAINST DPP. | 6.44e-01 |
| 9 | 56 | 69.1 | 760 | 3 | 091308 COSMID F46F11. | 6.44e-01 |
| 10 | 56 | 69.1 | 1232 | 13 | 093308 14S COHESIN SMC1 SUBUN | 6.44e-01 |
| 11 | 55 | 67.9 | 811 | 3 | 087145 HYPOTHETICAL 92.5 KD P | 1.10e+00 |
| 12 | 54 | 66.7 | 490 | 2 | 007382 HISTIDINE KINASE LTKIN | 1.80e+00 |
| 13 | 54 | 66.7 | 1233 | 13 | 073696 MITOSIS-SPECIFIC CHROM | 1.80e+00 |
| 14 | 53 | 65.4 | 241 | 2 | 053585 ENTEROTOXIN H PRECURSO | 2.94e+00 |
| 15 | 53 | 65.4 | 271 | 1 | 065075 HYPOTHETICAL 30.9 KD P | 2.94e+00 |
| 16 | 53 | 65.4 | 325 | 5 | 061207 H04221.1 PROTEIN (FRAG | 2.94e+00 |
| 17 | 53 | 65.4 | 393 | 4 | 060870 KINI7 PROTEIN. | 2.94e+00 |
| 18 | 53 | 65.4 | 725 | 4 | 014995 KIAA0178 (FRAGMENT). | 2.94e+00 |
| 19 | 53 | 65.4 | 880 | 3 | 006708 CHROMOSOME XII COSMID | 2.94e+00 |
| 20 | 53 | 65.4 | 1225 | 4 | 014683 KIAA0178 PROTEIN (FRAG | 2.94e+00 |

| | | | | | | |
|----|----|------|------|----|-------------------------------|----------|
| 21 | 53 | 65.4 | 1233 | 4 | 016351 SB1.8/DX5423E-MITOSIS- | 2.94e+00 |
| 22 | 52 | 64.2 | 127 | 2 | 021469 YCCG PROTEIN. | 4.78e+00 |
| 23 | 52 | 64.2 | 236 | 2 | 097163 TYPE A EXOTOXIN PRECUR | 4.78e+00 |
| 24 | 52 | 64.2 | 236 | 2 | 054779 TYPE A EXOTOXIN PRECUR | 4.78e+00 |
| 25 | 52 | 64.2 | 236 | 2 | 057453 TYPE A EXOTOXIN PRECUR | 4.78e+00 |
| 26 | 52 | 64.2 | 208 | 4 | 092599 MYELOBLAST KIAA0202 (F | 4.78e+00 |
| 27 | 51 | 63.0 | 109 | 5 | 044441 B0546.1 PROTEIN | 7.71e+00 |
| 28 | 51 | 63.0 | 258 | 2 | 085382 EXTRACELLULAR ENTEROTO | 7.71e+00 |
| 29 | 51 | 63.0 | 262 | 2 | 067006 FLAGELLAR HOOK BASAL-B | 7.71e+00 |
| 30 | 51 | 63.0 | 319 | 14 | 065408 POLYPROTEIN (FRAGMENTS | 7.71e+00 |
| 31 | 51 | 63.0 | 319 | 14 | 065409 POLYPROTEIN (FRAGMENTS | 7.71e+00 |
| 32 | 51 | 63.0 | 319 | 14 | 065407 POLYPROTEIN (FRAGMENTS | 7.71e+00 |
| 33 | 51 | 63.0 | 334 | 4 | 015008 BRCA2 (FRAGMENT). | 7.71e+00 |
| 34 | 51 | 63.0 | 336 | 5 | 021645 SIMILAR TO ACETICOLIN | 7.71e+00 |
| 35 | 51 | 63.0 | 674 | 11 | 035920 CALPAIN LARGE SUBUNIT | 7.71e+00 |
| 36 | 51 | 63.0 | 713 | 11 | 088666 CALPAIN I LARGE SUBUNI | 7.71e+00 |
| 37 | 51 | 63.0 | 713 | 11 | 097571 MU-CALPAIN LARGE SUBUN | 7.71e+00 |
| 38 | 51 | 63.0 | 713 | 11 | 035350 CALPAIN 1 | 7.71e+00 |
| 39 | 51 | 63.0 | 791 | 5 | 019148 COSMID F07C3. | 7.71e+00 |
| 40 | 51 | 63.0 | 804 | 5 | 044896 ZK84.4 PROTEIN. | 7.71e+00 |
| 41 | 51 | 63.0 | 3418 | 4 | 013879 BRCA2 GENE EXON 2 (AND | 7.71e+00 |
| 42 | 50 | 61.7 | 288 | 13 | 091491 DYSTROPHIN (FRAGMENT). | 1.23e+01 |
| 43 | 50 | 61.7 | 367 | 14 | 089736 POLYPROTEIN (FRAGMENT) | 1.23e+01 |
| 44 | 50 | 61.7 | 367 | 14 | 089735 POLYPROTEIN (FRAGMENT) | 1.23e+01 |
| 45 | 50 | 61.7 | 3685 | 4 | 014205 DYSTROPHIN (DMD). | 1.23e+01 |

ALIGNMENTS

| RESULT | ID | 1 | PRELIMINARY: | PRT: | 268 AA. |
|-----------------------|--|--|---------------------|------------|-------------|
| AC | 085217 | | | | |
| DT | 01-NOV-1998 | (TREMBL.REL. 08, CREATED) | | | |
| DT | 01-NOV-1998 | (TREMBL.REL. 08, LAST SEQUENCE UPDATE) | | | |
| DT | 01-NOV-1998 | (TREMBL.REL. 08, LAST ANNOTATION UPDATE) | | | |
| DE | ENTEROTOXIN J. | | | | |
| GN | SEQ. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OG | PLASMID P18485. | | | | |
| OC | BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | |
| NC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-KS11410; | | | | |
| RA | ZHANG S., IANDELO J.J., STEWART G.C.; | | | | |
| RT | "The enterotoxin D plasmid of Staphylococcus aureus encodes a second | | | | |
| RT | enterotoxin determinant (set)." | | | | |
| RL | SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS. | | | | |
| DR | EMBL; AF053140; G3572542; - | | | | |
| DR | PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1. | | | | |
| DR | PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. | | | | |
| KW | PLASMID. | | | | |
| SQ | SEQUENCE 268 AA: 31230 MW: 52EB1B06 CMC32. | | | | |
| Query Match | | 77.8% | Score 63; | DB 2; | Length 268; |
| Best local similarity | | 81.8%; | Pred. No. 1.71e-02; | | |
| Matches | 9; | Conservative | 1; | Mismatches | 1; |
| Indels | 0; | Gaps | 0; | | |
| DB | 170 NRRKATVQELDX 180 | | | | |
| OY | 3 NRRKATVQELDX 13 | | | | |
| RESULT | 2 | PRELIMINARY: | PRT: | 460 AA. | |
| ID | 060095 | | | | |
| AC | 060095 | | | | |
| DT | 01-AUG-1998 | (TREMBL.REL. 07, CREATED) | | | |
| DT | 01-AUG-1998 | (TREMBL.REL. 07, LAST SEQUENCE UPDATE) | | | |
| DT | 01-AUG-1998 | (TREMBL.REL. 07, LAST ANNOTATION UPDATE) | | | |
| DE | HYPOTHETICAL 52.7 KD PROTEIN. | | | | |
| GN | SPB14C8.15. | | | | |
| OS | SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). | | | | |
| OC | EUARIOTA; FUNGI; ASCOMYCOTA; ARCHIAASCOCYCETES; | | | | |

OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972H-;
RA LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AL022305; E1285407; -
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 460 AA; 52670 MW; 835D7303 CRC32;

Query Match 74.1%; Score 60; DB 3; Length 460;
Best Local Similarity 50.0%; Pred. No. 8.45e-02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 105 YKKKGKIEELN 116
OY 2 YNKKKATVOELD 13
1:111:1111:

RESULT 3
TN 045833 PRELIMINARY; PRT: 362 AA.
AC 045833;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE SPOULATION PROTEIN.
UN SPOID.
OS CLOSTRIDIUM ACETOBUTYLICUM.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
OC CLOSTRIDIUM.
RN [1]
RP SEQUENCE FROM N.A.
RA REID S.J., HANCOCK K., SANTANGELO J.D., WOODS D.R.;
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M87835; G144915; -
KW SPOULATION.
SQ SEQUENCE 362 AA; 40998 MW; 75E3556E CRC32;

Query Match 72.8%; Score 59; DB 2; Length 362;
Best Local Similarity 58.3%; Pred. No. 1.43e-01;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKDNVYEELD 78
OY 2 YNKKKATVOELD 13
1:111:1111:

RESULT 4
ID 054971 PRELIMINARY; PRT: 260 AA.
AC 054971;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE SUPERANTIGEN.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WELLER.
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSEY J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INFECT. IMMUN. 62:1867-1874(1994).
DR EMBL: L29565; G476764; -
KW PFAM: PF01123; Stap_Strp_toxin; 1.
RN SUPERANTIGEN.
SQ SEQUENCE 260 AA; 29797 MW; FE391C2B CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;
Best Local Similarity 81.8%; Pred. No. 2.39e-01;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKKQVTVQELD 183
OY 3 NKKKATVOELD 13
1111111111

RESULT 5
ID 054738 PRELIMINARY; PRT: 260 AA.
AC 054738;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS 1842;
RX MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSEY J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INFECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS 1842;
RX MEDLINE: 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSEY J.M., R R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
variants provides evidence for horizontal transfer of ssa within
Streptococcus pyogenes.";
RL INFECT. IMMUN. 64:1161-1165(1996).
DR EMBL: U48793; G1245174; -
KW PFAM: PF01123; Stap_Strp_toxin; 1.
SQ SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;
Best Local Similarity 81.8%; Pred. No. 2.39e-01;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 173 NKKQVTVQELD 183
OY 3 NKKKATVOELD 13
1111111111

RESULT 6
ID 054739 PRELIMINARY; PRT: 260 AA.
AC 054739; 054737;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE SUPERANTIGEN SSA.
GN SSA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSEY J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL INFECT. IMMUN. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96178602.

RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MOSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."

RL INSECT. IMMUN. 64:1161-1165(1996).
DR EMBL: U48794; G1245176; -;
DR EMBL: U48792; G1245172; -;
DR PFAM: PF01123; Strep-Stp toxin. 1.

SEQUENCE 260 AA; 29767 MW; C81448C1 CRC32;

Query Match 71.6%; Score 58; DB 2; Length 260;

Best Local Similarity 81.8%; Pred. No. 2.39e-01;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 173 NKQVTVQELD 183
||| |||||
QY 3 NKKKATVQELD 13

RESULT 7

ID 077384 PRELIMINARY; PRT: 3394 AA.

AC 077384;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE MAL3P6.11 PROTEIN.

GN MAL3P6.11.

OS PLASMODIUM FALCIPARUM.

OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM.

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN-3D7;

RA MURPHY L., LAMSON D., BARRELL B.;

RL SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: Z98551; E1331922; -;

SEQUENCE 3394 AA; 402947 MW; 4C3F2778 CRC32;

Query Match 71.6%; Score 58; DB 5; Length 3394;

Best Local Similarity 50.0%; Pred. No. 2.39e-01;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 373 YNKSNTIOQLN 384
||| |::|:
QY 2 YNKKATVQELD 13

RESULT 8

ID 091693 PRELIMINARY; PRT: 464 AA.

AC 091693;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DE MOTHERS AGAINST DPP.

GN XMAD.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOBATRACHIA; PIPOIDEA; PIPOIDAE; XENOPODINAE; XENOPUS.

RN [1]

RC SEQUENCE FROM N.A.

RX MEDLINE: 96312915.

RA THOMSEN G.H.;

RT "Xenopus mothers against decapentaplegic is an embryonic ventralizing
RT agent that acts downstream of the BMP-2/4 receptor.";

RL DEVELOPMENT 122:2359-2366(1996).

DR EMBL: U58834; G1381671; -;

PFAM: PF00968; Dwarfin. 1.

SEQUENCE 464 AA; 52346 MW; 4017799F CRC32;

Query Match 69.1%; Score 56; DB 13; Length 464;

Best Local Similarity 54.3%; Pred. No. 6.64e-01;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 42 KKKKAIOELE 52

QY 3 NKKKATVQELD 13
:||||:|
|||:|

RESULT 9

ID P91308 PRELIMINARY; PRT: 760 AA.

AC P91308;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DE COSMID F46F11.

GN F46F11.8.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECRETENTEA; RHABDITIA; RHABDITIDA;

OC RHABDITINA; RHABDITIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2;

RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LATSTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans."

RL NATURE 368:32-38(1994).

RN [2]

RC SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2;

RA PAULEY A., GATTUNG S.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RC SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2;

RA WATERSTON R.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: 088173; G1825648; -;

SEQUENCE 760 AA; 88595 MW; D1020BBA CRC32;

Query Match 69.1%; Score 56; DB 5; Length 760;

Best Local Similarity 33.3%; Pred. No. 6.64e-01;

Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

DB 569 YDSKNSIOELE 580
|:|::|:
QY 2 YNKKATVQELD 13

RESULT 10

ID 093308 PRELIMINARY; PRT: 1232 AA.

AC 093308;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE 14S COMESTIN SMC1 SUBUNIT.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOBATRACHIA; PIPOIDEA; PIPOIDAE; XENOPODINAE; XENOPUS.

RN [1]

RC SEQUENCE FROM N.A.

RX MEDLINE: 96315077.

RA LOSADA A., HIRANO M., HIRANO T.;

RT "Identification of Xenopus SMC protein complexes required for sister
RT chromatid cohesion.";

RL GENES DEV. 12:1986-1997(1998).

DR EMBL: AF051784; G3328231; -;

SEQUENCE 1232 AA; 142627 MW; FDEB5B84 CRC32;

DT 01-AUG-1998 (TREMBL,REL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBL,REL. 07, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 30.9 KD PROTEIN (FRAGMENT).
GN S850.
OS PICEA MARIANA.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC PICEA.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.;
RL GENETICS 0:0-0(1998).
DR EMBL: AF051236; G2982303; -.
KW HYPOTHETICAL PROTEIN.
FT NON_TER 1
SQ SEQUENCE 271 AA; 30897 MW; 1DEA85B1 CRC32;

Query Match 65.4%; Score 53; DB 10; Length 271;
Best Local Similarity 54.5%; Pred. No. 2.94e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
D5 115 YSKTKAVEDL 125
QY 2 YNKKKATVQEL 12

Search completed: Tue Aug 31 19:28:53 1999
Job time : 43 secs.

THIS PAGE BLANK (USPTO)

M E D I C I N E
(TM)

Release 3.1A John F. Collins, BioComputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msearch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 31 19:32:21 1999; Maspar time 3.55 Seconds

Tabular output not generated. 83.787 Million cell updates/sec

Title: >US-09-150-947-11

Description: (1-14) from US09150947.pep

Sequence: 1 XNNKKATVQELDX 14

Scoring table:

PAM 150

Searched: 170751 segs, 2126608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-gene35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.360; Variance 49.153; scale 0.353

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|--------------------------------|-----------|
| 1 | 81 | 100.0 | 12 34 | W64637 | Synthetic SEB peptide 1.54e-02 | |
| 2 | 81 | 100.0 | 13 34 | W64641 | Synthetic SEB peptide 1.54e-02 | |
| 3 | 81 | 100.0 | 13 34 | W64646 | Synthetic SEB peptide 1.54e-02 | |
| 4 | 81 | 100.0 | 14 34 | W64644 | Synthetic SEB peptide 1.54e-02 | |
| 5 | 81 | 100.0 | 14 34 | W64645 | Synthetic SEB peptide 1.54e-02 | |
| 6 | 81 | 100.0 | 24 34 | W64642 | Synthetic SEB peptide 1.54e-02 | |
| 7 | 81 | 100.0 | 35 34 | W64643 | Synthetic SEB peptide 1.54e-02 | |
| 8 | 64 | 79.0 | 10 34 | W64638 | Synthetic SEB peptide 1.96e+00 | |
| 9 | 59 | 72.8 | 28 19 | W04494 | Staphylococcal entero 7.72e+00 | |
| 10 | 59 | 72.8 | 36 36 | W72426 | Peptide #6 for reduci 7.72e+00 | |
| 11 | 59 | 72.8 | 38 36 | W72427 | Peptide #5 for reduci 7.72e+00 | |
| 12 | 59 | 72.8 | 91 27 | W24299 | Staphylococcus aureus 7.72e+00 | |
| 13 | 59 | 72.8 | 233 3 | R13203 | Staphylococcal entero 7.72e+00 | |
| 14 | 59 | 72.8 | 233 8 | R45011 | Staphylococcal entero 7.72e+00 | |
| 15 | 59 | 72.8 | 233 27 | W35373 | Staphylococcus entero 7.72e+00 | |
| 16 | 59 | 72.8 | 233 20 | W06738 | Staphylococcus entero 7.72e+00 | |

| | | | | | |
|----|----|------|--------|--------|--------------------------------|
| 17 | 58 | 71.6 | 12 34 | W64636 | Synthetic SEB peptide 1.01e+01 |
| 18 | 58 | 71.6 | 13 34 | W64640 | Synthetic SEB peptide 1.01e+01 |
| 19 | 58 | 71.6 | 239 34 | W64647 | Synthetic SEB protein 1.01e+01 |
| 20 | 58 | 71.6 | 239 8 | R45014 | Staphylococcal entero 1.01e+01 |
| 21 | 58 | 71.6 | 239 3 | R13206 | Staphylococcal entero 1.01e+01 |
| 22 | 58 | 71.6 | 255 20 | W06737 | Staphylococcus entero 1.01e+01 |
| 23 | 57 | 70.4 | 228 3 | R13205 | Staphylococcal entero 1.32e+01 |
| 24 | 57 | 70.4 | 228 8 | R45013 | Staphylococcal entero 1.32e+01 |
| 25 | 54 | 66.7 | 24 36 | W72423 | Peptide #2 for reduci 2.94e+01 |
| 26 | 54 | 66.7 | 28 36 | W72425 | Peptide #4 for reduci 2.94e+01 |
| 27 | 53 | 65.4 | 10 34 | W64639 | Synthetic SEB peptide 3.83e+01 |
| 28 | 53 | 65.4 | 230 8 | R45012 | Staphylococcal entero 3.83e+01 |
| 29 | 53 | 65.4 | 230 3 | R13204 | Staphylococcal entero 3.83e+01 |
| 30 | 53 | 65.4 | 245 27 | W35374 | Staphylococcus entero 3.83e+01 |
| 31 | 53 | 65.4 | 245 27 | W35375 | Staphylococcus entero 3.83e+01 |
| 32 | 52 | 64.2 | 221 3 | R13209 | Streptococcal pyrogen 4.97e+01 |
| 33 | 52 | 64.2 | 221 8 | R45017 | Streptococcal entero 4.97e+01 |
| 34 | 52 | 64.2 | 250 24 | W12145 | Streptococcus pyogene 4.97e+01 |
| 35 | 52 | 64.2 | 251 24 | W12147 | Streptococcus pyogene 4.97e+01 |
| 36 | 52 | 64.2 | 251 24 | W12153 | Streptococcus pyogene 4.97e+01 |
| 37 | 52 | 64.2 | 251 24 | W12097 | Streptococcus pyogene 4.97e+01 |
| 38 | 52 | 64.2 | 251 33 | W59781 | Amino acid sequence o 4.97e+01 |
| 39 | 52 | 64.2 | 251 33 | W59780 | Amino acid sequence o 4.97e+01 |
| 40 | 52 | 64.2 | 251 24 | W12151 | Streptococcus pyogene 4.97e+01 |
| 41 | 52 | 64.2 | 251 24 | W12150 | Streptococcus pyogene 4.97e+01 |
| 42 | 52 | 64.2 | 251 24 | W12152 | Streptococcus pyogene 4.97e+01 |
| 43 | 52 | 64.2 | 251 24 | W12146 | Streptococcus pyogene 4.97e+01 |
| 44 | 52 | 64.2 | 251 24 | W12149 | Streptococcus pyogene 4.97e+01 |
| 45 | 52 | 64.2 | 401 36 | W22779 | Human septin-2 protei 4.97e+01 |

ALIGNMENTS

RESULT 1
ID W64637 standard; peptide; 12 AA.
AC W64637;
DE 23-OCT-1998 (first entry)
DE Synthetic SEB peptide p12(151-161)
KW Enterotoxin B; SEB; Pyrogenic exotoxin; PERT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.
OS Staphylococcus aureus.
PN W09829444-A1.
PD 09-JUL-1998.
PF 30-DEC-1997; IL0438.
PR 30-DEC-1996; IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R.
DR WPI; 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
PS Claim 8; Page 41; 68pp; English.
CC W64636-W64637 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PERT or by a mixture of PERTs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PERTs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PERT.
SQ Sequence 12 AA;
Query Match 100.0%; Score 81; DB 34; Length 12;
Best local similarity 100.0%; Pred. No. 1.54e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YNKKKATVQELD 13

RESULT 2
ID W64641 standard; peptide; 13 AA.

DE 23-DEC-1998 (first entry)
DE Synthetic SEB peptide p12c(150-161).
KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
OS Synthetic.

OS Staphylococcus aureus.

FT Key Location/Qualifiers

FT Modified_site 1 /note= "N-terminal Tyr modified by presence of N-lauryl-cysteyl"

PN W09829444-A1.

PD 09-JUL-1998.

PR 30-DEC-1997; IL0438.

PS 30-DEC-1996; IL-119938.

PA (YISS) YISSUM RES & DEV CO.

PI Arad G, Kaempfer R;

DR WPI; 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.

PT antagonising toxin-mediated activation of T cells and prevention or

PT treatment of toxic shock caused by exotoxins(s)

PS Claim 16; Page 41; 68pp; English.

CC W64636-W64657 are peptides homologous to the amino acid sequence of a

CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide

CC capable of eliciting protective immunity against toxic shock induced by

CC PERT or by a mixture of PERTs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression

CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or

CC TNF-beta genes. The peptides may be used to prepare therapeutics or

CC vaccines for the treatment of prophylaxis of toxin-mediated activation

CC of T cells and eliciting protective immunity against toxic shock induced

CC by PERTs. They can also be used for the treatment of harmful effects

CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to

CC the peptides can also be used for alleviating toxic shock induced by PERT.

SQ Sequence 13 AA;

Query Match 100.0%; Score 81; DB 34; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.54e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ynkktatvqeld 13

QY 2 YNKKKATVQELD 13

RESULT 3
ID W64646 standard; peptide; 13 AA.

AC W64646;

DT 23-OCT-1998 (first entry)

DE Synthetic SEB peptide Ac-p12(150-161).

KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;

KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;

KW therapeutic; vaccine; food poisoning.

OS Synthetic.

OS Staphylococcus aureus.

FT Key Location/Qualifiers

FT Modified_site 1

FT /note= "N-terminal Tyr modified by N-acetyl group"

FT Misc_difference 14 /note= "D-form residue"

PN W09829444-A1.

PD 09-JUL-1998.

PR 30-DEC-1997; IL0438.

PS 30-DEC-1996; IL-119938.

PA (YISS) YISSUM RES & DEV CO.

PI Arad G, Kaempfer R;

DR WPI; 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.

PT antagonising toxin-mediated activation of T cells and prevention or

PT treatment of toxic shock caused by exotoxins(s)

PS Claim 24; Page 41; 68pp; English.

CC W64636-W64657 are peptides homologous to the amino acid sequence of a

CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide

CC capable of eliciting protective immunity against toxic shock induced by

CC PERT or by a mixture of PERTs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression

CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or

CC TNF-beta genes. The peptides may be used to prepare therapeutics or

CC vaccines for the treatment of prophylaxis of toxin-mediated activation

CC of T cells and eliciting protective immunity against toxic shock induced

CC by PERTs. They can also be used for the treatment of harmful effects

CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to

CC the peptides can also be used for alleviating toxic shock induced by PERT.

SQ Sequence 13 AA;

Query Match 100.0%; Score 81; DB 34; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.54e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ynkktatvqeld 12

QY 2 YNKKKATVQELD 13

RESULT 4
ID W64644 standard; peptide; 14 AA.

AC W64644;

DT 23-OCT-1998 (first entry)

DE Synthetic SEB peptide Cys-p12(150-161).

KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;

KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;

KW therapeutic; vaccine; food poisoning.

OS Synthetic.

OS Staphylococcus aureus.

PN W09829444-A1.

PD 09-JUL-1998.

PR 30-DEC-1997; IL0438.

PS 30-DEC-1996; IL-119938.

PA (YISS) YISSUM RES & DEV CO.

PI Arad G, Kaempfer R;

DR WPI; 98-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.

PT antagonising toxin-mediated activation of T cells and prevention or

PT treatment of toxic shock caused by exotoxins(s)

PS Claim 21; Page 41; 68pp; English.

CC W64636-W64657 are peptides homologous to the amino acid sequence of a

CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide

CC capable of eliciting protective immunity against toxic shock induced by

CC PERT or by a mixture of PERTs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression

CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or

CC TNF-beta genes. The peptides may be used to prepare therapeutics or

CC vaccines for the treatment of prophylaxis of toxin-mediated activation

CC of T cells and eliciting protective immunity against toxic shock induced

CC by PERTs. They can also be used for the treatment of harmful effects

CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to

CC the peptides can also be used for alleviating toxic shock induced by PERT.

SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 34; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.54e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ynkktatvqeld 13

QY 2 YNKKKATVQELD 13

RESULT 5

ID W64645 standard; peptide; 14 AA.
 AC W64645;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide D-A1a.
 KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 OS Synthetic.
 OS Staphylococcus aureus.
 PH Key
 FT Misc-difference 1 Location/Qualifiers
 FT MISC-difference 14 /note= "D-form residue"
 FT MISC-difference 14 /note= "D-form residue"
 PN W09829444-A1.
 PD 09-JUL-1998.
 PE 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI; 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PS treatment of toxic shock caused by exotoxin(s)
 PS Claim 23; Page 41; 68pp; English...
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T-cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 14 AA.

Query Match 100.0%; Score 81; DB 34; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 ynkktatvgeld 13
 |||||
 QY 2 YNKKKATVQELD 13

RESULT 6
 ID W64642 standard; peptide; 24 AA.
 AC W64642;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide dimer.
 KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 OS Synthetic.
 OS Staphylococcus aureus.
 PN W09829444-A1.
 PD 09-JUL-1998.
 PE 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI; 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PS treatment of toxic shock caused by exotoxin(s)
 PS Claim 18; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 24 AA.

Query Match 100.0%; Score 81; DB 34; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkktatvgeld 12
 |||||
 QY 2 YNKKKATVQELD 13

RESULT 7
 ID W64643 standard; peptide; 35 AA.
 AC W64643;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide trimer.
 KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 OS Synthetic.
 OS Staphylococcus aureus.
 PN W09829444-A1.
 PD 09-JUL-1998.
 PE 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR WPI; 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PS treatment of toxic shock caused by exotoxin(s)
 PS Claim 19; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PERTs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PERT. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PERT.
 SQ Sequence 35 AA.

Query Match 100.0%; Score 81; DB 34; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.54e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ynkktatvgeld 12
 |||||
 QY 2 YNKKKATVQELD 13

RESULT 8
 ID W64638 standard; peptide; 10 AA.
 AC W64638;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SEB peptide pSEB(152-161).
 KW Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KM toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 OS Synthetic.
 OS Staphylococcus aureus.

PN W09829444-A1.
PD 09-JUL-1998.
PE 30-DEC-1997: IL0438.
PR 30-DEC-1996: IL-119938.
PA (YISS) YISSUM RES & DEV CO.
PI Arad G, Kaempfer R;
DR WPI: 98-388042/33.
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.,
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxins(s)
PS Claim 10; Page 41; 68pp; English.
CC W64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by PET.
SQ Sequence 10 AA;

Query Match 79.0%; Score 64; DB 34; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.96e+00;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 kkatvgeid 10
|||:|||||
QY 4 KKKATVOELD 13

RESULT 9
AC W04494;
DI 10-DEC-1996 (first entry)
DE Staphylococcal enterotoxin A; agonist; T-cell proliferation;
KW Staphylococcal enterotoxin A; agonist; T-cell proliferation;
KW treatment; immunodeficiency; autoimmune disease; TNF-alpha;
KW tumour necrosis factor alpha.
OS Staphylococcus spp.
PN US545716-A.
PD 13-AUG-1996.
PE 08-SEP-1992: 941497.
PR 08-SEP-1992: US-941497.
PT 23-MAR-1994; US-220378.
PA (UYFL) UNIV FLORIDA.
PI Griegs ND, Johnson HM, Pontzer CH;
DR WPI: 96-383718/38.
PT Peptide fragments of Staphylococcal enterotoxin A (SEA) - useful as
PT SEA agonists for stimulating T-cell proliferation, e.g. in treatment
PT of immunodeficiency and autoimmune diseases
PS Example 1; Columns 15-16; 17pp; English.
CC The present peptide, comprising residues 146-173 of Staphylococcal
CC enterotoxin A (SEA), is useful as an SEA agonist for stimulating
CC T-cell proliferation, e.g. in the treatment of immunodeficiency and
CC autoimmune diseases. Supernatant from PBMC stimulated with
CC 100 micro of the peptide for 18 hrs., was collected and assayed
CC for TNF-alpha activity by cytotoxicity on L-929 cells. The result
CC given as units/ml of TNF-alpha activity was 1.85, compared to 24.1
CC for the most effective agonist, comprising SEA residues 121-149.
SQ Sequence 28 AA;

Query Match 72.8%; Score 59; DB 19; Length 28;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 nkknvteid 11
|||:|||||
QY 3 NKKRATVOELD 13

RESULT 10
ID W72426 standard; peptide; 36 AA.
AC W72426;
DI 22-DEC-1998 (first entry)
DE Peptide #5 for reducing symptoms of toxic shock syndrome.
KW Toxic shock syndrome; immunogenic response; bacterial infection;
KW Staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KW autoimmune disease.
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PE 01-APR-1998; 006663.
PR 07-APR-1997; US-838413.
PA (UYRQ) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
PS Claim 4; Page 54; 69pp; English.
CC The present invention describes peptides having consensus sequences #1
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGCX1TX23X4X5N #1,
CC KXKX78X9X10X11X12X13D14X15X16X17X18X27X19X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
CC are used: (i) for diagnostic detection of SPE or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit biogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
SQ Sequence 36 AA;

Query Match 72.8%; Score 59; DB 36; Length 36;
Best Local Similarity 81.8%; Pred. No. 7.72e+00;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvteid 22
|||:|||||
QY 3 NKKRATVOELD 13

RESULT 11
ID W72427 standard; peptide; 38 AA.
AC W72427;
DI 22-DEC-1998 (first entry)
DE Peptide #6 for reducing symptoms of toxic shock syndrome.
KW Toxic shock syndrome; immunogenic response; bacterial infection;
KW Staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KW autoimmune disease.
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
PN W09845325-A1.
PD 15-OCT-1998.
PE 01-APR-1998; 006663.
PR 07-APR-1997; US-838413.
PA (UYRQ) UNIV ROCKEFELLER.
PI Bannan JD, Zabriskie JB;
DR WPI: 98-568335/48.
PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
PS Claim 4; Page 54; 69pp; English.
CC The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kd.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1TX3X4X5N #1,
 CC KX6X78X9X10X11X12X13DX14X15X16RX17X18X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SEP). Ab
 CC are used: (i) for diagnostic detection of SPEA or SEA, SEP and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 CC Sequence 38 AA;

Query Match 72.8%; Score 59; DB 36; Length 38;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 12 nkknvtvgeld 22
 |||: |||||
 QY 3 NKKKATVOELD 13

RESULT 12
 ID W24299 standard; Protein: 91 AA.
 AC W24299;
 DT 14-APR-1998 (first entry)
 DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
 KM Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen;
 KW vaccine; disease; protection; isolation.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Misc-difference 29
 FT note="unspecified amino acid"
 FT
 FT W09731114-A2.
 PN 28-AUG-1997.
 PF 25-FEB-1997; G00524.
 PR 26-FEB-1996; GB-004045.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 PI Burnham MKR, Hodgson JE;
 DR WPI: 97-435166/40.
 DR N-PSDB: V01865.
 PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for
 PT isolating antagonist of the polypeptide(s) useful as anti-bacterials
 PS Claim 11; Page 33; 117pp; English.
 CC The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from Staphylococcus aureus. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds
 CC that bind and inhibit the activity of the polypeptide. Such compounds
 CC can be used as anti-bacterial compounds. The polypeptide may also be
 CC used as an immunogen to vaccinate an animal for protection against
 CC Staphylococcus aureus caused disease.
 CC Sequence 91 AA;

Query Match 72.8%; Score 59; DB 27; Length 91;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 40 nkknvtvgeld 50
 |||: |||||
 QY 3 NKKKATVOELD 13

RESULT 13
 ID R13203 standard; protein: 233 AA.
 AC R13203;
 DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin A.
 KW SEA; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.
 PN W09110680-A.
 PF 25-JUL-1991.
 PF 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237964/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure; Fig 1; 74pp; English.
 CC SEA was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC ibuprofen to attenuate toxic reaction to SEA. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophobic profiles.
 CC See also R13204-R13211.
 CC Sequence 233 AA;

Query Match 72.8%; Score 59; DB 3; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtvgeld 156
 |||: |||||
 QY 3 NKKKATVOELD 13

RESULT 14
 ID R45011 standard; protein: 233 AA.
 AC R45011;
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SEA.
 KM Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Misc-difference 49
 FT note="Given in the specification as O, no further
 FT details given"
 FT
 FT W09324136-A.
 PN 09-DEC-1993.
 PF 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS Disclosure; Fig 1; 90pp; English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC Sequence 233 AA;

Query Match 72.8%; Score 59; DB 8; Length 233;
 Best Local Similarity 81.8%; Pred. No. 7.72e+00;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtvgeld 156
 |||: |||||
 QY 3 NKKKATVOELD 13

RESULT 15

ID W35373 standard; peptide: 233 AA.
 AC W35373;
 DT 20-APR-1998 (first entry)
 DE Staphylococcus enterotoxin SEA wild-type superantigen.
 KM SEI: SEA; Staphylococcus enterotoxin: superantigen; conjugate;
 KW treatment: cancer; infection; autoimmune disease; antibody.
 OS Staphylococcus sp.
 PN W09736932-A1.
 PD 09-OCT-1997.
 PE 26-MAR-1997; SE0537.
 PK 12-AUG-1996; US-695692.
 PR 29-MAR-1996; SE-001245.
 PA (PHAA) PHARMACIA & UPJOHN AB.
 PI Aarlammen L, Antonsson P, Bjoerk P, Dohlsten M,
 Forsberg G, Hansson J, Kalland T;
 DR WPI: 97-503052/46.
 PT Conjugate of target seeking moiety and modified superantigen -
 useful for activating the immune system to treat cancer, viral
 PT infections, parasitic infestations and autoimmune diseases
 PS Claim 8: Pages 36-37; 58pp; English.
 CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
 CC SEA superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to
 CC T cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 SQ Sequence 233 AA;

Query Match 72.8%; Score 59; DB 27; Length 233;

Best Local Similarity 81.8%; Pred. No. 7.72e+00; Mismatches 1; Indels 0; Gaps 0;

Db 146 nkknvtyqeld 156
 |||:|||||
 QY 3 NKKKATVQELD 13

Search completed: Tue Aug 31 19:32:37 1999
 Job time : 16 secs.

WORLDWIDE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:31:47 1999; MasPar time 3.56 Seconds
Tabular output not generated. 157.313 Million cell updates/sec

Title: >US-09-150-947-11
Description: (1-14) from US09150947.pep
Perfect Score: 81
Sequence: 1 XNKKKATVOELDX 14

Scoring table:
PAM 150
Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 24.268; Variance 31.113; scale 0.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|--------------------------------|-----------|
| 1 | 59 | 72.8 | 233 | 2 | A29566 enterotoxin A - Staph | 2.55e+01 |
| 2 | 59 | 72.8 | 237 | 2 | A28664 enterotoxin A precursor | 2.55e+01 |
| 3 | 59 | 72.8 | 362 | 2 | S27530 sporulation protein - | 2.55e+01 |
| 4 | 58 | 71.6 | 265 | 1 | ENSAB5 enterotoxin B precursor | 4.14e+01 |
| 5 | 57 | 70.4 | 258 | 2 | A33953 enterotoxin D precursor | 6.68e+01 |
| 6 | 53 | 65.4 | 257 | 2 | A28179 enterotoxin E precursor | 4.30e+00 |
| 7 | 53 | 65.4 | 671 | 2 | A40692 signal recognition pa | 4.30e+00 |
| 8 | 53 | 65.4 | 880 | 2 | S51473 probable membrane pro | 4.30e+00 |
| 9 | 53 | 65.4 | 1233 | 2 | S15483 gene SBI.8/DX5423E pr | 4.30e+00 |
| 10 | 52 | 64.2 | 127 | 2 | B69767 conserved hypotetica | 6.76e+00 |
| 11 | 52 | 64.2 | 146 | 2 | S49746 probable membrane pro | 6.76e+00 |
| 12 | 52 | 64.2 | 226 | 2 | S18786 exotoxin type A precu | 6.76e+00 |
| 13 | 52 | 64.2 | 236 | 2 | S18783 exotoxin type A precu | 6.76e+00 |
| 14 | 52 | 64.2 | 251 | 2 | S29659 exotoxin type A precu | 6.76e+00 |
| 15 | 51 | 63.0 | 224 | 2 | S58590 ribosomal protein S3 | 1.05e+01 |
| 16 | 51 | 63.0 | 239 | 1 | R3R23 ribosomal protein S3 | 1.05e+01 |
| 17 | 51 | 63.0 | 262 | 2 | C70372 flagellar hook basal | 1.05e+01 |
| 18 | 51 | 63.0 | 412 | 2 | S48861 rRNA (guanosine-2'-O- | 1.05e+01 |
| 19 | 51 | 63.0 | 3418 | 1 | G02334 breast cancer tumor s | 1.05e+01 |
| 20 | 50 | 61.7 | 274 | 2 | B64087 outer membrane protei | 1.64e+01 |
| 21 | 50 | 61.7 | 391 | 2 | S18666 KIN17 protein - mouse | 1.64e+01 |
| 22 | 50 | 61.7 | 1075 | 1 | OYRTHX heat-stable enterotox | 1.64e+01 |
| 23 | 50 | 61.7 | 1223 | 2 | I38111 phosphotyrase kinase | 1.64e+01 |

| 24 | 50 | 61.7 | 3685 | 1 | A27605 | dystrophin, muscle - | 1.64e+01 |
|--|---|--|---|--|---|-----------------------|----------|
| 25 <td>49<td>60.5<td>290<td>2<td>S66072<th>hypothetical protein</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>290<td>2<td>S66072<th>hypothetical protein</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>290<td>2<td>S66072<th>hypothetical protein</th><th>2.52e+01</th></td></td></td> | 290 <td>2<td>S66072<th>hypothetical protein</th><th>2.52e+01</th></td></td> | 2 <td>S66072<th>hypothetical protein</th><th>2.52e+01</th></td> | S66072 <th>hypothetical protein</th> <th>2.52e+01</th> | hypothetical protein | 2.52e+01 |
| 26 <td>49<td>60.5<td>384<td>2<td>S46523<th>transcription factor</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>384<td>2<td>S46523<th>transcription factor</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>384<td>2<td>S46523<th>transcription factor</th><th>2.52e+01</th></td></td></td> | 384 <td>2<td>S46523<th>transcription factor</th><th>2.52e+01</th></td></td> | 2 <td>S46523<th>transcription factor</th><th>2.52e+01</th></td> | S46523 <th>transcription factor</th> <th>2.52e+01</th> | transcription factor | 2.52e+01 |
| 27 <td>49<td>60.5<td>452<td>2<td>T01694<th>calcium-dependent pro</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>452<td>2<td>T01694<th>calcium-dependent pro</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>452<td>2<td>T01694<th>calcium-dependent pro</th><th>2.52e+01</th></td></td></td> | 452 <td>2<td>T01694<th>calcium-dependent pro</th><th>2.52e+01</th></td></td> | 2 <td>T01694<th>calcium-dependent pro</th><th>2.52e+01</th></td> | T01694 <th>calcium-dependent pro</th> <th>2.52e+01</th> | calcium-dependent pro | 2.52e+01 |
| 28 <td>49<td>60.5<td>455<td>2<td>S55019<th>MAD polypeptide - fru</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>455<td>2<td>S55019<th>MAD polypeptide - fru</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>455<td>2<td>S55019<th>MAD polypeptide - fru</th><th>2.52e+01</th></td></td></td> | 455 <td>2<td>S55019<th>MAD polypeptide - fru</th><th>2.52e+01</th></td></td> | 2 <td>S55019<th>MAD polypeptide - fru</th><th>2.52e+01</th></td> | S55019 <th>MAD polypeptide - fru</th> <th>2.52e+01</th> | MAD polypeptide - fru | 2.52e+01 |
| 29 <td>49<td>60.5<td>465<td>2<td>S68987<th>transcription activat</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>465<td>2<td>S68987<th>transcription activat</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>465<td>2<td>S68987<th>transcription activat</th><th>2.52e+01</th></td></td></td> | 465 <td>2<td>S68987<th>transcription activat</th><th>2.52e+01</th></td></td> | 2 <td>S68987<th>transcription activat</th><th>2.52e+01</th></td> | S68987 <th>transcription activat</th> <th>2.52e+01</th> | transcription activat | 2.52e+01 |
| 30 <td>49<td>60.5<td>599<td>2<td>T02994<th>CDPK-related protein</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>599<td>2<td>T02994<th>CDPK-related protein</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>599<td>2<td>T02994<th>CDPK-related protein</th><th>2.52e+01</th></td></td></td> | 599 <td>2<td>T02994<th>CDPK-related protein</th><th>2.52e+01</th></td></td> | 2 <td>T02994<th>CDPK-related protein</th><th>2.52e+01</th></td> | T02994 <th>CDPK-related protein</th> <th>2.52e+01</th> | CDPK-related protein | 2.52e+01 |
| 31 <td>49<td>60.5<td>607<td>2<td>T03023<th>calcium-dependent pro</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>607<td>2<td>T03023<th>calcium-dependent pro</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>607<td>2<td>T03023<th>calcium-dependent pro</th><th>2.52e+01</th></td></td></td> | 607 <td>2<td>T03023<th>calcium-dependent pro</th><th>2.52e+01</th></td></td> | 2 <td>T03023<th>calcium-dependent pro</th><th>2.52e+01</th></td> | T03023 <th>calcium-dependent pro</th> <th>2.52e+01</th> | calcium-dependent pro | 2.52e+01 |
| 32 <td>49<td>60.5<td>625<td>2<td>T02033<th>calcium/calmodulin-de</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>625<td>2<td>T02033<th>calcium/calmodulin-de</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>625<td>2<td>T02033<th>calcium/calmodulin-de</th><th>2.52e+01</th></td></td></td> | 625 <td>2<td>T02033<th>calcium/calmodulin-de</th><th>2.52e+01</th></td></td> | 2 <td>T02033<th>calcium/calmodulin-de</th><th>2.52e+01</th></td> | T02033 <th>calcium/calmodulin-de</th> <th>2.52e+01</th> | calcium/calmodulin-de | 2.52e+01 |
| 33 <td>49<td>60.5<td>803<td>2<td>I66600<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>803<td>2<td>I66600<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>803<td>2<td>I66600<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td> | 803 <td>2<td>I66600<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td> | 2 <td>I66600<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td> | I66600 <th>dipeptidyl aminopepti</th> <th>2.52e+01</th> | dipeptidyl aminopepti | 2.52e+01 |
| 34 <td>49<td>60.5<td>803<td>2<td>A41793<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>803<td>2<td>A41793<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>803<td>2<td>A41793<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td> | 803 <td>2<td>A41793<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td> | 2 <td>A41793<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td> | A41793 <th>dipeptidyl aminopepti</th> <th>2.52e+01</th> | dipeptidyl aminopepti | 2.52e+01 |
| 35 <td>49<td>60.5<td>831<td>2<td>B64528<th>conserved hypotetica</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>831<td>2<td>B64528<th>conserved hypotetica</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>831<td>2<td>B64528<th>conserved hypotetica</th><th>2.52e+01</th></td></td></td> | 831 <td>2<td>B64528<th>conserved hypotetica</th><th>2.52e+01</th></td></td> | 2 <td>B64528<th>conserved hypotetica</th><th>2.52e+01</th></td> | B64528 <th>conserved hypotetica</th> <th>2.52e+01</th> | conserved hypotetica | 2.52e+01 |
| 36 <td>49<td>60.5<td>865<td>2<td>I54331<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>865<td>2<td>I54331<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>865<td>2<td>I54331<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td></td> | 865 <td>2<td>I54331<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td></td> | 2 <td>I54331<th>dipeptidyl aminopepti</th><th>2.52e+01</th></td> | I54331 <th>dipeptidyl aminopepti</th> <th>2.52e+01</th> | dipeptidyl aminopepti | 2.52e+01 |
| 37 <td>49<td>60.5<td>1134<td>2<td>A60234<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>1134<td>2<td>A60234<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>1134<td>2<td>A60234<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td></td> | 1134 <td>2<td>A60234<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td> | 2 <td>A60234<th>Iga Fc receptor precu</th><th>2.52e+01</th></td> | A60234 <th>Iga Fc receptor precu</th> <th>2.52e+01</th> | Iga Fc receptor precu | 2.52e+01 |
| 38 <td>49<td>60.5<td>1164<td>1<td>FC50AG<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>1164<td>1<td>FC50AG<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>1164<td>1<td>FC50AG<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td></td> | 1164 <td>1<td>FC50AG<th>Iga Fc receptor precu</th><th>2.52e+01</th></td></td> | 1 <td>FC50AG<th>Iga Fc receptor precu</th><th>2.52e+01</th></td> | FC50AG <th>Iga Fc receptor precu</th> <th>2.52e+01</th> | Iga Fc receptor precu | 2.52e+01 |
| 39 <td>49<td>60.5<td>1369<td>2<td>JC4860<th>protein-tyrosine kina</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>1369<td>2<td>JC4860<th>protein-tyrosine kina</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>1369<td>2<td>JC4860<th>protein-tyrosine kina</th><th>2.52e+01</th></td></td></td> | 1369 <td>2<td>JC4860<th>protein-tyrosine kina</th><th>2.52e+01</th></td></td> | 2 <td>JC4860<th>protein-tyrosine kina</th><th>2.52e+01</th></td> | JC4860 <th>protein-tyrosine kina</th> <th>2.52e+01</th> | protein-tyrosine kina | 2.52e+01 |
| 40 <td>49<td>60.5<td>3678<td>2<td>S28916<th>dystrophin - mouse</th><th>2.52e+01</th></td></td></td></td></td> | 49 <td>60.5<td>3678<td>2<td>S28916<th>dystrophin - mouse</th><th>2.52e+01</th></td></td></td></td> | 60.5 <td>3678<td>2<td>S28916<th>dystrophin - mouse</th><th>2.52e+01</th></td></td></td> | 3678 <td>2<td>S28916<th>dystrophin - mouse</th><th>2.52e+01</th></td></td> | 2 <td>S28916<th>dystrophin - mouse</th><th>2.52e+01</th></td> | S28916 <th>dystrophin - mouse</th> <th>2.52e+01</th> | dystrophin - mouse | 2.52e+01 |
| 41 <td>48<td>59.3<td>303<td>2<td>E69164<th>conserved hypotetica</th><th>3.86e+01</th></td></td></td></td></td> | 48 <td>59.3<td>303<td>2<td>E69164<th>conserved hypotetica</th><th>3.86e+01</th></td></td></td></td> | 59.3 <td>303<td>2<td>E69164<th>conserved hypotetica</th><th>3.86e+01</th></td></td></td> | 303 <td>2<td>E69164<th>conserved hypotetica</th><th>3.86e+01</th></td></td> | 2 <td>E69164<th>conserved hypotetica</th><th>3.86e+01</th></td> | E69164 <th>conserved hypotetica</th> <th>3.86e+01</th> | conserved hypotetica | 3.86e+01 |
| 42 <td>48<td>59.3<td>324<td>2<td>S48122<th>transcription factor</th><th>3.86e+01</th></td></td></td></td></td> | 48 <td>59.3<td>324<td>2<td>S48122<th>transcription factor</th><th>3.86e+01</th></td></td></td></td> | 59.3 <td>324<td>2<td>S48122<th>transcription factor</th><th>3.86e+01</th></td></td></td> | 324 <td>2<td>S48122<th>transcription factor</th><th>3.86e+01</th></td></td> | 2 <td>S48122<th>transcription factor</th><th>3.86e+01</th></td> | S48122 <th>transcription factor</th> <th>3.86e+01</th> | transcription factor | 3.86e+01 |
| 43 <td>48<td>59.3<td>332<td>2<td>S15347<th>transcription factor</th><th>3.86e+01</th></td></td></td></td></td> | 48 <td>59.3<td>332<td>2<td>S15347<th>transcription factor</th><th>3.86e+01</th></td></td></td></td> | 59.3 <td>332<td>2<td>S15347<th>transcription factor</th><th>3.86e+01</th></td></td></td> | 332 <td>2<td>S15347<th>transcription factor</th><th>3.86e+01</th></td></td> | 2 <td>S15347<th>transcription factor</th><th>3.86e+01</th></td> | S15347 <th>transcription factor</th> <th>3.86e+01</th> | transcription factor | 3.86e+01 |
| 44 <td>48<td>59.3<td>844<td>2<td>T00529<th>bZIP-like protein - A</th><th>3.86e+01</th></td></td></td></td></td> | 48 <td>59.3<td>844<td>2<td>T00529<th>bZIP-like protein - A</th><th>3.86e+01</th></td></td></td></td> | 59.3 <td>844<td>2<td>T00529<th>bZIP-like protein - A</th><th>3.86e+01</th></td></td></td> | 844 <td>2<td>T00529<th>bZIP-like protein - A</th><th>3.86e+01</th></td></td> | 2 <td>T00529<th>bZIP-like protein - A</th><th>3.86e+01</th></td> | T00529 <th>bZIP-like protein - A</th> <th>3.86e+01</th> | bZIP-like protein - A | 3.86e+01 |
| 45 <td>48<td>59.3<td>1381<td>2<td>S60004<th>hypothetical protein</th><th>3.86e+01</th></td></td></td></td></td> | 48 <td>59.3<td>1381<td>2<td>S60004<th>hypothetical protein</th><th>3.86e+01</th></td></td></td></td> | 59.3 <td>1381<td>2<td>S60004<th>hypothetical protein</th><th>3.86e+01</th></td></td></td> | 1381 <td>2<td>S60004<th>hypothetical protein</th><th>3.86e+01</th></td></td> | 2 <td>S60004<th>hypothetical protein</th><th>3.86e+01</th></td> | S60004 <th>hypothetical protein</th> <th>3.86e+01</th> | hypothetical protein | 3.86e+01 |

ALIGNMENTS

| RESULT | 1 | A29566 | #type complete |
|-----------------------|-----|----------------|---|
| ENTRY | 1 | A29566 | enterotoxin A - Staphylococcus aureus |
| TITLE | | A29566 | enterotoxin A - Staphylococcus aureus |
| ORGANISM | | A29566 | Staphylococcus aureus |
| DATE | | A29566 | 05-Jun-1988 #sequence-revision 05-Jun-1988 #text-change 18-Jun-1993 |
| ACCESSIONS | | A29566 | A29566 |
| REFERENCE | | A29566 | Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J. |
| #authors | | A29566 | J. Biol. Chem. (1987) 262:7006-7013 |
| #journal | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #title | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #cross-references | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #accession | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #molecule-type | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #residues | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| GENETICS | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #gene | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| #map-position | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| SUMMARY | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| Query Match | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| Best Local Similarity | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| Matches | | A29566 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| DB | 146 | NKKNVVOELD 156 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| QY | 3 | NKKNVVOELD 13 | Complete amino acid sequence of staphylococcal enterotoxin A. |
| RESULT | 2 | A28664 | #type complete |
| ENTRY | | A28664 | enterotoxin A precursor - Staphylococcus aureus (strain |
| TITLE | | A28664 | FR1337) |
| ORGANISM | | A28664 | #formal_name Staphylococcus aureus |
| DATE | | A28664 | 30-Jun-1989 #sequence-revision 30-Jun-1989 #text-change 20-Mar-1998 |
| ACCESSIONS | | A28664 | A28664 |
| REFERENCE | | A28664 | Betty, M.J.; Mekalanos, J.J. |
| #authors | | A28664 | J. Bacteriol. (1988) 170:34-41 |
| #journal | | A28664 | Nucleotide sequence of the type A staphylococcal enterotoxin |
| #title | | A28664 | gene. |
| #cross-references | | A28664 | Complete amino acid sequence of staphylococcal enterotoxin |
| #accession | | A28664 | Complete amino acid sequence of staphylococcal enterotoxin |
| #molecule-type | | A28664 | Complete amino acid sequence of staphylococcal enterotoxin |
| #residues | | A28664 | Complete amino acid sequence of staphylococcal enterotoxin |
| #cross-references | | A28664 | Complete amino acid sequence of staphylococcal enterotoxin |

```
##experimental_source strain FR1337
SUMMARY #length 257 #molecular-weight 29669 #checksum 2543

Query Match 72.8% Score 59; DB 2; Length 257;
Best Local Similarity 81.8%; Pred. No. 2.55e-01;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 170 NKKKATVOELD 180
|||:|||||
QY 3 NKKKATVOELD 13

RESULT 3
ENTRY S27530 #type complete
TITLE sporulation protein - Clostridium acetobutylicum
ORGANISM #formal_name Clostridium acetobutylicum
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
09-Sep-1997

ACCESSIONS S27530
REFERENCE S27530
#authors Reid, S.J.; Hancock, K.; Santangelo, J.D.; Woods, D.R.
#submission Submitted to the EMBL Data Library, March 1992
#description Cloning and sequencing of a SpoIIID gene from Clostridium
acetobutylicum.
#accession S27530
#status Preliminary
#molecule_type DNA
#residues 1362 #label REI
#cross-references EMBL:M87835; NID:g144914; PID:g144915
SUMMARY #length 362 #molecular-weight 40998 #checksum 3634

Query Match 72.8% Score 59; DB 2; Length 362;
Best Local Similarity 58.3%; Pred. No. 2.55e-01;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 67 YHKKNSVEELD 78
|||:|||||
QY 2 YHKKATVOELD 13

RESULT 4
ENTRY ENSAB6 #type complete
TITLE enterotoxin B precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change
11-Sep-1998

ACCESSIONS S27360; A92065; S27240; A01815
REFERENCE S27360
#authors Jones, C.L.; Khan, S.A.
#journal J. Bacteriol. (1986) 166:29-33
#title Nucleotide sequence of the enterotoxin B gene from
Staphylococcus aureus.
#cross-references EMBL:M1118; NID:g152999; PID:g153000
#accession S27360
#molecule_type DNA
#residues 1-266 #label JON
#experimental_source strain S6
REFERENCE A92065
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3518-3525
#title The primary structure of staphylococcal enterotoxin B. III.
The cyanogen bromide peptides of reduced and aminoethylated
enterotoxin B, and the complete amino acid sequence.
#cross-references MUID:71007902
#accession A92065
#molecule_type protein
#residues 28-55; 'NND', '59-68', 'NE', '71', 'FDLYL', '78-117', '119-127', 'N',
'129', 'D', '131-132', 'ENT', '136-148', 'GN', '151-156', 'Y',
'157-184', 'EQ', '187-232', 'N', '234-245', 'ND', '248-266' #label
HDA
#experimental_source strain S-6
REFERENCE A92064
```

```
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3511-3517
#title The primary structure of staphylococcal enterotoxin B. II.
Isolation, composition, and sequence of chymotryptic
peptides.
#cross-references MUID:71007901
#contents annotation; chymotryptic peptides
REFERENCE A92063
#authors Huang, I.Y.; Bergdoll, M.S.
#journal J. Biol. Chem. (1970) 245:3493-3510
#title The primary structure of staphylococcal enterotoxin B. I.
Isolation, composition, and sequence of tryptic peptides
from oxidized entero-toxin B.
#cross-references MUID:71007900
#contents annotation; tryptic peptides
REFERENCE A90548
#authors Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
Dunnehy, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin B.
#cross-references MUID:66035792
#contents annotation; biological source of protein
REFERENCE S27240
#authors Alakhov, V.Y.; Klinisky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.;
Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
Shemchukova, O.B.; Severin, E.S.
#journal Eur. J. Biochem. (1992) 209:823-828
#title Identification of functionally active fragments of
staphylococcal enterotoxin B.
#accession S27240
#molecule_type protein
#residues 28-42; 128-148 #label ALA
#classification #superfamily enterotoxin B
#keywords enterotoxin; extracellular protein; toxin
FEATURE 1-27
28-266 #domain signal sequence #status predicted #label SIG\
120-140 #product enterotoxin B #status experimental #label MAT\
SUMMARY #length 266 #molecular-weight 31436 #checksum 4249

Query Match 71.6% Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 4.14e-01;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 178 NKKKATVOELD 188
|||:|||||
QY 3 NKKKATVOELD 13

RESULT 5
ENTRY A33953 #type complete
TITLE enterotoxin D precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
09-Sep-1997

ACCESSIONS A33953
REFERENCE A33953
#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:4799-4806
#title Genetic and molecular analyses of the gene encoding
staphylococcal enterotoxin D.
#cross-references MUID:89359112
#accession A33953
#status Preliminary
#molecule_type DNA
#residues 1-258 #label BAY
#cross-references GB:M28521; NID:g1492109; PID:g758691
SUMMARY #length 258 #molecular-weight 29746 #checksum 39

Query Match 70.4% Score 57; DB 2; Length 258;
Best Local Similarity 72.7%; Pred. No. 6.68e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```



```

Db      171 DKKRATVOELD 181
QY      3 NKKRATVOELD 13

RESULT  6
ENTRY   A28179 #type complete
TITLE   enterotoxin F precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE    30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
        09-Sep-1997
ACCESSIONS
REFERENCE #authors A28179
          #journal A28179
          #title    J. Bacteriol. (1988) 170:2954-2960
                Cloning and nucleotide sequence of the type E staphylococcal
                enterotoxin gene.
          #cross-references MUID:88257005
          #accession A28179
          ##molecule_type DNA
          ##residues 1-257 #label COU
          ##cross-references GB:M21319; NID:g153001; PID:g153002
SUMMARY  #length 257 #molecular-weight 29358 #checksum 2562

Query Match
Best Local Similarity 72.7%; Pred. No. 4.30e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Lb      170 SKRETVQELD 180
QY      3 NKKRATVOELD 13

RESULT  7
ENTRY   A40692 #type complete
TITLE   signal recognition particle 72k chain - dog
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE    21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
        10-Sep-1997
ACCESSIONS
REFERENCE #authors A40692; S32167
          #journal Lutcke, H.; Prehn, S.; Ashford, A.J.; Remus, M.; Frank, R.;
                Dobberstein, B.
          #title    J. Cell Biol. (1993) 121:977-985
                Assembly of the 66- and 72-kD proteins of signal recognition
                particle with 7S RNA.
          #cross-references MUID:93273803
          #accession A40692
          ##status preliminary
          ##molecule_type mRNA; protein
          ##residues 1-671 #label IUT
          ##cross-references EMBL:X67813; NID:g297767; PID:g297768
                sequence extracted from NCBI backbone (NCBIP:132901)
SUMMARY  ##note #length 671 #molecular-weight 74493 #checksum 6822

Query Match
Best Local Similarity 65.4%; Score 53; DB 2; Length 671;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db      460 YGRKKAISDLE 471
QY      2 YNKKRATVOELD 13

RESULT  8
ENTRY   S51473 #type complete
TITLE   probable membrane protein YLR386w - yeast (Saccharomyces
ORGANISM #formal_name Saccharomyces cerevisiae
DATE    23-Feb-1995 #sequence_revision 12-May-1995 #text_change
        21-Nov-1997
ACCESSIONS
S51473

```

```

REFERENCE S51466
#authors Du, Z.
#submission Submitted to the EMBL Data Library, December 1994
#description The sequence of S. cerevisiae cosmid L3502.
#accession S51473
##molecule_type DNA
##residues 1-880 #label DU2
##cross-references EMBL:U0104; NID:g609423; PID:g609424; MIPS:YLR386w
GENETICS
#map_position 12R
KEYWORDS transmembrane protein
FEATURE
FEATURE 426-442
SUMMARY  #domain transmembrane #status predicted #label TM
          #length 880 #molecular-weight 99771 #checksum 5346

Query Match
Best Local Similarity 50.0%; Pred. No. 4.30e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db      14 YEKRAALELE 25
QY      2 YNKKRATVOELD 13

RESULT  9
ENTRY   I54383 #type complete
TITLE   gene SBI.8/DXS423E protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change
        28-Feb-1997
ACCESSIONS
REFERENCE #authors I54383
          #journal Rocques, P.J.; Clark, J.; Ball, S.; Crew, J.; Gill, S.;
                Christodoulou, Z.; Borts, R.H.; Louis, E.J.; Davies, K.E.;
                Cooper, C.S.
          #title    Hum. Mol. Genet. (1995) 4:243-249
                The human SBI.8 gene (DXS423E) encodes a putative chromosome
                segregation protein conserved in lower eukaryotes and
                prokaryotes.
          #cross-references MUID:95276737
          #accession I54383
          ##status preliminary; translated from GB/EMBL/DBJ
          ##molecule_type mRNA
          ##residues 1-1233 #label RES
          ##cross-references GB:S78271; NID:g999379; PID:g999380
GENETICS
SUMMARY  #gene SBI.8/DXS423E
          #length 1233 #molecular-weight 143204 #checksum 7067

Query Match
Best Local Similarity 65.4%; Score 53; DB 2; Length 1233;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db      326 YKRRGDMDELE 337
QY      2 YNKKRATVOELD 13

RESULT  10
ENTRY   B69767 #type complete
TITLE   conserved hypothetical protein yccC - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE    05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
        24-Sep-1998
ACCESSIONS
REFERENCE #authors B69767
          #journal Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
                Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessières, P.;
                Bolotin, A.; Borchert, S.; Bortiss, R.; Boursier, L.; Brans,
                A.; Braun, M.; Bignelli, S.C.; Bron, S.; Brouillet, S.;
                Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
                Choi, S.K.; Codani, J.J.; Connetton, I.F.; Cummings, N.J.;
                Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;

```

Ehrlich, S.D.; Emmerson, P.T.; Ertlan, K.D.; Errington, J.; Fabre, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guisepi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karmata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardinois, S.; Laber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolk, S.; Prescott, A.M.; Prescecian, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.; Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Seror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstara, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Vandenbol, R.; Wedler, E.; Wedler, H.; Weltzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

#Journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
#cross-references MUID:98044033
#accession B69767
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-127 #label KUN
#cross-references GB:299105; GB:AL009126; NID:g2632457; PID:e1182223;
#experimental_source strain 168

GENETICS
#gene yzcC
SUMMARY
#length 127 #molecular-weight 13950 #checksum 9937

Query Match 64.2%; Score 52; DB 2; Length 127;
Best Local Similarity 45.5%; Pred. No. 6.76e+00;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 107 FTKKQTVHDM 117
: ||| ||:::
OY 2 YNKKRAIVQEL 12

RESULT 11
ENTRY 549746 #type complete
TITLE probable membrane protein YM033w - yeast (*Saccharomyces cerevisiae*)
ORGANISM #formal_name *Saccharomyces cerevisiae*
DATE 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 21-Nov-1997

ACCESSIONS
#accession S49746
#residues 549746
#cross-references EMBL:246559; NID:g575680; PID:g575686; MIPS:YML033w

GENETICS
#map_position 13L
KEYWORDS transmembrane protein
FEATURE
19-35 #domain transmembrane #status predicted #label TM

SUMMARY
#length 146 #molecular-weight 17729 #checksum 5607

Query Match 64.2%; Score 52; DB 2; Length 146;
Best Local Similarity 54.5%; Pred. No. 6.76e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 40 YNKKRAIVQEL 50
: ||| ||:::
OY 2 YNKKRAIVQEL 12

RESULT 12
ENTRY 518786 #type fragment
TITLE exotoxin type A precursor (allele 2) - *Streptococcus pyogenes* phage (strain MGAS250 isolate California and others)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name *Streptococcus pyogenes* phage
#variety strain MGAS250 isolate California; strain MGAS251 isolate California; strain MGAS256 isolate California; strain MGAS285 isolate Colorado; strain MGAS480 isolate Yugoslavia; strain MGAS492 isolate United Kingdom; strain MGAS496 isolate Germany
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998

ACCESSIONS
#accession 518786; 518787; 518788; 518790; 518792; 518795; 518799
#cross-references MUID:92044323
#accession 518786
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEU
#cross-references EMBL:X61561; NID:g47297; PID:g47298
#experimental_source strain MGAS250 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL data Library, September 1991

ACCESSIONS
#accession 518787
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEA
#cross-references EMBL:X61562; NID:g47299; PID:g47300
#experimental_source strain MGAS251 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL data Library, September 1991

ACCESSIONS
#accession 518788
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEZ
#cross-references EMBL:X61563; NID:g47301; PID:g47302
#experimental_source strain MGAS256 isolate California unassigned phage
#note the nucleotide sequence was submitted to the EMBL data Library, September 1991

ACCESSIONS
#accession 518790
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEY
#cross-references EMBL:X61564; NID:g47305; PID:g47306
#experimental_source strain MGAS285 isolate Colorado unassigned phage
#note the nucleotide sequence was submitted to the EMBL data Library, September 1991

ACCESSIONS
#accession 518792
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 #label NEO
#cross-references EMBL:X61565; NID:g47311; PID:g47312
#experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL data Library, September 1991

#accession S18795
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 ##label NEH
#cross-references EMBL:X61566; NID:q47317; PID:q47318
#experimental_source strain MGAS492 isolate United Kingdom unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18799
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 ##label NES
#cross-references EMBL:X61567; NID:q47325; PID:q47326
#experimental_source strain MGAS496 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22 #domain signal sequence (fragment) #status predicted
#product exotoxin type A (fragment) #status predicted
#label MAT
#label MAT
23-236 #length 236 #checksum 1685

SUMMARY
Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6.76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKMTA0ELD 168
|||:|||||
QY 3 NKKATV0ELD 13

RESULT 13
ENTRY S18783
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isolate Nebraska and others) (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal name Streptococcus pyogenes phage
#variety strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS491 isolate United Kingdom; strain MGAS624 isolate Germany; strain MGAS495 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 02-Jul-1998
S18783; S18793; S18794; S18801; S18798
S18782
#cross-references EMBL:X61568; NID:q47289; PID:q47290
#experimental_source strain MGAS158 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18793
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 ##label NEL
#cross-references EMBL:X61569; NID:q47313; PID:q47314
#experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18794
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 ##label NEZ
#cross-references EMBL:X61570; NID:q47315; PID:q47316
#experimental_source strain MGAS491 isolate United Kingdom unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18801
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-236 ##label NEY
#cross-references EMBL:X61572; NID:q47333; PID:q47334
#experimental_source strain MGAS624 isolate Germany unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

GENETICS
#gene speA3
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22 #domain signal sequence (fragment) #status predicted
#product exotoxin type A (fragment) #status predicted
#label SIG
#label SIG
23-236 #length 236 #checksum 612

SUMMARY
Query Match 64.2%; Score 52; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 6.76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 158 NKKMTA0ELD 168
|||:|||||
QY 3 NKKATV0ELD 13

RESULT 14
ENTRY S29659
TITLE exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
ALTERNATE_NAMES erythrogenic toxin; scarlet fever toxin
ORGANISM #formal name Streptococcus pyogenes phage T12
DATE 22-Nov-1993 #sequence_revision 02-Aug-1996 #text_change 25-Mar-1998
S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800

REFERENCE
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references EMBL:M9350; NID:q1877426; PID:q1877430
#accession S29659
#molecule_type DNA
#residues 1-251 ##label WEE
#cross-references GB:040453; EMBL:M9350; NID:q1877426; PID:q1877430
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references M92044323

```
#accession S18782
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-244 ##label NEI
##cross-references EMBL:X61560; NID:q47287; PID:q47288
##experimental_source Streptococcus pyogenes strain MGAS156 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18784
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-244 ##label NEA
##cross-references EMBL:X61556; NID:q47291; PID:q47292
##experimental_source Streptococcus pyogenes strain MGAS165 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18785
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-244 ##label NEZ
##cross-references EMBL:X61559; NID:q47293; PID:q47294
##experimental_source Streptococcus pyogenes strain MGAS167 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18791
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-244 ##label NEY
##cross-references EMBL:X61555; NID:q47309; PID:q47310
##experimental_source Streptococcus pyogenes strain MGAS327 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18796
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-244 ##label NEO
##cross-references EMBL:X61557; NID:q47319; PID:q47320
##experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18797
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-244 ##label NEH
##cross-references EMBL:X61558; NID:q47321; PID:q47322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

#accession S18800
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 9-228 ##label NES
##cross-references EMBL:X61554; NID:q47327; PID:q47328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
Zealand unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

GENETICS
#gene speA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURES
1-30
31-251
SUMMARY #domain signal sequence #status predicted #label SIG\
#product exotoxin type A #status predicted #label MAT
#length 251 #molecular-weight 29246 #checksum 1475

Query Match 64.2%; Score 52; DB 2; Length 251;
```

```
Best Local Similarity 72.7%; Pred. No. 6,76e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 166 NKKMTVAOEID 176
|||:| |||
Qy 3 NKKMTVAOEID 13

RESULT 15
ENTRY S58590 #type complete
TITLE ribosomal protein S3 - maize chloroplast
ORGANISM #formal_name Chloroplast Zea mays #common_name maize
DATE 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change
17-Mar-1999
ACCESSIONS S58590
REFERENCE S58531
#authors Maier, R.M.; Neckerhmann, K.; Igloi, G.L.; Koessel, H.
#journal J. Mol. Biol. (1995) 251:614-628
#title Complete sequence of the maize chloroplast genome: gene
content, hotspots of divergence and fine tuning of genetic
information by transcript editing.
#cross-references MUID:95395841
#accession S58590
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-224 ##label MAI
##cross-references EMBL:X86563; NID:9902200; PID:9902260
#note the nucleotide sequence was submitted to the EMBL Data
Library, April 1995

GENETICS
#gene rps3
#genome chloroplast
CLASSIFICATION #superfamily Escherichia coli ribosomal protein S3
KEYWORDS chloroplast; protein biosynthesis; ribosome
SUMMARY #length 224 #molecular-weight 25916 #checksum 3426

Query Match 63.0%; Score 51; DB 2; Length 224;
Best Local Similarity 50.0%; Pred. No. 1.05e+01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKKGAIEEID 102
|||:| |||
Qy 4 KKKATVQELD 13
```

Search completed: Tue Aug 31 19:32:04 1999
Job time : 17 secs.

MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm
(7M)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 31 19:30:15 1999; Maspar time 2.62 Seconds
Tabular output not generated. 151,002 Million cell updates/sec

Title: >US-09-150-947-11
Description: (1-14) from US09150947.ppe
Perfect Score: 81
Sequence: 1 XYNKKATVQELDX 14

Scoring table:
PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 24.929; Variance 27.412; scale 0.909

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description | Pred. No. |
|------------|-------|-------|--------|----|-----------------------------------|-----------|
| 1 | 59 | 72.8 | 257 | 1 | ETXA_STAAU ENTEROTOXIN TYPE A PRE | 4.80e-02 |
| 2 | 58 | 71.6 | 266 | 1 | ETXB_STAAU ENTEROTOXIN TYPE B PRE | 8.32e-02 |
| 3 | 57 | 70.4 | 258 | 1 | ETXD_STAAU ENTEROTOXIN TYPE D PRE | 1.43e-01 |
| 4 | 53 | 65.4 | 257 | 1 | ETXE_STAAU ENTEROTOXIN TYPE E PRE | 1.18e+00 |
| 5 | 53 | 65.4 | 670 | 1 | SR72_CANPA SIGNAL RECOGNITION PAR | 1.18e+00 |
| 6 | 52 | 64.2 | 146 | 1 | YMD3_YEAST HYPOHETICAL 17.7 KD P | 1.97e+00 |
| 7 | 52 | 64.2 | 251 | 1 | SPDA_STRAY EXOTOXIN TYPE A PRECUR | 1.97e+00 |
| 8 | 51 | 63.0 | 187 | 1 | YCF4_MAIZE HYPOHETICAL 21.2 KD P | 3.26e+00 |
| 9 | 51 | 63.0 | 224 | 1 | R32_ORYSA CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 10 | 51 | 63.0 | 239 | 1 | R32_ORYSA CHLOROPLAST 30S RIBOSO | 3.26e+00 |
| 11 | 51 | 63.0 | 412 | 1 | PT56_YEAST RIBOSE METHYLTRANSFERA | 3.26e+00 |
| 12 | 51 | 63.0 | 566 | 1 | LIGA_MOUSE LIGATIN (FRAGMENT) | 3.26e+00 |
| 13 | 51 | 63.0 | 3418 | 1 | BRC2_HUMAN BREAST CANCER TYPE 2 S | 3.26e+00 |
| 14 | 50 | 61.7 | 268 | 1 | NO20_MEDTR EARLY NODULIN 20 PRECU | 5.36e+00 |
| 15 | 50 | 61.7 | 274 | 1 | HEU_HAELN LIPOPROTEIN E PRECURSO | 5.36e+00 |
| 16 | 50 | 61.7 | 386 | 1 | YAWH_SCHPO HYPOHETICAL 44.5 KD P | 5.36e+00 |
| 17 | 50 | 61.7 | 1072 | 1 | HSEB_RAT HEAT-STABLE ENTEROTOXI | 5.36e+00 |
| 18 | 50 | 61.7 | 1223 | 1 | KPBL_HUMAN PHOSPHORILASE B KINASE | 5.36e+00 |
| 19 | 50 | 61.7 | 3685 | 1 | DMD_HUMAN DYSTROPHIN | 5.36e+00 |
| 20 | 49 | 60.5 | 290 | 1 | YABG_BACSU HYPOHETICAL 33.3 KD P | 8.72e+00 |
| 21 | 49 | 60.5 | 455 | 1 | MAD_DROME MOTHERS AGAINST DPP PR | 8.72e+00 |
| 22 | 49 | 60.5 | 559 | 1 | KIF2_XENLA KINESIN-LIKE PROTEIN K | 8.72e+00 |
| 23 | 49 | 60.5 | 670 | 1 | SR72_HUMAN SIGNAL RECOGNITION PAR | 8.72e+00 |

| | | | | | | |
|----|----|------|------|---|-----------------------------------|----------|
| 24 | 49 | 60.5 | 859 | 1 | DPP6_RAT DIPEPTIDYL PEPTIDASE I | 8.72e+00 |
| 25 | 49 | 60.5 | 863 | 1 | DPP6_BOVIN DIPEPTIDYL PEPTIDASE I | 8.72e+00 |
| 26 | 49 | 60.5 | 865 | 1 | DPP6_HUMAN DIPEPTIDYL PEPTIDASE I | 8.72e+00 |
| 27 | 49 | 60.5 | 1164 | 1 | BAG_STRAG IGA FC RECEPTOR PRECUR | 8.72e+00 |
| 28 | 49 | 60.5 | 3678 | 1 | DMD_MOUSE DYSTROPHIN | 8.72e+00 |
| 29 | 48 | 59.3 | 1330 | 1 | VG67_BPPHS EARLY PROTEIN GP16.7 | 1.41e+01 |
| 30 | 48 | 59.3 | 261 | 1 | HCD2_MOUSE ENTEROTOXIN TYPE C-1 P | 1.41e+01 |
| 31 | 48 | 59.3 | 266 | 1 | ETC1_STAAU ENTEROTOXIN TYPE C-1 P | 1.41e+01 |
| 32 | 48 | 59.3 | 266 | 1 | ETC2_STAAU ENTEROTOXIN TYPE C-2 P | 1.41e+01 |
| 33 | 48 | 59.3 | 266 | 1 | ETC3_STAAU ENTEROTOXIN TYPE C-3 P | 1.41e+01 |
| 34 | 48 | 59.3 | 269 | 1 | YD54_SCHPO HYPOHETICAL 31.2 KD P | 1.41e+01 |
| 35 | 48 | 59.3 | 293 | 1 | R15_CAEL PROBABLE 60S RIBOSOMAL | 1.41e+01 |
| 36 | 48 | 59.3 | 302 | 1 | CAN1_RABIT CALPAIN 1, LARGE [CATA | 1.41e+01 |
| 37 | 48 | 59.3 | 330 | 1 | HBPB_ARATH TRANSCRIPTION FACTOR H | 1.41e+01 |
| 38 | 48 | 59.3 | 332 | 1 | HBPB_WHEAT TRANSCRIPTION FACTOR H | 1.41e+01 |
| 39 | 48 | 59.3 | 346 | 1 | VG1M_HSVJ GLYCOPROTEIN M | 1.41e+01 |
| 40 | 48 | 59.3 | 359 | 1 | TCGA_TOBAC TGACG-SEQUENCE SPECIFI | 1.41e+01 |
| 41 | 48 | 59.3 | 560 | 1 | GGPI_ARATH GLUCOSE-6-PHOSPHATE IS | 1.41e+01 |
| 42 | 48 | 59.3 | 634 | 1 | DNK2_SYNP7 DNK PROTEIN 2 (HEAT S | 1.41e+01 |
| 43 | 47 | 58.0 | 383 | 1 | YAGN_RHISN HYPOHETICAL 45.0 KD P | 2.26e+01 |
| 44 | 47 | 58.0 | 433 | 1 | PR12_CAEL PROBABLE DNA PRIMASE L | 2.26e+01 |
| 45 | 47 | 58.0 | 556 | 1 | SYR_BACSU ARGINYL-TRNA SYNTHETAS | 2.26e+01 |

ALIGNMENTS

| RESULT | ID | ETXA_STAAU | STANDARD | PRT | 257 AA. |
|--------|--|------------|----------|-----|---------|
| AC | P13163 | | | | |
| DT | 01-JAN-1990 (REL. 13, CREATED) | | | | |
| DT | 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) | | | | |
| DT | 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) | | | | |
| DE | ENTEROTOXIN TYPE A PRECURSOR (SEA). | | | | |
| GN | ENTX. | | | | |
| OS | STAPHYLOCOCCUS AUREUS. | | | | |
| OC | BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; | | | | |
| OC | STAPHYLOCOCCUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-FRI137; | | | | |
| RX | MEDLINE: 88086892. | | | | |
| RA | BETLEY M.J., MEKALANOS J.J.; | | | | |
| RT | "Nucleotide sequence of the type A staphylococcal enterotoxin gene"; | | | | |
| RL | J. BACTERIOL. 170:34-41(1988). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 25-257. | | | | |
| RX | MEDLINE: 87222293. | | | | |
| RA | HIANG I.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J.; | | | | |
| RT | "Complete amino acid sequence of staphylococcal enterotoxin A."; | | | | |
| RL | J. BIOL. CHEM. 262:7006-7013(1987). | | | | |
| RN | [3] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). | | | | |
| RX | MEDLINE: 95354648. | | | | |
| RA | SCHAD E.M., ZAITSEVA I., ZAITSEV V.N., DOHLSTEN M., KALLAND T.; | | | | |
| RT | SCHLIEVERT P.M., OHLENDORF D.H., SVENSSON L.A.; | | | | |
| RL | "Crystal structure of the superantigen staphylococcal enterotoxin | | | | |
| RT | type A."; | | | | |
| EMBO | J. 14:3292-3301(1995). | | | | |
| RN | [4] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). | | | | |
| RX | MEDLINE: 97113025. | | | | |
| RA | SUNDSTROM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEN M., | | | | |
| RT | ABRAHAMSEN L.; | | | | |
| RL | "The Co-crystal structure of staphylococcal enterotoxin type A with | | | | |
| RT | zn2+ at 2.7-A resolution. Implications for major histocompatibility | | | | |
| RT | complex class II binding."; | | | | |
| RL | J. BIOL. CHEM. 271:32212-32216(1996). | | | | |
| RN | [5] | | | | |
| RP | 3D-STRUCTURE MODELLING. | | | | |
| RX | MEDLINE: 96022987. | | | | |
| RA | SNAMINATIAN S., FUREY W.F. JR., PLETCHER J., SAX M.; | | | | |
| RT | "Residues defining V beta specificity in staphylococcal | | | | |
| RT | enterotoxins."; | | | | |

RL NAT. STRUCT. BIOL. 2:680-686(1995).
 RN [6]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE: 97334373.
 RA "SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity.";
 RL J. MOL. BIOL. 269:270-280(1997).
 CC -1- SUBUNIT: MONOMER.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M18970; G153121; -
 DR PIR: A28664; A28664.
 DR PIR: A29566; A29566.
 DR PDB: 1SEF; 11-JUL-96.
 DR PDB: 1SEF; 15-OCT-95.
 DR PDB: 1SEF; 19-NOV-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 1 25 257 ENTEROTOXIN A.
 FT DISULFID 120 130
 FT METAL 25 25 ZINC.
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 2).
 SQ SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;
 Query Match 72.8%; Score 59; DB 1; Length 257;
 Best Local Similarity 81.8%; Pred. No. 4,80e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 170 NKKKATVOELD 180
 Oy 3 NKKKATVOELD 13
 RESULT 2
 ID ETKAV STAAU STANDARD; PRT: 266 AA.
 AC P01552;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
 GN ENTB.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86168029.
 RA JONES C.L., KHAN S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
 RT aureus.";
 RL J. BACTERIOL. 166:29-33(1986).
 RL [2]
 RP SEQUENCE OF 40-91 FROM N.A.

RX MEDLINE: 85298255.
 RA PANELLI D.M., JONES C.L., JOHNS M.B., MUSEY G.J., KHAN S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in
 RT Escherichia coli and Staphylococcus aureus.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:5850-5854(1985).
 RN [3]
 RP SEQUENCE OF 28-266 (S-6).
 RX MEDLINE: 71007902.
 RA HUANG I.-Y., BERGDOLL M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The
 RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
 RT B, and the complete amino acid sequence.";
 RL J. BIOL. CHEM. 245:3518-3525(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE: 93063291.
 RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
 RN NATURE 359:801-806(1992).
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RX MEDLINE: 94203282.
 RA JARDEZYK T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G.,
 RA CHI Y.I., STAUPEACHER C., STROMINGER J.L., WILEY D.C.;
 RT "Three-dimensional structure of a human class II histocompatibility
 RT molecule complexed with superantigen.";
 RL NATURE 368:711-718(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE: 98181012.
 RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal
 RT enterotoxin B at 1.5-A resolution: implications for superantigen
 RT recognition by MHC class II molecules and T-cell receptors.";
 RL J. MOL. BIOL. 277:61-79(1998).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M1118; G153000; -
 DR PIR: A01815; ENSAB6.
 DR PIR: S27360; S27360.
 DR PDB: 1SEB; 20-JUN-96.
 DR PDB: 2SEB; 28-JAN-98.
 DR PDB: 3SEB; 27-MAY-98.
 DR PDB: 1SE3; 16-JUN-97.
 DR PDB: 1SE4; 15-OCT-97.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PFAM: PF01123; Staph_strep_toxin; 1.
 KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
 FT SIGNAL 1 27
 FT CHAIN 1 28 266 ENTEROTOXIN B.
 FT DISULFID 120 140
 FT METAL 56 58
 FT CONFLICT 69 77 DDN -> NND (IN REF. 3).
 FT CONFLICT 118 118 DDLYFDLI -> NEFFDLYL (IN REF. 3).
 FT CONFLICT 128 130 MISSING (IN REF. 3).
 FT CONFLICT 133 135 DIN -> NID (IN REF. 3).
 FT CONFLICT 149 150 QTD -> ENT (IN REF. 3).
 FT CONFLICT 156 156 NG -> GN (IN REF. 3).
 FT CONFLICT 185 186 Y -> YY (IN REF. 3).
 FT CONFLICT 233 233 OE -> EO (IN REF. 3).
 FT CONFLICT 246 247 D -> N (IN REF. 3).
 DN -> ND (IN REF. 3).

SC SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
Query Match 71.6%; Score 58; DB 1; Length 266;
Best Local Similarity 81.8%; Pred. No. 8.32e-02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 178 NKKKATVOELD 188
1111111111
QY 3 NKKKATVOELD 13

RESULT 3
ID ETXD-STAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE D PRECURSOR (SED).
GN ENTD.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89359112.
RA BAYLES K.W., IANDOLO J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";
RT J. BACTERIOL. 171:4799-4806(1989).
RL [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE; 97157473.
RA SUNDBLOM M., ABRAHAMSEN L., ANTONSSON P., MEHINDATE K., MOURAD W., DOHLSTEN M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization.";
RT EMBO J. 15:6832-6840(1996).
CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M28521; G758691; .
DR PIR; A33953; A33953.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph-Strep_toxin; 1.
KW HSSP; P13163; ISXT.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; ZINC.
FT SIGNAL 1 25
FT CHAIN 1 258 ENTEROTOXIN D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 2D1A120 CRC32;

Query Match 70.4%; Score 57; DB 1; Length 258;
Best Local Similarity 72.7%; Pred. No. 1.43e-01;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
DB 171 DKKNTVOELD 181
1111111111

QY 3 NKKKATVOELD 13

RESULT 4
ID ETXE-STAU STANDARD; PRT; 257 AA.
AC P12993;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN ENTE.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC STAPHYLOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC STRAIN-MJ265;
RX MEDLINE; 88257005.
RA COUCH J.L., SOLLIS M.T., BENTLEY M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.";
RT J. BACTERIOL. 170:2954-2960(1988).
RL [2]
RP 3D-STRUCTURE MODELLING.
RX MEDLINE; 96022987.
RA SWAMINATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RT "Residues defining v beta specificity in staphylococcal enterotoxins.";
RT NAT. STRUCT. BIOL. 2:680-686(1995).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M21319; G153002; .
DR PIR; A28179; A28179.
DR PDB; 1SEE; 15-OCT-95.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph-Strep_toxin; 1.
KW ENTEROTOXIN; TOXIN; SIGNAL; SUPERANTIGEN; 3D-STRUCTURE.
FT SIGNAL 1 27
FT CHAIN 1 257 ENTEROTOXIN E.
SQ SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;

Query Match 65.4%; Score 53; DB 1; Length 257;
Best Local Similarity 72.7%; Pred. No. 1.18e+00;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 170 SKKEVTVOELD 180
1111111111
QY 3 NKKKATVOELD 13

RESULT 5
ID SR72-CANFA STANDARD; PRT; 670 AA.
AC P33731;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).
GN SRP72.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.

```

RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE: 93273803.
RA LIETCKE H., PREHN S., ASHFORD A.J., REMUS M., FRANK R.,
RA DOBERSTEIN B.:
RT "Assembly of the 68- and 72-kD proteins of signal recognition
RT particle with 7S RNA."
RL J. CELL BIOL. 121:977-985(1993).
CC -1- FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE
CC IN TARGETING SECRETORY PROTEINS TO THE ROUGH ENDOPLASMIC
CC RETICULUM MEMBRANE. SRP72 BINDS THE 7S RNA ONLY IN PRESENCE OF
CC SRP68. THIS RIBONUCLEOPROTEIN COMPLEX MIGHT INTERACT DIRECTLY WITH
CC THE DOCKING PROTEIN IN THE ER MEMBRANE AND POSSIBLY PARTICIPATE
CC IN THE ELONGATION ARREST FUNCTION.
CC -1- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE
CC OF 300 NUCLEOTIDES AND SIX PROTEIN SUBUNITS: SRP72, SRP68, SRP54,
CC SRP19, SRP14 AND SRP9.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- DOMAIN: THE C-TERMINAL IS ESSENTIAL FOR THE INTERACTION WITH THE
CC SRP68/7S RNA COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE SRP72 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X67813; G297768; -
DR PIR: S32167; S32167.
DR PIR: A40692; A40692.
KW SIGNAL RECOGNITION PARTICLE; RIBONUCLEOPROTEIN.
FT INT_MET 0 0 PROBABLE.
FT MOD_RES 1 1 BLOCKED.
FT DOMAIN 551 560 POLY-LYS.
FT DOMAIN 661 664 POLY-LYS.
SQ SEQUENCE 670 AA; 74362 MW; 9CB38962 CRC32;

Query Match 65.4%; Score 53; DB 1; Length 670.
Best Local Similarity 33.3%; Pred. No. 1.18e+00;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 459 YGRKKEAIDLE 470
| : | | : : | :
Qy 2 YNKKATVQELD 13

RESULT 6
ID YMD3_YEAST STANDARD; PRT; 146 AA.
AC 003712;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOHETICAL 17.7 KD PROTEIN IN AMD1-RAD52 INTERGENIC REGION.
GN YMD033W.
OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCAROMYCETALES;
OC SACCAROMYCETACEAE; SACCAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA BADCOCK K., CHURCHER C., BARRELL B.G., RAUANDREAM M.A., WALSH S.V.;
RL SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST YDR4458C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

```

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z46659; G575686; -
KW HYPOHETICAL PROTEIN.
SQ SEQUENCE 146 AA; 17729 MW; 9A378D91 CRC32;

Query Match 64.2%; Score 52; DB 1; Length 146;
Best Local Similarity 54.5%; Pred. No. 1.97e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 40 YRKKARIEEL 50
| : | | : : | |
Qy 2 YNKKATVQELD 12

RESULT 7
ID SPEA_STRPY STANDARD; PRT; 251 AA.
AC P08095;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE (SPE A).
GN SPEA.
OS STREPTOCOCCUS PYOGENES.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86166804.
RA WEEKS C.R., FERRETTI J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from streptococcus pyogenes bacteriophage
RT T12."
RL INFECT. IMMUN. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86284313.
RA JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL MOL. GEN. GENET. 203:354-356(1986).
CC -1- DISEASE: THE STREPTOCOCCAL PYOGENIC TOXINS A, B, AND C ARE
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC FEVER.
CC -1- THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYOGENIC EXOTOXINS ARE ALL RELATED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U40453; G1877430; -
DR EMBL: X03929; G47442; -
DR PIR: A26152; A26152.
DR PIR: S29659; S29659.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
DR HSSP: P01552; 1SEB.
KW TOXIN; SIGMAL.
FT SIGNAL 1 30
FT CHAIN 31 251
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
EXOTOXIN TYPE A.
K -> E (IN REF. 2).
VT -> MK (IN REF. 2).
SQEVFAQDDP -> LPKGICSRPK (IN REF. 2).

```



```

FT CONFLICT 40 40 H -> Q (IN REF. 2)
FT CONFLICT 43 43 S -> N (IN REF. 2)
FT CONFLICT 47 59 NUCNTFLXEDGP -> TKIYIFMRVTL (IN
FT CONFLICT 129 129 REF. 2)
FT CONFLICT 129 129 I -> L (IN REF. 2)
FT CONFLICT 165 178 TNKKVTAOELDYK -> QIKNGCSRISYT (IN
FT REF. 2)
SQ SEQUENCE 251 AA; 29246 MM; 535FE465 CRC32;

Query Match
Best Local Similarity 72.7%; Score 52; DB 1; Length 251;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 166 NKKVTAOELD 176
|||: ||||
Oy 3 NKKKATVOELD 13

RESULT 8
ID YCF4_CYAPA STANDARD: PRT: 187 AA.
AC P48192:
DT 01-FEB-1986 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 21.2 KD PROTEIN YCF4.
GN YCF4.
OS CYANOPHORA PARADOXA.
OC CYANELLE.
OC EURAROTIA; GLAUCOCYSTOPHYCEAE; CYANOPHORACEAE; CYANOPHORA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LB555 / PRINGSHEIM;
RA STIREWALT V.L., MICHALOWSKI C.B., LUFFELHARDT W., BOHNERT H.J.,
RA BRYANT D.A.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- SIMILARITY: BELONGS TO THE YCF4 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U0821; GI016091; -
CC DR MENDEL; 7950; CYAPA:ycf4.1.
CC KW CYANELLE; HYPOTHETICAL PROTEIN.
CC SQ SEQUENCE 187 AA; 21207 MM; B5D7E756 CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 187;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 97 YNKKKGTV 104
||||: |||
Oy 2 YNKKKATV 9

RESULT 9
ID R33_MAIZE STANDARD: PRT: 224 AA.
AC P06586:
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ZEA MAYS (MAIZE).
OC CHLOROPLAST.
OC EURAROTIA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 87231045.
RA MCLAUGHLIN W.E., LARRINDA I.M.;
RT "The sequence of the maize plastid encoded rps3 locus.";
RL NUCLEIC ACIDS RES. 15:4689-4689(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95395841.
RA MAIER R.M., NECKERMANN K., IGLOI G.L., KOESSEL H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. MOL. BIOL. 251:614-628(1995).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y00340; G12469; -
CC DR EMBL: M31336; G552741; -
CC DR EMBL: X86563; G902260; -
CC DR MAIZEDB: 66303; -
CC DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
CC DR PFAM: PF00189; S3_C; 1.
CC DR PFAM: PF00417; S3_N; 1.
CC DR MENDEL: 13473; ZEMA:rps3.1.
CC KW RIBOSOMAL PROTEIN; CHLOROPLAST.
CC SQ SEQUENCE 224 AA; 25916 MM; 3ED95CF6 CRC32;

Query Match
Best Local Similarity 63.0%; Score 51; DB 1; Length 224;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 93 KKKGAIEELE 102
||||: |||
Oy 4 KKKATVOELD 13

RESULT 10
ID R33_ORYZA STANDARD: PRT: 239 AA.
AC P12146;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S3.
GN RPS3.
OS ORYZA SATIVA (RICE).
OC CHLOROPLAST.
OC EURAROTIA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ORYZA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA SUGIURA M.;
RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [2]
RP COMPLETE GENOME.
RX MEDLINE: 89364698.
RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,
RA MORI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-O.,
RA KANNO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct trna genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL MOL. GEN. GENET. 217:185-194(1989).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X15901; G12025; -
 CC PIR: J00265; R3R23;
 CC PROSITE: PS00548; RIBOSOMAL_S3; 1.
 CC PFAM: PF00189; S3_N; 1.
 CC MENDEL: 13258; ORYsa: rps3.1.
 CC RIBOSOMAL PROTEIN: CHLOROPLAST.
 CC SEQUENCE 239 AA; 27518 MW; 38E916EE CRC32;
 SO
 Query Match 63.08; Score 51; DB 1; Length 239;
 Best Local Similarity 50.08; Pred. No. 3.26e+00;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Db 108 KKKKATEELE 117
 QY 4 KKKATVOELD 13
 RESULT 11
 ID PT56_YEAST STANDARD: PRT: 412 AA.
 AC P25270;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE RIBOSE METHYLTRANSFERASE PET56 (EC 2.1.1.-) (MITOCHONDRIAL LARGE
 DE RIBOSOMAL RNA RIBOSE METHYLASE) (21S RNA [GM2251] 2'-O-
 DE METHYLTRANSFERASE).
 GN PET56 OR YOR201C.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94090319.
 RA SIRM-CONNOLLY K.; MASON T.L.;
 RT "Functional requirement of a site-specific ribose methylation in
 RT ribosomal RNA.";
 RL SCIENCE 262:1886-1889(1993).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA HUGHES B.; POHL T.M.;
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN (3)
 RP SEQUENCE OF 1-95 FROM N.A.
 RX MEDLINE: 86093663.
 RA STRUHL K.;
 RT Nucleotide sequence and transcriptional mapping of the yeast
 RT pet56-his3-dead gene region.";
 RL NUCLEIC ACIDS RES. 13:8587-8601(1985).
 CC -1- FUNCTION: ENCODES AN ESSENTIAL RIBOSE METHYLTRANSFERASE THAT
 CC SPECIFICALLY MODIFIES TO 2'-O-METHYLGUANOSINE A UNIVERSALLY
 CC CONSERVED NUCLEOTIDE, G-2270, IN THE PEPTIDYL TRANSFERASE CENTER
 CC OF THE MITOCHONDRIAL LARGE RIBOSOMAL RNA (21S). THIS MODIFICATION
 CC SEEMS TO BE IMPORTANT FOR THE NORMAL ACCUMULATION OF THIS LATTER
 CC 21S SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: L19947; G431760; -
 DR EMBL: X03245; G3779; -
 DR EMBL: 275107; E252073; -
 DR PIR: S07682; S07682.
 DR SGD: L0001392; PET56.
 DR PFAM: PF00588; SpoU_methylase; 1.
 CC MITOCHONDRION; TRANSFERASE; METHYLTRANSFERASE.
 KW
 SO SEQUENCE 412 AA; 46387 MW; B3436655 CRC32;
 Query Match 63.08; Score 51; DB 1; Length 412;
 Best Local Similarity 50.08; Pred. No. 3.26e+00;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Db 79 YGKKRAVERL 89
 QY 2 YNKKATVOELD 12
 RESULT 12
 ID LIGA_MOUSE STANDARD: PRT: 566 AA.
 AC Q61211;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE LIGATIN (FRAGMENT).
 GN LGTN.
 OS MUS MUSCULUS (HOUSE)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIOGNATHI; MURIDAE; MURINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97224508.
 RA MALNAR-DRAGOJEVIC D.; TRACHUTULEC Z.; VINCEK V.;
 RT Assignment of the mouse ligatin gene (Lgtn) to chromosome 1F by in
 RT situ hybridization.";
 RL GENOMICS 40:192-193(1997).
 CC -1- FUNCTION: TRAFFICKING RECEPTOR FOR PHOSPHOLIPOPROTEINS. LOCALIZES
 CC PHOSPHOLIPOPROTEINS WITHIN ENDOSOMES AND AT THE CELL PERIPHERY
 CC WHERE THEY PARTICIPATE IN SPECIFIC METABOLIC PROCESSES AS WELL AS
 CC INTERCELLULAR ADHESION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U58337; G1377880; -
 DR MGD; MGI:109342; LGTN.
 KW MEMBRANE.
 FT NON_TER 1
 FT 566 566
 SO SEQUENCE 566 AA; 62239 MW; AAB58F4B CRC32;
 Query Match 63.08; Score 51; DB 1; Length 566;
 Best Local Similarity 50.08; Pred. No. 3.26e+00;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Db 503 YNKKATVVRNLE 514
 QY 2 YNKKATVOELD 13
 RESULT 13
 ID BRC2_HUMAN STANDARD: PRT: 3418 AA.
 AC P51567;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN.

GN BRCA2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96172838.
 PA TAVTIGIAN S.V., ROMMENS J.M., COUCH F.J., NEUHAUSEN S., BELL R.,
 BA BERRY S., BOGDEN R., CHEN O., DAVIS T., FRYE C., HATIER T.,
 JAMULAPATI S., JANECKI T., JIANG P., KEHRER R., SCHROEDER M.,
 SNYDER S., STRINGFELLOW M., STROUP C., SWEDLUND B., TENG D.,
 RA THOMAS A., TRAN T., WEAVER-FELDAUS J., WONG A., LEBLANC J.-F.,
 BELANGER C., TRANCHANT M., SAMSON C., DUMONT M.,
 KACHIKUR-MORISON J., MCSWENEY D., PENG Y., SHIZUYA H.,
 SLEPAC T., SIMON M.I., LABRIE F., SHATTUCK-EIDENS D., SKOLNICK M.,
 RA GOLDGAR D., WEBER B.L., SIMARD J., KAMB A.,
 RT "The complete BRCA2 gene and mutations in chromosome 13q-linked
 kindreds.";
 RL NAT. GENET. 12:333-337(1996).
 RN [2]
 RP VARIANTS ASN-372: ASP-991: SER-1147: MET-1915 AND CYS-2034.
 RX MEDLINE: 96241588.
 RA COUCH F.J., FARID L.M., DESHANO M.L., TAVTIGIAN S.V., CALZONE K.,
 RA CAMPEAU L., PENG Y., BOGDEN B., CHEN O., NEUHAUSEN S.,
 RA SHATTUCK-EIDENS D., GODWIN A.K., DALY M., RADFORD D.M., SEDLACEK S.,
 RA ROMMENS J., SIMARD J., GARBER J., MERAJVER S., WEBER B.L.,
 RT "BRCA2 germline mutations in male breast cancer cases and breast
 cancer families.";
 RL NAT. GENET. 13:123-125(1996).
 RN [3]
 RP VARIANT GLU-3095.
 RX MEDLINE: 96225456.
 RA LANGASTER J.M., WOOSTER R., MANGION J., PHELAN C.M., COCHRAN C.,
 RA GUMBS C., SEUL S., BARFOOT R., COLLINS N., BIGWELL G., PATEL S.,
 RA HAMOUDI R., LARSSON C., WISEMAN R.W., BERCHUCK A., ILEHART J.D.,
 RA MARKS J.R., ASHWORTH A., STRATTON M.R., FUTRELL P.A.,
 RT "BRCA2 mutations in primary breast and ovarian cancers.";
 RL NAT. GENET. 13:238-240(1996).
 RN [4]
 RP VARIANTS.
 RX MEDLINE: 96225457.
 RA TENG D.H.-F., BOGDEN R., MITCHELL J., BAUMGARD M., BELL R., BERRY S.,
 RA DAVIS T., HA P.C., KEHRER R., JAMULAPATI S., CHEN O., OFFIT K.,
 RA SKOLNICK M.H., TAVTIGIAN S.V., JHANWAR S., SWEDLUND B., WONG A.K.C.,
 RA KAMB A.,
 RT "Low incidence of BRCA2 mutations in breast carcinoma and other
 cancers.";
 RL NAT. GENET. 13:241-244(1996).
 RN [5]
 RP VARIANT ASN-2415.
 RX MEDLINE: 96225458.
 RA MIKI Y., KATAGIRI T., KASUMI F., YOSHIMOTO T., NAKAMURA Y.,
 RT "Mutation analysis in the BRCA2 gene in primary breast cancers.";
 RL NAT. GENET. 13:245-247(1996).
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS OF EXPRESSION IN BREAST AND
 THYMS, WITH SLIGHTLY LOWER LEVELS IN LUNG, OVARY, AND SPLEEN.
 CC -1- DISEASE: BREAST CANCER (BC) IS AN EXTREMELY COMMON MALIGNANCY,
 AFFECTING ONE IN EIGHT WOMEN DURING THEIR LIFETIME. A POSITIVE
 FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OF
 DEVELOPMENT OF THE DISEASE, AND THIS LINK IS STRIKING FOR EARLY-
 ONSET BREAST CANCER. MUTATIONS IN BRCA2 ARE THOUGHT TO BE
 RESPONSIBLE FOR SOME INHERITED BREAST CANCER. IT IS LINKED WITH
 MALE BREAST CANCER.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U043746; G1161384; -

DR MIM: 600185; -
 DR PFAM: PF00634; BRCA2_repeat; 8.
 KM DISEASE MUTATION: POLYMORPHISM: REPEAT.
 FT NP_BIND 262 269
 FT DOMAIN 1009 2082
 FT REPEAT 1009 1033
 FT REPEAT 1219 1243
 FT REPEAT 1428 1452
 FT REPEAT 1524 1548
 FT REPEAT 1671 1695
 FT REPEAT 1844 1868
 FT REPEAT 1978 2002
 FT REPEAT 2058 2082
 FT VARIANT 75 75
 FT VARIANT 289 289
 FT VARIANT 355 355
 FT VARIANT 372 372
 FT VARIANT 630 630
 FT VARIANT 728 728
 FT VARIANT 991 991
 FT VARIANT 1147 1147
 FT VARIANT 1302 1302
 FT VARIANT 1529 1529
 FT VARIANT 1880 1880
 FT VARIANT 1915 1915
 FT VARIANT 2034 2034
 FT VARIANT 2274 2274
 FT VARIANT 2415 2415
 FT VARIANT 2421 2421
 FT VARIANT 3095 3095
 FT VARIANT 3103 3103
 FT VARIANT 3357 3357
 FT VARIANT 3412 3412
 SQ SEQUENCE 3418 AA: 384280 MW: F5785BCB CRC32:
 Query Match 63.0%; Score 51; DB 1; Length 3418;
 Best Local Similarity 50.0%; Pred. No. 3.26e+00;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Db 3159 FNKKKNTVENID 3170
 Oy 2 YNKKKATVQELD 13
 RESULT 14
 ID NO20_MEDTR STANDARD; PRT; 268 AA.
 AC P93329;
 DT 15-DEC-1998 (REL. 37, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE EARLY NODULIN 20 PRECURSOR (N-20).
 GN ENOD20.
 OS MEDICAGO TRUNCATULA (BARREL MEDIC).
 OC EUPHYLLIOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
 CC FABALES; FABACEAE; PAPILIONOIDEAE; MEDICAGO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV, JEMALONG;
 RA GREENE E.A., ERARD M., DEDIED A., BARKER D.G.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X99467; E258656; -
 DR NODULATION; SIGNAL.

RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."

RL INFECT. IMMUN. 64:1161-1165(1996).

DR EMBL: U48794; G1245176; -

DR EMBL: U48792; G1245172; -

DR PFAM: PF01123; Strep-strep toxin; 1.

SO SEQUENCE 260 AA: 29767 MW; C81448C1 CRC32;

Db 173 NKKTATQELD 183

Oy 3 NKKTATQELD 13

RESULT 7
ID 077384; PRELIMINARY; PRT; 3394 AA.

AC 077384; (TREMREL. 08, CREATED)

DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)

DE MAL3P6.11 PROTEIN.

OS PLASMODIUM FALCIPARUM.

OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDIA; PLASMODIUM.

RN SEQUENCE FROM N.A.

RP STRAIN-307;

RA SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: Z98551; E1331922; -

SO SEQUENCE 3394 AA: 402947 MW; 4C3F2778 CRC32;

Db 373 YNKSNTIQQUN 384

Oy 2 YNKSNTIQQUN 13

RESULT 8
ID 091693; PRELIMINARY; PRT; 464 AA.

AC 091693; (TREMREL. 01, CREATED)

DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)

DE MOTHERS AGAINST DPP.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

RN MESOBATRACHIA; PIPOIDEA; PIPIIDAE; XENOPODINAE; XENOPUS.

RP SEQUENCE FROM N.A.

RX MEDLINE: 96312915.

RA THOMSEN G.H.;

RT "Xenopus mothers against decapentaplegic is an embryonic ventralizing

RT agent that acts downstream of the BMP-2/4 receptor."

RL DEVELOPMENT 123:2359-2366(1996).

DR EMBL: U58834; G1381671; -

DR PFAM: PF00968; Dwarfin; 1.

SO SEQUENCE 464 AA: 52346 MW; 4017799F CRC32;

Db Query Match 69.1%; Score 56; DB 13; Length 464;

Best Local Similarity 54.5%; Pred. No. 6.64e-01;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 42 KKKKGATQELE 52

Oy 3 NKKTATQELD 13

RESULT 9
ID P91308; PRELIMINARY; PRT; 760 AA.

AC P91308; (TREMREL. 03, CREATED)

DT 01-MAY-1997 (TREMREL. 03, LAST SEQUENCE UPDATE)

DE COSMID F46F11.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;

RN RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,

RA SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans."

SO NATURE 368:32-38(1994).

Db 569 YDSKNSIQDLE 580

Oy 2 YNKSNTIQQUN 13

RESULT 10
ID 093308; PRELIMINARY; PRT; 1232 AA.

AC 093308; (TREMREL. 08, CREATED)

DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)

DE 14S COHESIN SMC1 SUBUNIT.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

RN MESOBATRACHIA; PIPOIDEA; PIPIIDAE; XENOPODINAE; XENOPUS.

RP SEQUENCE FROM N.A.

RX MEDLINE: 96315077.

RA LOSADA A., HIRANO M., HIRANO T.;

RT "Identification of Xenopus SMC protein complexes required for sister

RT chromatid cohesion."

RL GENES DEV. 12:1986-1997(1998).

DR EMBL: AF051784; G3328231; -

SO SEQUENCE 1232 AA: 142627 MW; FDE5B84 CRC32;

Query Match 69.1%; Score 56; DB 13; Length 1232;
 Best Local Similarity 50.0%; Pred. No. 6.64e-01;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRKADMELE 337
 1:1:1:1:1:1:
 QY 2 YNKKKATVQELD 13

RESULT 11 PRELIMINARY; PRT: 811 AA.
 AC P87145;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 92.5 KD PROTEIN C25H2.03 IN CHROMOSOME II.
 GN SPB25H2.03.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA DURSO G., LYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,
 RA RAJANDREAN M.A., CONNOR R.E.;
 RT SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: TO YEAST INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 DR EMBL: 295397; E316120; -;
 KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT TRANSMEM 362 382 POTENTIAL.
 FT TRANSMEM 602 622 POTENTIAL.
 FT TRANSMEM 630 650 POTENTIAL.
 SQ SEQUENCE 811 AA; 92452 MW; E1E2FB77 CRC32;

Query Match 67.9%; Score 55; DB 3; Length 811;
 Best Local Similarity 58.3%; Pred. No. 1.10e+00;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 14 YDKRKATAYELE 25
 1:1:1:1:1:1:
 QY 2 YNKKKATVQELD 13

RESULT 12 PRELIMINARY; PRT: 490 AA.
 AC 007382;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HISTIDINE KINASE LKINA.
 GN LKINA.
 OS LACTOCOCCUS LACTIS CREMORIS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC LACTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MG1363;
 RX MEDLINE: 97316457.
 RA O'CONNELL-MOTHERWAY M., FITZGERALD G.F., VAN SINDEREN D.;
 RT Cloning and sequence analysis of putative histidine protein kinases
 isolated from Lactococcus lactis MG1363."
 RL APPL. ENVIRON. MICROBIOL. 63:2454-2459(1997).
 DR EMBL: U81166; G2182835; -;
 PRAM: PF00512; signal: 1.
 SQ SEQUENCE 490 AA; 55864 MW; 05197910 CRC32;

Query Match 66.7%; Score 54; DB 2; Length 490;
 Best Local Similarity 70.0%; Pred. No. 1.80e+00;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 7 FNKKKEVVEE 16
 1:1:1:1:1:1:
 QY 2 YNKKKATVQE 11

RESULT 13 PRELIMINARY; PRT: 1233 AA.
 AC 073696;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE MTOSIS-SPECIFIC CHROMOSOME SEGREGATION PROTEIN SMC1 HOMOLOG.
 GN SMC1.
 OS FGUG RUBRIPES (JAPANESE PUFFERFISH) (YAKIFUGU RUBRIPES).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
 OC TETRAODONTIFORMES; TETRAODONTIOIDEI; TETRAODONTIDAE; FUGU.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RIBOLDI TUNNICLIFFE G.R., PLATZER M., NYAKATURA G., ELGAR G.S.,
 RA BRENNER S., ROSENTHAL A.;
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF026198; G3098266; -;
 SQ SEQUENCE 1233 AA; 143100 MW; FBD2FB59 CRC32;

Query Match 66.7%; Score 54; DB 13; Length 1233;
 Best Local Similarity 50.0%; Pred. No. 1.80e+00;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 326 YKKRKADMELE 337
 1:1:1:1:1:1:
 QY 2 YNKKKATVQELD 13

RESULT 14 PRELIMINARY; PRT: 241 AA.
 AC 053585;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ENTEROTOXIN H PRECURSOR.
 GN SEH.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DA508;
 RA RER K., BANNAN J.D., PANCHOLI V., CHEUNG A.L., ROBBINS J.C.,
 RA FISCHETTI V.A., ZABRISKIE J.B.;
 RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U11702; G510692; -;
 DR PRAM: PF01123; Staph-strep-toxin; 1.
 KW SIGNAL.
 FT SIGNAL. 1 24 POTENTIAL.
 FT CHAIN 25 241 ENTEROTOXIN H.
 SQ SEQUENCE 241 AA; 27858 MW; AE5AB04A CRC32;

Query Match 65.4%; Score 53; DB 2; Length 241;
 Best Local Similarity 72.7%; Pred. No. 2.94e+00;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 153 NKKKATVQELD 163
 1:1:1:1:1:1:
 QY 3 NKKKATVQELD 13

RESULT 15 PRELIMINARY; PRT: 271 AA.
 AC 065075;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
GN HYPOTHETICAL 30.9 KD PROTEIN (FRAGMENT).
OS SB50.
OS PICEA MARIANA.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC PICEA.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.,
RL GENETICS 0:0-0(1998).
DR EMBL; AF051236; G2982303; -.
KW HYPOTHETICAL PROTEIN.
FT NON_TER 1
SQ SEQUENCE 271 AA; 30897 MW; 1DEA85B1 CRC32;

Query Match 65.4%; Score 53; DB 10; Length 271;
Best Local Similarity 54.5%; Pred. No. 2.94e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 115 YSKTKAMVEDL 125
Qy 2 YNKKRATVOEL 12

Search completed: Tue Aug 31 19:31:30 1999
Job time : 52 secs.

THIS PAGE BLANK (USPTO)